BRIEF REPORT



Nonstructural p26 proteins encoded by the 3'-proximal genes of velariviruses and criniviruses are orthologs

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Abstract

The 3'-most genes in RNA-2 of the *Crinivirus* genus members (family *Closteroviridae*) code for non-structural p26 proteins that share amino acid sequence similarity [Stewart LR, Hwang MS, Falk BW (2009) Virus Res 145:293-299]. In this study, sensitive bioinformatic tools have been used to identify the homologous p26 proteins encoded by the 3' genes in monopartite genomes of the members of *Velarivirus*, another *Closteroviridae* genus, and mint vein banding-associated virus, an unassigned member of the family. The p26 proteins showed similarity in their predicted secondary structures, but an amino acid sequence alignment showed no strictly conserved positions, thus indicating a high plasticity of these non-structural proteins. The implications of the sequence analysis for possible functions of the crinivirus and velarivirus p26 proteins are discussed.

The family *Closteroviridae* includes about 50 filamentous plant viruses with large positive-sense RNA genomes that show numerous traces of recombination events, such as gene duplication and gene capture [1–3]. Closteroviruses contain up to 12 genes, most of which are arranged in two conserved modules: the replicative module, which encodes proteins responsible for RNA synthesis and membrane modification, and the five-gene block, which encodes proteins involved in particle formation and cell-to-cell movement [2–4] (Fig. 1). In addition, closteroviruses carry variable accessory genes in the 3' part of their genome (Fig. 1). Some products of the 3' genes are conserved in some members of the *Closteroviridae* [3, 5], whereas others have no apparent homologs and are species-specific.

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The members of the genus *Crinivirus* have bipartite genomes with RNA-1 and RNA-2 bearing the replicase module and the five-gene block, respectively, plus some additional 3' ORFs [6, 7] (Fig. 1). The 3' genes in RNA-2 of criniviruses code for proteins with a molecular weight of about 26 kDa (p26) that have certain similarity in amino acid sequence and predicted secondary structure [3, 5] (Fig. 1). In this study, our purpose was to identify the p26-related proteins in members of the other genera and unassigned virus species of the family *Closteroviridae*.

The p26 protein sequences (Supplementary Table S1) were downloaded from the Refseq database using BLASTp and PSI-BLAST searches (www.ncbi.nlm.nih.gov) [8]. Multiple alignments were produced with the T-Coffee program [9]. HMMER2.0 toolbox [10] was used for Hidden Markov Model (HMM) reconstruction and sequence comparisons, HHpred [11] for HMM profile comparisons, and JPRED4 [12] for secondary structure predictions.

Initial BLAST and PSI-BLAST searches did not reveal any putative p26 protein homologs outside the genus *Crinivirus* when the crinivirus p26 sequences were used as a query (Supplementary Table S1). At the next step, we used HMMER 2.0, a sensitive tool for detecting remote protein homologs [10]. The hidden Markov model for the crinivirus p26 proteins was constructed and used for directed search for the 3' ORF products in members of other *Closteroviridae* genera (*Velarivirus, Closterovirus,* and *Ampelovirus*). Low probability values (indicating a statistically significant similarity) were obtained for the 27- to 29-kDa proteins encoded

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Fig. 1 Genome maps of representatives of the genera *Crinivirus* (lettuce infectious yellows virus, LIYV) and *Velarivirus* (little cherry virus 1, LChV-1) drawn approximately to scale. The arrow indicates the RNA 3' end. ORFs are shown as boxes. Encoded domains: PCP, papain-like cysteine proteinase; Mtr, methyltransferase; Hel, heli-

case; Pol, RNA polymerase. Proteins: p6, small hydrophobic protein; HSP70h, HSP70-related protein; p60,~60 kDa proteins; CP and CPm, major and minor coat proteins, respectively. The ORFs for p26 proteins are shaded

 Table 1
 Significance of similarities between the crinivirus p26 hidden Markov model and the velarivirus p26 proteins

Sequence ID	Score	E-value
Cordyline virus 1 ADU03662	-141.2	0.066
Cordyline virus 2 AFJ05053	-138.7	0.049
Cordyline virus 3 AGF73886	-126.8	0.012
Cordyline virus 4 AGF73893	-136.9	0.04
Grapevine leafroll-associated virus 7 AEQ59451	-130.0	0.018
Little cherry virus-1 CEO12417	-125.1	0.0098

by the 3'-most ORFs of velariviruses (below, also referred to as p26 proteins) (Table 1). Figure 2 shows a sequence alignment of the p26 proteins of criniviruses and velariviruses. Although some positions in the alignment are occupied by similar amino acid residues, none of them is strictly conserved (Fig. 2). Analysis of secondary structure suggests that the p26 proteins of velariviruses and criniviruses are alpha-helical with a few beta-strands (Fig. 2), which corroborates the previous data for the crinivirus proteins [5]. Six alpha-helices in the p26 proteins have a similar location (Fig. 2), suggesting that these proteins share a common three-dimensional structure.

We also performed an additional HMM database search using the combined multiple alignment of crinivirus and velarivirus p26 proteins (Fig. 2) as a query for HMMER2.0. The 24-kDa protein of mint vein banding-associated virus (MVBaV), an unassigned member of the family *Closteroviridae* [13], was detected as a possible remote homolog (Fig. 3). A significant probability value (0.009) was obtained, supporting the relatedness of the MVBaV p24 to the p26 of criniviruses and velariviruses (Fig. 3). Attempts to include the MVBaV p24 into the multiple alignment using T-Coffee [9] were not successful due to the lack of detectable similarity in the C-terminal regions (Fig. 3). Additional HHPred database searches did not reveal any putative homologs of crinivirus/velarivirus p26 proteins among the available HMM profiles [11].

The data presented here indicate that the p26 genes are not *Crinivirus* taxon-specific as has been thought but are conserved across the monopartite genomes of *Velarivirus* members and mint vein banding-associated virus. Taking into account the 3'-proximal location of the p26 genes

Fig. 2 Multiple alignment and predicted secondary structure of the p26 proteins of representatives of the genera Crinivirus and Velarivirus. Predicted alpha-helices (H) and beta-strands (B) are indicated. Criniviruses: PYVV (potato yellow vein virus, YP_054414.1), TVCV (tetterwort vein chlorosis virus, ALE18225.1), CYSDV (cucurbit yellow stunting disorder virus, NP 851578.1), bean yellow disorder virus (BnYDV, ABY66971.1), CCYV (cucurbit chlorotic yellows virus, YP_006522433.1), LCV (lettuce chlorosis virus, YP_003002364.1), BPYV (beet pseudo-yellows virus, AAQ97392.1), SPaV (strawberry pallidosis-associated virus, YP_025091.1), DVCV (diodia vein chlorosis virus, ADU25040.1), SPCSV (sweet potato chlorotic stunt virus, AEO37527.1), ToCV (tomato chlorosis virus, AJY78063.1), TICV (tomato infectious chlorosis virus, YP_003204962.1), LIYV (lettuce infectious yellows virus, NP_619699.1). Velariviruses: LChV-1 (little cherry virus 1, acc. CEO12417.1), GLRaV-7 (grapevine leafroll-associated virus 7, acc. AEQ59451.1), CoV-1 (cordyline virus 1, acc. ADU03662.1), CoV-2 (cordyline virus 2, AFJ05053.1), CoV-3 (cordyline virus 3, AGF73886.1), CoV-4 (cordyline virus 4, AGF73893.1)

Crinivirus

DCO.DCT GOCGTC		ННННННННННН	ннн ннннннн	ІНННННННННННН
PVCV	MENPELISY	-PS-N-GNTQFAS-DEFIAYQ-INAVVN	ALQKYALYSADELSAFR-	DHCGVI-LNLIS-
TVCV	MMEYPIE	YARND-GGNNESL-INIISHN-FNSIVN	IIENYCMYDVHVIDAAI-	ETSHIL-INMCK-
CYSDV	MEFPTN	DIEHI-QEDGEDF-PAIISKN-LNSVLN	AIQNHSLYDMIMLDNAI-	ETCYTL-IIMCQ-
BnYDV	MEVDYPIQ	EFELT-TDSGKSM-GELIAKN-FHTIVN	VIQSHQMFDIMNLEHVA-	NLCYTL-HVMID-
CCYV	MSL	FNTIVN	IIQSHALFDKIHLENYR-	ELCNVL-HVMIN-
LCV	MSNMEVDYPIQ	GFEFG-GGGDKAM-AEVISKN-FNTIVN	IIQNHEMYDMIHLNHLH-	ELCQVL-RVMIN-
BPYV	MRRMDFPVL	TSETT-GEQ-AND-LDMLASN-VNIILN	ILQDHRQHDNFELQNAL-	NSCSTV-INVCN-
SPaV	MTSSFHDLTTS	DFOIS-NPV-ONE-RGIISDN-INFIIN	ITVENATSYTNAELEHAK-	LCCOAL-LTESN-
DVCV	MTSNVFDLTLPSDDOVR	DODIS-RSS-TMT-NDRIASN-INOVIN	VTNDFKBYTVAELEHNL-	LCCEAL-MTYAA-
SPCSV	MSGWD-DIPMOON	YVSSS-VENDDDI-AKICART-FNRAVN	ULTDYSOHTIPFLRESR-	FELGCI-BSLCE-
TOCY	MEWAYNSDD	-VNSC-ACSCEDV-NTTVAKN-FYSITH	WMSNVPNVTDDFTKDAV_	NVCYCI -INICE-
TOCV	MDCDDDEVC	VNOG AGOGEDV NIIVANN FISIIN	ALCNDA IMEMORIANEZ	OLCICI INTECE
	MUSPEREVS	DECE ODVDKEIDUOELODE PWCVIS	RESIDAIMIWDELIMER-	NULTINE DIGUN
	MNNFPEIFD	-DESI-CDIDKEIDHQELSDI-FWCLMD	FISSERGESVADINSGM-	NILINI-KKSLN-
velarivirus				
Sec.structure		НННННННННННННННН	НННН ННННННН	ІННННННННННННН
LChV-1	MLNTFGHE	GSSTN-K-RVDTF-ATQVSKKLLEFMHN	VVTTLNGKNLSINELRGML-	PQVLECKRFFEA-
GLRaV-7	MDLETRNDN	-TM-FR-ERD		KCKIF-SCIID-
CoV-1	MDKNCVANSTE	FTDTSDFENKKEI-NRVFSCI-VEAVDN	IIDEICSLKVNNFNKLKN	ILSDHLRLI-EHFLKK
CoV-2	MEDNSVVQTCD	GFDTSDLEDDRVR-NKLFSDM-MDEVDO	IKSEICSSTTANSHKLKS	MLKTLSLI-HHFLKK
CoV-3	MDLESRSTE	KNRLK-NOILTSA-IDYFFN	I.KYYII.KENAITI.ERKKN	ILLSKIRYL-YDFFKA
CoV-4	MSSSYNNFD	MEOKR-NTMFTKI-FNCIND	TESSILENDSMTVSSLLC	NISOLKTI-LSEVSK
			LEGGE BEIGGENERS	
Sec structure	BBBB	нннн	нинининининини	инниннин в
DVIN	PHCESUNMESDNSK-I-	FFSI TNNSVDEETII DNKCIVEDT	T SVYELODI I NNEVVTI	NELIDV-KT-CIVTE
TYCY	TCSCEINI VSI NNK-D-		I KCMOI EEI I XOI I BVI	SFIPSV-MT-CIMDD
CYCDV	VIVEDUNIVOATND D		TCCMOIDDI WKOITDII	NELKOC KE KIMDO
CISDV	KLIEDVNLISAINP-R-		LSSWQIDDLVKQLIPII	NERMET KC CIMND
BHIDV	NHEGIVNLIAENNP-R-	DSFRDAGVRPEVLVNRRDRIFPT	LTTWQLRDTLSQLEPVI	JNFVIEL-KG-GLMIND
CCYV	ENNNDINIYSENNR-T-	·LGSFRDAGLDINNISARRNKLFPT	LTPWQIRDVLQQLESVI	JWFVTDL-KT-GLMDD
LCV	DCTEDINLFSENNK-L-	·VGSFRDAGLDMNNISSRRNKLFST	TTPRQLRDTLDQLETVL	JNFLTDA-RF-GVMND
BPYV	LQTEDVNLFSTHSK-V-	·YQDLKSAGVSHEELSSQRSKYFST	'LSTEDLKYLMFDVANIF	RLLLVA-RK-NLVDN
SPaV	QNNFKVSLFGKNSK-I-	YNALRNSSHSDEEIERCKDYYFPT	LRSFDVIDVIELMQDFFAVI	LEFLINM-RK-GYFDF
DVCV	LNTFDVSLFSENSS-T-	·FKVLRDSGHDEEEIKQNKQFYFPV	'LNDFDVKTIMYDISKVI	JKFLIRY-KM-GYFEN
SPCSV	NDDFNINLGADNNN-L-	FQGLNKLGVRADSLRVNSERFFPS	ISSKVMTNVIDSISSVM	MEFVIDL-NH-SGFST
ToCV	RLDRDVILVSPNSP-V-	YNNYRDAGIPHNLLMENTARYFPV	VNPSELGKILLGHISVI	KFLEYF-TR-YGVDD
TICV	SLPNNLILYHTNTM-P-	HEILGSRRINDTDIDLHSSRYFQN	VTKQVVRFLLEDYLIII	NMKLHM-KK-GLLDV
LIYV	GSGKVVSITDSYNK-TY	FHSQRGLTNVDSRINID	ILKIDFISIIDDLQIIF	RGLIYK-DK-GFLDS
Sec.structire		UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	нининининин нинин	
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LChV-1	RRDETLETIGSRSK-M-	·FSS-EVLEIDEDTVNEFKELFLMR	IPIKLLIOYCDDFILVF	DILKNFLDK-TLINE
LChV-1 GLRaV-7	RRDETLETIGSRSK-M- KISSALNTLSSTSS-S-	FSS-EVLEIDEDTVNEFKELFLMR	IPIKLLIQYCDDFILVF	DILKNFLDK-TLINE
LChV-1 GLRaV-7 CoV-1	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTELDRKSBEL-	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV	IPIKLLIQYCDDFILVF LTQGHTGFLTESCGVPL	DILKNFLDK-TLINE SEFLDEV-GR-DLLVS
LChV-1 GLRaV-7 CoV-1 CoV-2	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENI DVTVIDKDAKEL-	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VE-TYVTVNDKFILDNEQVMTTT IE-PFIUDEPFIINNEHUVTT	IPIKLLIQYCDDFILVF LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVI PMVIELKKI	TDILKNFLDK-TLINE EFLDEV-GR-DLLVS KLKKCI-LSGQVFSR
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-2	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSUNYUNITETKEL	FSS-EVLEIDEDTVNEFKELFLM ·IVSKQQALSDISLSKDILKKLGLFAAPV ·VETYVTVNDKFILDNEQVMTTT ·IERFIVLDERFILNNEHVVTTT ·ETEINEFESIDEREFMERST	IPIKLLIQYCDDFILVF LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC	FDILKNFLDK-TLINE JEFLDEV-GR-DLLVS JKLKKCI-LSGQVFSR CSLKIDF-SLRVVLTK
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL-	FSS-EVLEIDEDTVNEFKELFLMM IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESIDSEEMFTST	IPIKLLIQYCDDFILVF LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC VKISELGDQLNELINII	FDILKNFLDK-TLINE EFLDEV-GR-DLLVS KLKKCI-LSGQVFSR CSLKIDF-SLRVVLTK HLKQDI-YTKRVLNN
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL-	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESLIDSEEMFTST VSSVIGDDDEFFLENETLIVDS	IPIKLLIQYCDDFILVE LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC VKISELGDQLNELINII VKSKDLVPNIVELIKLI	DDILKNFLDK-TLINE LEFLDEV-GR-DLLVS LKLKKCI-LSGQVFSR SLKIDF-SLRVVLTK LHLKQDI-YTKRVLNN LELKHRL-KTFSLLDS
LChV-1 GLRAV-7 CoV-1 CoV-2 CoV-3 CoV-4	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL-	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESLIDSEEMFTST VSSVIGDDDEFFLENETLIVDS	IPIKLLIQYCDDFILVE LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC VKISELGDQLNELINII VKSKDLVPNIVELIKLI	DDILKNFLDK-TLINE DEFLDEV-GR-DLLVS .KLKKCI-LSGQVFSR SLKIDF-SLRVVLTK .HLKQDI-YTKRVLNN .ELKHRL-KTFSLLDS
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-2 CoV-3 CoV-4	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL-	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESLIDSEEMFTST VSSVIGDDDEFFLENETLIVDS	IPIKLLIQYCDDFILVE LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC VKISELGDQLNELINII VKSKDLVPNIVELIKLI	PDILKNFLDK-TLINE DILKNFLDK-TLINE LFLDEV-GR-DLLVS LKLKKCI-LSGQVFSR SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN LELKHRL-KTFSLLDS
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-2 CoV-3 CoV-4	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL-	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESLIDSEEMFTST VSSVIGDDDEFFLENETLIVDS	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVIPMVLELKGLC VKISELGDQLNELINII VKSKDLVPNIVELIKLI	DELEMBER DELEMBER DEFLDEV-GR-DLLVS JKLKKCI-LSGQVFSR JKLKCI-LSGQVFSR JKLKQDI-SLRVVLTK JHLKQDI-YTKRVLNN JELKHRL-KTFSLLDS
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL-	BBBB HHHHHHHHHHHH	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI 'MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB	DDILKNFLDK-TLINE LEFLDK-TLINE LEFLDK-GR-DLLVS KLKKCI-LSGQVFSR SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN JELKHRL-KTFSLLDS BBBB
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESIDSEEMFTST VSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK	IPIKLLIQYCDDFILVF LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTFFVSL	DDILKNFLDK-TLINE LEFLDEV-GR-DLLVS .KLKKCI-LSGQVFSR .SLKIDF-SLRVVLTK .HLKQDI-YTKRVLNN .ELKHRL-KTFSLLDS BBBB
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VH-KITCV-SELNDSLYYYLKNK	IPIKLLIQYCDDFILVF LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV	BBBBB BBBBB BBBBB BBBBBB
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA	FSS-EVLEIDEDTVNEFKELFLMM IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT FERFIVLDERFILNNEHVVTTT FSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VH-KITCV-SELNDSLYYYLKNK	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI 'VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV	BBBB BBBB EKSL
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENSVYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT FERFIVLDERFILNNEHVVTTT FSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VH-KITCV-SELNDSLYYYLKNK VY-KINNV-KDLINSVHHFLNDM	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV FKFGENVKA	DILKNFLUK-TLINE LEFLDEV-GR-DLUVS SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN JELKHRL-KTFSLLDS BBBB DISL DISL EFSL
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV CCYV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFS FRVSNLFT FKINNLFS	FSS-EVLEIDEDTVNEFKELFLMM IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VH-KITCV-SELNDSLYYYLKNK VY-KINNV-KDLINSVHHFLNDM IY-KINNV-GDLINSVHSYLNSH	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI 'MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV FKFGENVKA YNFRDNINA	BBBB BBBB BERNE BBBBB BBBB BBBB BBBBB BBBB BBBB BBBBB BBBBB BBBBB BBBBB BBBBB BBBBB BBBBB BBBBBB
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LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV CCYV LCV BPYV SPaV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NENLRVTYIDKRAKEL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT FKINNLFS FKINNLFS FKINNLFS	FSS-EVLEIDEDTVNEFKELFLMM IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT FERFIVLDERFILNNEHVVTTT FSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VY-KITCV-SELNDSLYYYLKNK VY-KINNV-KDLINSVHHFLNDM IY-KINNV-GDLINSVHSHNSH NY-NVTDI-PSFNRATEYFSKT NY-NIYDS-KSLNSAVAKHIEAN	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI 'VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV FKFGENVKA YNFRDNINA YRFGSNIQ2 VSLGYYTKL	DILKNFLDK-TLINE DEJLKDF-LDK-TLINE EFLDEV-GR-DLLVS SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN LELKHRL-KTFSLLDS BBBB DISL DISL EFSL EFSL EFSL EFSI EFSI EFSI
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV CCYV LCV BPYV SPaV DVCV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT FKINNLFS FKINNLFS FKINNLFS FKINNLFS FKINNLFA	FSS-EVLEIDEDTVNEFKELFLMR ·IVSKQQALSDISLSKDILKKLGLFAAPV ·VETYVTVNDKFILDNEQVMTTT ·ERFIVLDERFILNNEHVVTTT ·SSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VH-KITCV-SELNDSLYYYLKNK VY-KINNV-RDLINSVHHFLNDM IY-KINNV-GDLINSVHGFLNSH NY-NVTDI-PSFNRAITEYFSKT HY-NIYDS-KSINSAVAKHIEAN YY-HVNNF-QRINFAIKDMTLTD	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI 'MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL YNFGRNTVP YNFGRNTVP YNFRDNINA YRFGSNIQA YPMSYYCQQ VSLGYTTKL MQVNDQVDA	DDILKNFLDK-TLINE DDILKNFLDK-TLINE LEFLDEV-GR-DLUVS SLKIDF-SLRVVLTK SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN JELKHRL-KTFSLLDS BBBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBB BBBBB BBBB BBBB BBBBB BBBBB BBBBB BBBBB BBBBB BB
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV CCYV LCV BPYV SPaV DVCV SPCSV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT FKINNLFS FKINNLFS FKINNLFS FKINNLFS FUISIFT LDVTNLFH FDINTIFA	FSS-EVLEIDEDTVNEFKELFLMM IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FE-TELHIEEESLIDSEMFTST VS-SVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VY-KINCV-SELNDSLYYYLKNK VY-KINNV-KDLINSVHHFLNDM IY-KINNV-GDLINSVHSYLNSH IY-KINNV-GDLINSVHGFLNSH HY-NIYDS-KSLNSAVAKHIEAN YY-HVNNF-QRINFAIRDMTLTD IY-LINNY-GRINFAIRDMTLTD	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI 'MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI 	DILKNFLDK-TLINE JEFLDEV-GR-DLLVS JKLKKCI-LSGQVFSR SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN JELKHRL-KTFSLLDS BBBBB BBBBBB
LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV CCYV LCV BPYV SPaV DVCV SPCV SPCSV ToCV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT FKINNLFS FKINNLFS FKINNLFS FDINTIFA LWVGEIMT	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT FETELHIEESLIDSEEMFTST VSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VY-KINV-RSLLTSLQTFLTSY VY-KINNV-GDLINSVHFLNDM IY-KINNV-GDLINSVHSFLNSH IY-KINNV-GDLINSVHSFLNSH YY-NTDI-PSFNRAITEYFSKT YY-HVNNF-QRINFAIKDMTLTD IY-HVNNF-QRINFAIKDMTLTD IY-VLWST-GDVNAALHSIYODD	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI 'VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV YNFGRNTVP YNFRDNINA YNFRONIQA YPKSYYCQQ YPKSYYCQQ YNFQENVKL YNFPEVQF	DILKNFLDK-TLINE JEFLDEV-GR-DLLVS JKLKKCI-LSGQVFSR SLKIDF-SLRVVLTK HLKQDI-YTKRVLNN JELKHRL-KTFSLLDS BBBB CONSTRATION CONSTRATI
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LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-2 CoV-4 Sec.structure PYVV TVCV CYSDV BnYDV CCYV LCV BPYV SPaV DVCV SPESV ToCV TICV LIYV	HHHHH RDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT FKINNLFS FKINNLFS FKINNLFS FKINNLFS FLISIFT LDVTNLFH FDINTIFA LDVDDILR ADLLDLDK	FSS-EVLEIDEDTVNEFKELFLMR IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT IERFIVLDERFILNNEHVVTTT FETELHIEEESLIDSEEMFTST VSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VY-KINCV-SELNDSLYYYLKNK VY-RINDV-RSLITSLQTFLTSY VY-KINNV-GDLINSVHGFLNSH IY-KINNV-GDLINSVHGFLNSH IY-KINNV-GDLINSVHGFLNSH IY-KINNV-GDLINSVHGFLNSH YY-HVNNF-QRINFAIKDMTLTD YY-HVNNF-QRINFAIKDMTLTD YY-HVNNF-QDLNSAKHIEAN YY-HVNNF-QRINFAIKDMTLTD YY-HVNF-QRINFAIKDMTLTD NF-VLWST-GDVNAALHSIYQQD MI-KSTNL-EVLKSIVLSYICSS KT-TTRKF-QEYFNILKIKIIEKIGM	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI 'VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV YNFGRNTVP YNFRDNINA YNFRONIQA YPMSYYCQQ YPMSYYCQQ YNFPGEN	DDILKNFLDK-TLINE LEFLDEV-GR-DLLVS .KLKKCI-LSGQVFSR .SLKIDF-SLRVVLTK .HLKQDI-YTKRVLNN .ELKHRL-KTFSLLDS BBBB BBBB
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LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-4 Sec.structure PYVV TVCV CYSDV BNYDV CCYV LCV BPYV SPaV DVCV SPaV DVCV SPCV TOCV TICV LIYV Sec.structure LChV-1 GLRaV-7 CoV-1 CoV-2 CoV-3 CoV-3	HHHHH RRDETLETIGSRSK-M- KISSALNTLSSTSS-S- NENANVTFLDRKSREL- NESSSVNYVNIEIKKL- NEDITIKYVNADHKRL- BBB BB VILSSCID FNVNNLFA FRVSNLFT FKINNLFS FKINNLFS FKINNLFS DVTNLFH FDINTIFA LDVTNLFH ADLIDLDK HHHHHH KDIAEMFD SDCEDILQ	FSS-EVLEIDEDTVNEFKELFLMM IVSKQQALSDISLSKDILKKLGLFAAPV VETYVTVNDKFILDNEQVMTTT FERFIVLDERFILNNEHVTTT FSSVIGDDDEFFLENETLIVDS BBBB HHHHHHHHHHH EF-NVKNF-RGLKNILRAKLTTK VH-KITCV-SELNDSLYYYLKNK VY-RINDV-RSLLTSLQTFLTSY VY-KINNV-GDLINSVHHFLNDM -IY-KINNV-GDLINSVHHFLNDM -IY-KINNV-GDLINSVHFLNSH YY-NVTDI-PSFNRATEYFSKT YY-NVTDI-SFNRATEYFSKT YY-HVNNF-QRINFAIKDMTLTD IY-DVNSF-DKLVDAIYRFLLYT MY-NVTDI-SFNRATEYFSKT MY-NNT-QRINFAIKDMTLTD IY-DVNSF-DKLVDAIYRFLLYT MF-VLWSF-DKLVDAIYRFLLYT KT-TTRKF-QEYFNILKIKIIEKIGM HH BBHHHHHHHHHH KF-GTNVKLKMLSELTEVVLKN NIPNSTK-DGILELTRVHITDK NIPRRTK-EGILEIVKQKIFEK	IPIKLLIQYCDDFILVF 'LTQGHTGFLTESCGVPI MRMSEIIPKVSELTKVI VKLADVLPMVLELKGLC 'VKISELGDQLNELINII VKSKDLVPNIVELIKLI BBB BB YPLTRFVSL FNFGENVLV FKFGENVLV YNFRDNINA YRFGSNIQA YRFGSNIQA YNFREVQF FHFPVEVRA FHFPVEVRA FFFPVEVRA FGFGDRVSKIRAAFMNI FSIGNHFNV YQVSNLLLI	BBBB JKLKKCI-LSGQVFSR SLKIDF-SLRVVLTK JLKKCI-LSGQVFSR SLKIDF-SLRVVLTK JHLKQDI-YTKRVLNN JELKHRL-KTFSLLDS BBBB BBBB

Sec.structure	ннннннннн	ННННННННН	BBBBBBB	ВВ	
PYVV	DDNGKQDIARFLKNMRTDDVDPK	-KVLRKIVQDLNLA	FMFELSFHYLN	-DGL-IIFKIN-N	1-KH
TVCV	FVDNSDKLENLMLKQKIRKYLDK	-NAREYLKEYITKN	IMFELNFSFTC	-FGI-NIKQIK-N	1 - F
CYSDV	YIDDSEKLEKLIKGYKSKRYLTK	-SVRNELVNYFSNNI	LVYQISFLFDN	-IGI-NIKPIK-N	1 - F
BnYDV	LIKDGKSVERMIKNFKKQKYLDE	-NLRIKFKDFISEN	LVYEINFEFKN	-LGF-YLKPIK-N	IFN
CCYV	MIRDDDCVDSVIKNFKRKKFLNE	-KSRQKMKTLLANCI	LVYEITFNFGN	-LGL-YMNPLK-N	I - F
LCV	MIKDGKTIDEVIKKYKKEKYLND	-INRRKIKDLLSNHI	LVYEISFHFGG	-LGL-PIKPLK-N	I - F
BPYV	DVADEYRFSHLLKSIKFPNKRSY	-IKKGELIEICKESI	LIFKISINYDH	-LGL-NIKTIK-B	"D
SPaV	NLSDDFEVKNLIIKYKKFSKNNE	-SKKLAMLKLLNESI	LIFKITFTFSH	-VGL-EINSIS-S	-PRQAF
DVCV	DVDNSYWLKTLLKKCANFSKTGE-	-EKRLILKTYINEH	LKFKFAFRYNI	-SSF-KIPEVS-N	1K
SPCSV	NLFNDDILKIISKAKKKIRPLSD	-SERVLMAKSITKG	IHFEFHFTYRS	-LGL-YLPKVT-N	-SLTVCNKNR
ToCV	LFLNSSEIDRRLSNIRRKGYPNS	-ENFNWFKNMISNY]	LYFDFVFRYSG	-TRI-NIERIS-N	1-YYI
TICV	IFEEDHRLKSLLKLFKKNKSLTS	-KEIGVIRATINNG	IIGKFTIK-RSFG	-FGI-PFENIN	L
LIYV	SPLDKQRKCSISSSHKKTNRLND	-LNNYITYLNDN:	IVLTFRWKG	-VGF-GGLSLN-I	-IKI
Sec.structure	ввнининининининин	НННННН	ннн нн	BBBB	BB
LChV-1	IVK-SECLKGFTTTLSSLFMYNK	-GHRNSYARAITLNI	LKLFIEH	-SGL-LNGELAYN	ILVVG
GLRaV-7	V-IDEPILKKIIAEIRGSILCNS	-NKRKELLELLNKK	FLIIYSYYNSVFG	DVYI - V	I
CoV-1	RSDVLAYMKSVAKGNSYFTF	-LKHKPVDVEMNRN	IIITLL	F	
CoV-2	RRDTLTYLKSLAKGNSYFSL	-IRQKSIDFELNKNI	LIMSFEKV	F	
CoV-3	PIMILKTVQSFSKNLPSTIF	-VRASSLLKDINSTN	MVISFDTTYKQ	-LK	
CoV-4	KRDIIKTIIAMVNKSPLYNF	LYNTKSTCSDLNKSI	LQIFFYKG	-QGCVKSTTI	

Fig. 2 (continued)

Fig. 3 Sequence alignment between the hidden Markov model consensus sequence for the crinivirus and velarivirus p26 proteins and a remote homolog, mint vein bandingassociated virus 24-kDa protein (NC_038420.1). Due to the lack of detectable similarity in the C-terminal regions, only partial sequences are shown

domain 1	1, from 1 to 180: score -94.5, E = 0.0093
cons	<pre>*->MesnsrdfptedvetsgesdkdintiisknfnsivNiisnisytvae M + +d++ + + +f +i+ i+</pre>
MVBaV	1 MVDVDYD D IFKYIMSYIY 18
cons	LehaknllntcktllnfcnKnededVnlfssnskelfesLrdagvdeeei + ++ +++f + e+ + ++f+ + + + L+ ++++e +
MVBaV	9EVLSGFYTFTDEPLNYTTFDM-VCNQLTSIPDEVV 52
cons	lenkeryfptltskdlidilddlikvLefLidlkkkgllddfdvndifsF + ++y ++ sk ++ + ++v++ ++l+k +++d+++ +++
MVBaV	3 YDVCNKYMINVASKKTQVQTFNVFDTIDYLTKISVVDSVRQLCD- 96
cons	CmyPkinnfedlnnavkefllekfnfgdnvna ++ +n ++++ ++++ ++ ++ ++ ++ ++
MVBaV	7 -NIVFNQKMRYHIRKLPGVPEVFDKvsgcsvmstndvktwlls 13
cons	efsldvddskrlksllkkiKknkylnkskrkslkkllNknLvfefsFryk e++ + d+ +++s++ +++ + +++ + +nL ++ k
MVBaV	9 ELKAVDETYFDSVTIDSFELHFNIRDAIDRNLSMKE-K 17
cons	gFGlGlnikpikNlf<-* + ik
MVBaV	6 NIKR-A 180

(Fig. 1), similarity of the predicted secondary structures, and statistically significant similarity of the amino acid sequences (Table 1, Fig. 2), it is likely that the p26 proteins of criniviruses and velariviruses are orthologs that may perform the same or similar function(s). It should be noted that members of the genera *Crinivirus* and *Velarivirus* are markedly different from each other in their biological properties and the genome structure. Criniviruses have divided genomes, are transmitted by whiteflies, and infect herbaceous hosts, whereas velariviruses possess monopartite genomes, have no known vectors, and infect woody hosts [2] (Fig. 1). The absence of conserved amino acid positions in the p26 alignment suggests high plasticity of these

Mint:

non-structural proteins, which may indicate their involvement in the response of virus systems to rapidly changing environmental conditions. On the other hand, the p26 protein of lettuce infectious yellows virus (LIYV), the type member of the genus *Crinivirus*, induces specific ultrastructures in the infected cells – conical plasmalemma deposits over plasmadesmata – that are thought to be associated with the vascular transport of the virus [7, 14, 15]. In support of this, a knockout LIYV p26 mutant proved to be unable to spread systemically in a *Nicotiana benthamiana* host [15]. Although the *Closteroviridae* members other than LIYV do not induce plasmalemma deposits, the involvement of crinivirus and velarivirus p26 proteins in systemic transport cannot be excluded and needs to be tested experimentally.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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