Acta virologica **65**: 365 – 372, 2021 doi: 10.4149/av_2021_402

Two novel poty-like viruses identified from the transcriptome data of purple witchweed (*Striga hermonthica*)

Dongjin Choi[1], Chaerim Shin[1], Ken Shirasu[2,3], Yoonsoo Hahn[1*]

[1]Department of Life Science, Chung-Ang University, Seoul 06974, South Korea; [2]RIKEN Center for Sustainable Resource Science, Yokohama, Kanagawa 230-0045, Japan; [3]Graduate School of Science, The University of Tokyo, Bunkyo, Tokyo 113-0033, Japan

Received May 12, 2021; accepted June 3, 2021

Summary. – Potyvirids (the family *Potyviridae*) are the largest family of plant RNA viruses. Two novel potyvirid viruses, Striga-associated poty-like virus 1 (SaPlV1) and Striga-associated poty-like virus 2 (SaPlV2), were identified from the transcriptome data of purple witchweed (*Striga hermonthica*). SaPlV1 was most closely related to bellflower veinal mottle virus (BVMoV), the only member of the genus *Bevemovirus*, and then to macluraviruses (the genus *Macluravirus*). The SaPlV1 genome encodes a 2462-amino acid (aa) polyprotein that may be cleaved into nine mature peptides. The cleavage sites of SaPlV1, BVMoV, and macluravirus polyproteins shared strong sequence similarities. SaPlV2 was most closely related to celery latent virus, the sole species of the genus *Celavirus*, which is the most divergent potyvirid genus. The SaPlV2 polyprotein contained 3329 aa and it may be cleaved into at least seven or eight mature peptides. Phylogenetic analysis suggested that SaPlV1 and SaPlV2 may be novel species of the genera *Bevemovirus* and *Celavirus*, respectively. The genome sequences of SaPlV1 and SaPlV2 are useful resources for studying the genome evolution of potyvirids.

Keywords: Striga-associated poty-like virus 1; Striga-associated poty-like virus 2; Potyviridae; Bevemovirus; Celavirus; purple witchweed; *Striga hermonthica*

Introduction

Potyviridae is the largest family of plant-infecting RNA viruses containing 235 species approved by the International Committee on Taxonomy of Viruses (ICTV) (https://talk.ictvonline.org; ICTV Master Species List #36, March 2021) (Gibbs *et al.*, 2020; Palani *et al.*, 2021). Potyvirids (members of the family *Potyviridae*) are classified into 12 genera: *Arepavirus*, *Bevemovirus*, *Brambyvirus*, *Bymovirus*, *Celavirus*, *Ipomovirus*, *Macluravirus*, *Poacevirus*, *Potyvirus*, *Roymovirus*, *Rymovirus*, and *Tritimovirus* (Palani *et al.*, 2021). Members of the genus *Bymovirus* have a bipartite genome, whereas those from the remaining 11 genera have a monopartite positive-sense single-stranded RNA genome (Revers and Garcia, 2015).

The genomic RNA of potyvirids encodes an open reading frame (ORF) for a large polyprotein, which undergoes proteolytic cleavage by virus-encoded proteases (Adams *et al.*, 2005; Goh and Hahn, 2021; Palani *et al.*, 2021). The polyprotein of potyviruses (the genus *Potyvirus*) is processed into ten mature peptides (from N-terminus to C-terminus): protein 1 protease (P1), helper component-protease (HC-Pro), protein 3 (P3), 6-kilodalton (kDa) peptide 1 (6K1), cylindrical inclusion protein (CI), 6-kDa peptide 2 (6K2), viral protein genome-linked (VPg), nuclear inclusion a protease (NIa-Pro), nuclear inclusion b protein (NIb), and coat protein (CP) (Adams *et al.*, 2005; Goh and Hahn, 2021). P1 and HC-Pro proteases cleave themselves from the polyprotein, and NIa-Pro cleaves the remaining seven junctions. The NIb protein is an RNA-dependent RNA polymerase (RdRp)

---

[*] Corresponding author. E-mail: hahny@cau.ac.kr; phone: +82-2-820-5812.

Abbreviations: BVMoV = Bellflower veinal mottle virus; CeLV = Celery latent virus; ORF = open reading frame; PIPO = pretty interesting *Potyviridae* ORF; RdRp = RNA-dependent RNA polymerase; SaPlV1 = Striga-associated poty-like virus 1; SaPlV2 = Striga-associated poty-like virus 2 that is responsible for viral genome replication (Shen *et al.*, 2020). Potyvirids from other genera have the same or similar genomic organization.

Eight mature peptides, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb, and CP, are commonly produced from potyvirid polyproteins (Revers and Garcia, 2015). However, the P1 and HC-Pro segments among potyvirids are variable, probably resulting from diversifying evolution involving recombination and gene duplication (Valli *et al.*, 2007). For example, macluraviruses (the genus *Macluravirus*) lack the P1 coding region and HC-Pro is absent in cassava brown streak virus (Mbanzibwa *et al.*, 2009; Revers and Garcia, 2015; Elangovan *et al.*, 2019).

An additional short ORF termed "pretty interesting *Potyviridae* ORF" (PIPO) is universally present within the P3 coding region of potyvirid genomes (Chung *et al.*, 2008). A polymerase slippage inserts an additional A nucleotide within the highly conserved GAAAAAA (GA_6) motif. This insertion, termed "+1A insertion event," results in the formation of a "trans-frame" fusion protein with the N-terminal half of P3 and PIPO; this protein is named the P3N-PIPO protein (Olspert *et al.*, 2015; Rodamilans *et al.*, 2015; White, 2015).

The majority of ICTV-approved *Potyviridae* species (190 out of 235) belong to the genus *Potyvirus*. The other 11 genera each contain one to ten recognized species. The genus *Bevemovirus* has a single approved species, the *Bellflower veinal mottle virus* (BVMoV), which was isolated from a bellflower (*Campanula takesimana*) (Seo *et al.*, 2017). The BVMoV polyprotein is predicted to be cleaved to produce nine mature proteins, HC-Pro, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb, and CP; this is the same as that of macluravirus polyproteins. Phylogenetic analysis using BVMoV and selected potyvirid polyprotein sequences suggested that the genus *Bevemovirus* is the sister taxon of the genus *Macluravirus* (Seo *et al.*, 2017).

Celavirus is another genus represented by only one species, the *Celery latent virus* (CeLV), which was first identified in celery (*Apium graveolens* var. *dulce*) and celeriac (*A. g.* var. *rapaceum*) without visible symptoms (Bos *et al.*, 1978; Rose *et al.*, 2019). The CeLV polyprotein has a low sequence similarity to other potyvirid polyproteins, suggesting that *Celavirus* is the most divergent genus of the family *Potyviridae* (Rose *et al.*, 2019).

RNA-Seq data obtained from plant tissue samples often contain genomic RNA or mRNA fragments derived from latently infected RNA viruses (Bejerman *et al.*, 2020; Park and Hahn, 2021). Comprehensive analyses of diverse plant transcriptome data have yielded many novel RNA virus genome sequences (Park *et al.*, 2018; Goh *et al.*, 2021; Park *et al.*, 2021; Park and Hahn, 2021). In this study, we identified the genome sequences of two novel viruses belonging to the genera *Bevemovirus* and *Celavirus* (the family *Potyviridae*) from the transcriptome data of purple witchweed (*Striga hermonthica*) (Yoshida *et al.*, 2019). Purple witchweed is a hemiparasitic plant that infests grain crops, such as sorghum, maize, and sugar cane, and causes major grain losses (Spallek *et al.*, 2013).

Materials and Methods

The purple witchweed transcriptome data analyzed in this study are available in the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI) (Yoshida *et al.*, 2019). The SRA Acc. Nos. are DRR183243, DRR183244, DRR183245, DRR183246, DRR183247, DRR183248, DRR183249, and DRR183250. RNA-Seq reads were trimmed using the sickle program (version 1.33; https://github.com/najoshi/sickle) with the parameter "-q 30 -l 55." Filtered high-quality reads from all nine sequencing runs were pooled into a single dataset and assembled into contigs using the rnaviralSPAdes pipeline of the SPAdes assembler (version 3.15.1; http://cab.spbu.ru/software/spades) (Bushmanova *et al.*, 2019).

Known viral RdRp domain sequences were downloaded from the Pfam database (release 33.1; https://pfam.xfam.org). Pfam Acc. Nos. for the viral RdRp families are PF00602, PF00603, PF00604, PF00680, PF00946, PF00972, PF00978, PF00998, PF02123, PF03035, PF03431, PF04196, PF04197, PF05788, PF05919, PF06317, PF07925, PF08467, PF08716, PF08717, PF12426, and PF17501. The DIAMOND program (version 2.0.4; http://www.diamondsearch.org/index.php) was used to compare the purple witchweed contigs and known viral RdRp sequences.

Sequencing depth was examined by mapping high-quality RNA-Seq reads to the contig sequence using the bwa-mem2 program (version 2.0pre2; https://github.com/bwa-mem2/bwa-mem2). Conserved domains in the polyprotein sequences were predicted using the InterPro web server (version 84.0; https://www.ebi.ac.uk/interpro). The SignalP web server (version 5.0; https://services.healthtech.dtu.dk/service.php?SignalP) was used to predict the signal peptide.

Pairwise identities of the protein sequences were calculated using the needle program of the EMBOSS package (version 6.6.0.0; http://emboss.open-bio.org). Multiple sequence alignments were performed using the MAFFT program (version 7.475; https://mafft.cbrc.jp/alignment/software) (Nakamura *et al.*, 2018). Gap-rich segments in the aligned sequences were removed using the trimAl program (version 1.4.rev22; http://trimal.cgenomics.org) with the "-gappyout" option (Capella-Gutierrez *et al.*, 2009). A maximum-likelihood phylogenetic tree was constructed using the IQ-TREE program (version 2.1.2; http://www.iqtree.org) (Minh *et al.*, 2020). Bootstrap supports were calculated from 1,000 replicates using the UFBoot2 method implemented in the IQ-TREE program. Sequence logos were generated using the WebLogo 3 server (http://weblogo.threeplusone.com) (Crooks *et al.*, 2004).

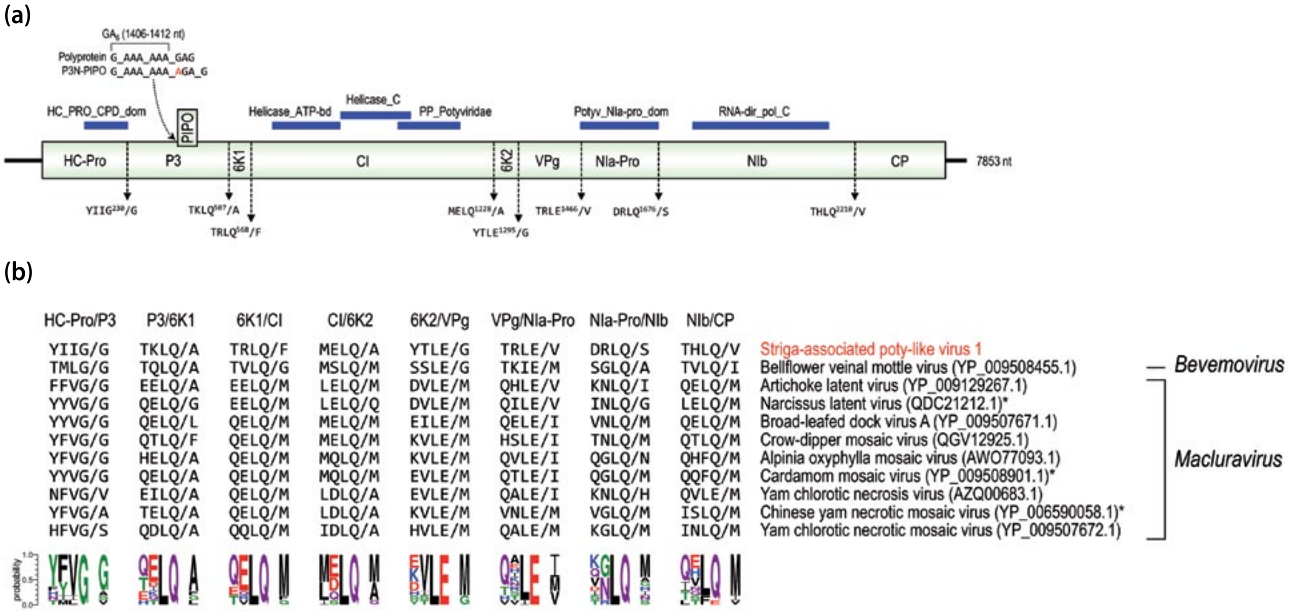

Fig. 1

Genome organization and cleavage sites of SaPlV1

(a) Schematic figure of the SaPlV1 genome is presented. ORFs for the large polyprotein and PIPO are depicted as boxes. Predicted InterPro domains are marked above the polyprotein ORF with the corresponding InterPro short name. The GA_6 motif causing a polymerase slippage is shown above the genome (the +1A insertion is indicated in red and the underscores ('_') indicate the codon boundaries). Predicted cleavage sites are presented below the polyprotein ORF. **(b)** Five aa resides at the eight cleavage sites of the SaPlV1, BVMoV, and nine macluravirus polyprotein sequences are presented. The slash ('/') indicates the cleaved bond. Three macluraviruses with annotated cleavage site information are indicated by asterisks. Sequence logos showing the frequencies of residues at each position are displayed at the bottom.

Results and Discussion

We re-analyzed the transcriptome data obtained for the investigation of gene expression dynamics during haustorium development in purple witchweed (Yoshida *et al.*, 2019). Transcriptome contigs assembled from high-quality RNA-Seq reads were compared with known viral RdRp sequences. Several contigs were found to contain a viral RdRp motif. Two different contigs showing significant sequence similarity to potyvirid RdRp motifs were chosen for further studies. To obtain a high-quality contig sequence, the sequencing depth of each contig was examined by mapping RNA-Seq reads to a contig, and bases supported by only one read were trimmed off at both ends. Two putative viral contigs that were 7853 and 10767 nucleotides (nt) in length were obtained.

BLASTX searches of the NCBI protein database using two contigs as query sequences confirmed that they encoded a large protein showing significant sequence similarity to known potyvirid polyproteins. Therefore, the 7853-nt and 10767-nt contigs were considered genome sequences of novel potyvirids and tentatively named Striga-associated poty-like virus 1 (SaPlV1) and Striga-associated poty-like virus 2 (SaPlV2), respectively. The genome sequences were deposited in the NCBI database (Acc. Nos. MW699352 and MW699353, respectively).

Genome sequence of Striga-associated poty-like virus 1 (SaPlV1)

The SaPlV1 genome was 7853-nt long and predicted to encode a 2462-amino acid (aa) polyprotein (Fig. 1a and Table 1). The InterPro domain analysis indicated that the SaPlV1 polyprotein has conserved domains that are typically found in other potyvirid polyproteins, including the HC-Pro cysteine protease, helicase, NIa protease, and RdRp domains.

A sequence similarity search of all known viral proteins revealed that the SaPlV1 polyprotein was the most similar to the BVMoV polyprotein (NCBI Acc. No. YP_009508455.1), with 52.6% identity in the 2496-aa overlap. BVMoV is a species within the genus *Bevemovirus* (Seo *et al.*, 2017). The next similar sequences were polyproteins of various macluraviruses (the genus *Macluravirus*) such as the narcissus latent virus (QDC21212.1), cardamom mosaic virus (YP_009508901.1), and Chinese yam necrotic mosaic virus (YP_006590058.1), with 32%–34% identity in an approximately 2700-aa overlap (Kondo and Fujita, 2012;

Table 1. ORFs and domains of SaPlV1 and SaPlV2 genome sequences

Virus	ORF	ORF position (nt)	Protein length (aa)	Domain position (aa)	InterPro domain[a]
SaPlV1	Polyprotein	309–7679	2462	113–230	HC_PRO_CPD_dom (IPR031159): Helper-component proteinase (HC-Pro) cysteine protease (CPD) domain-like methyltransferase (MT) domain
				625–810	Helicase_ATP-bd (IPR014001): Helicase superfamily 1/2, ATP-binding domain
				810–1000	Helicase_C (IPR001650): Helicase, C-terminal
				967–1136	PP_Potyviridae (IPR013648): Polyprotein, *Potyviridae*
				1463–1674	Potyv_NIa-pro_dom (IPR001730): Potyvirus NIa protease (NIa-pro) domain
				1769–2139	RNA-dir_pol_C (IPR001205): RNA-directed RNA polymerase, C-terminal domain
	PIPO	1412–1573	53		
SaPlV2	Polyprotein	278–10267	3329	1180–1342	Helicase_C (IPR001650): Helicase, C-terminal
				2067–2285	Potyv_NIa-pro_dom (IPR001730): Potyvirus NIa protease (NIa-pro) domain
				2381–2726	RNA-dir_pol_C (IPR001205) RNA-directed RNA polymerase, C-terminal domain
	PIPO	2047–2439	130		

[a] InterPro domain in the format of "short name (accession number): full name."

Elangovan *et al.*, 2019; Wylie *et al.*, 2019). Thus, SaPlV1 is the most closely related to BVMoV and possibly, a novel member of the genus *Bevemovirus*.

The polyprotein of potyvirids is post-translationally cleaved at conserved cleavage sites to produce mature peptides (Adams *et al.*, 2005; Revers and Garcia, 2015; Goh and Hahn, 2021; Palani *et al.*, 2021). BVMoV and macluravirus polyproteins are processed into nine mature peptides: HC-Pro, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb, and CP (Revers and Garcia, 2015; Seo *et al.*, 2017). The HC-Pro/P3 cleavage site is self-cleaved by HC-Pro, and the remaining seven sites are processed by NIa-Pro. To predict the putative cleavage sites and mature peptides of the SaPlV1 polyprotein, the polyprotein sequences of SaPlV1, BVMoV, and nine macluraviruses were multiply aligned (Supplementary Fig. S1 and Fig. 1b).

Based on the annotated cleavage sites of three macluraviruses (narcissus latent virus, cardamom mosaic virus, and Chinese yam necrotic mosaic virus), eight cleavage sites were predicted in the SaPlV1 polyprotein (see Fig. 1a for their positions). The predicted HC-Pro/P3 cleavage site was YIIG/G, which is highly similar to the potyvirus HC-Pro recognition sequence YXVG/G, where 'X' indicates any aa and the slash ('/') indicates the cleaved bond (Adams *et al.*, 2005; Goh and Hahn, 2021). Seven other predicted cleavage sites, which were processed by NIa-Pro, were TKLQ/A (P3/6K1), TRLQ/F (6K1/CI), MELQ/A (CI/6K2), YTLE/G (6K2/VPg), TRLE/V (VPg/NIa-Pro), DRLQ/S (NIa-Pro/NIb), and THLQ/V (NIb/CP). When the SaPlV1 NIa-Pro recognition sites were compared with those of BVMoV and macluraviruses, two consensus sequences were deduced: XXLQ/X for five sites (P3/6K1, 6K1/CI, CI/6K2, NIa-Pro/NIb, and NIb/CP) and XXLE/X for two sites (6K2/VPg, VPg/NIa-Pro) (see Fig. 1b). The same pattern was also observed in bymoviruses (the genus *Bymovirus*), which are

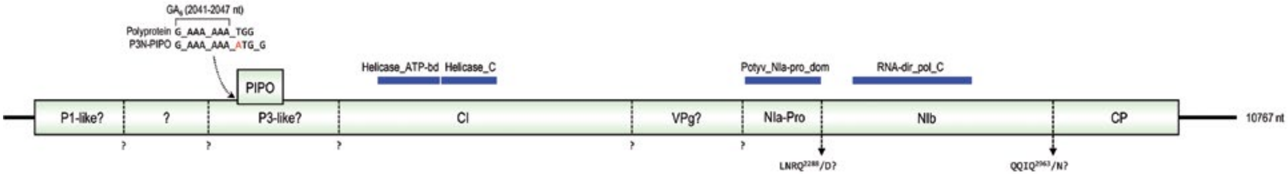

Fig. 2

Schematic figure of the putative genome organization of SaPlV2
Predicted genomic features of SaPlV2 are presented. See Fig. 1a for details.

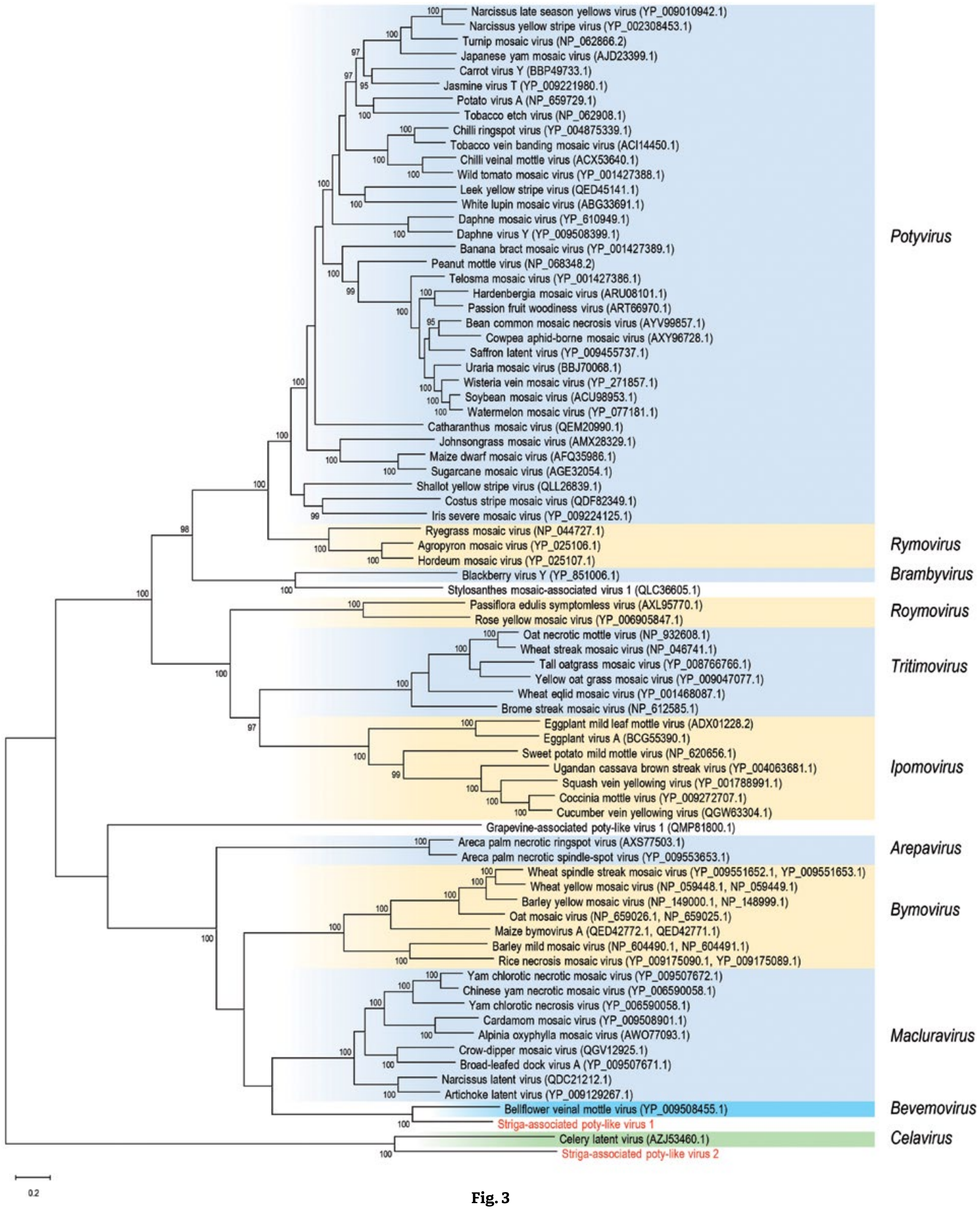

Fig. 3

Phylogenetic relationships of SaPlV1 and SaPlV2 among *Potyviridae* viruses

A maximum-likelihood phylogenetic tree was constructed from the polyprotein sequences of SaPlV1, SaPlV2, and selected members of the family *Potyviridae*. The NCBI protein sequence accession numbers are shown in parentheses. Bootstrap supporting values of 95% or higher are shown at the nodes.

more closely related to BVMoV and macluraviruses than to other potyvirids (Palani *et al.*, 2021).

Potyviruses have an additional overlapping ORF termed PIPO within the P3 segment (Revers and Garcia, 2015; Gibbs *et al.*, 2020). The trans-frame fusion protein P3N-PIPO is produced by a +1A insertion in the A-tract of the GA_6 motif by polymerase slippage (Olspert *et al.*, 2015; White, 2015). There was only one GA_6 motif in the SaPlV1 genome sequence within the P3 segment (nt 1406–1412) (Fig. 1a). To examine if the +1A insertion product was present in the purple witchweed transcriptome data, RNA-Seq reads were mapped to the SaPlV1 genome sequence. There were 18 reads spanning the GA_6 motif. Among them, 17 (94.44%) were the wild-type and 1 (5.56%) was the +1A insertion product, suggesting that this position may be a polymerase slippage site.

The SaPlV1 small polyprotein sequence containing the 54-aa PIPO segment was deduced by inserting an A nucleotide within the A-tract of the GA_6 motif. When the predicted SaPlV1 and BVMoV small polyprotein sequences were compared, the P3N and PIPO boundaries of both viruses exactly matched (Supplementary Fig. S2). The PIPO segments of the two viruses exhibited high sequence similarity, further indicating that the predicted GA_6 motif was a genuine polymerase slippage site for the production of the trans-frame fusion protein P3N-PIPO.

Genome sequence of Striga-associated poty-like virus 2 (SaPlV2)

The SaPlV2 genome was 10767-nt long and predicted to encode a 3329-aa polyprotein (Fig. 2 and Table 1). The SaPlV2 polyprotein had InterPro domains that are shared by potyvirid polyproteins, including helicase, NIa protease, and RdRp domains. No HC-Pro cysteine protease domains were detected. Sequence similarity search revealed that the CeLV polyprotein (3640-aa, NCBI Acc. No. AZJ53460.1) was the most similar to the SaPlV2 polyprotein, with 44.9% identity in a 3917-aa overlap, whereas the other potyvirid polyproteins showed lower (15%–20%) sequence identities. Thus, SaPlV2 is the most closely related to CeLV among the currently known viruses.

CeLV is the sole species in the genus *Celavirus* (Rose *et al.*, 2019). Because CeLV is distantly related to other potyvirids, annotation of proteolytic cleavage sites and mature peptides of its polyprotein is highly limited. The CeLV polyprotein was assumed to be cleaved into at least seven or eight mature peptides: one or two P1-like proteases, a P3-like peptide, CI, VPg, NIa-Pro, NIb, and CP (Rose *et al.*, 2019). However, only two cleavage sites (NIa-Pro/NIb and NIb/CP) have been previously predicted. Therefore, the annotation of the SaPlV2 polyprotein is difficult.

The SaPlV2 and CeLV polyprotein sequences shared a strong sequence similarity with their N-terminal regions (Supplementary Fig. S3). The SaPlV2 polyprotein was approximately 300-aa shorter than the CeLV polyprotein at the N-terminus. There was an in-frame stop codon upstream of the SaPlV2 polyprotein ORF, indicating that the SaPlV2 polyprotein was full-length. The CeLV polyprotein was predicted to contain a signal peptide at its N-terminus (Rose *et al.*, 2019). However, no signal peptide was predicted for the SaPlV2 polyprotein. Despite the difference in their N-terminal regions, it was assumed that the SaPlV2 polyprotein may be processed into seven or eight mature peptides similar to those of CeLV. The SaPlV2 and CeLV polyproteins lacked the HC-Pro segment. Among the six or seven potential cleavage sites, two were predicted in the SaPlV2 polyprotein: LNRQ/D (NIa-Pro/NIb) and QQIQ/N (NIb/CP) (see Fig. 2 and Supplementary Fig. S3).

A putative GA_6 polymerase slippage motif for the P3N-PIPO fusion was found within the SaPlV2 P3-like segment (nt 2041–2047). A total of 191 purple witchweed RNA-Seq reads mapped to the putative GA_6 motif: 175 (91.62%) were the wild-type and 16 (8.38%) were the +1A insertion products, implying that the position was a polymerase slippage site. The predicted SaPlV2 PIPO contained 130 aa whereas the CeLV PIPO contained 189 aa. Sequence alignment of the SaPlV2 and CeLV small polyproteins with the P3N-PIPO fusion revealed that the PIPO segments of the two viruses shared many conserved residues, although their start positions were different (Supplementary Fig. S4).

Phylogenetic positions of SaPlV1 and SaPlV2 among potyvirids

To investigate the phylogenetic positions of SaPlV1 and SaPlV2 among potyvirids, polyprotein sequences of 76 selected potyvirids were collected from 12 genera of the family *Potyviridae*. In the case of the genus *Bymovirus*, which has a bipartite genome, two polyprotein sequences were concatenated. Multiple sequence alignment was generated using the MAFFT program, followed by filtering out the gap-rich segments using the trimAl program. A maximum-likelihood tree was constructed using the IQ-TREE program (Fig. 3).

SaPlV1 and BVMoV, the founding and only member of the genus *Bevemovirus*, clearly formed a strong clade with 100% bootstrap support. SaPlV2 and CeLV, the type species of the genus *Celavirus*, also formed a distinct clade with 100% bootstrap support. Phylogenetic relationships and similarities of genome organizations strongly suggested that SaPlV1 and SaPlV2 may be novel members of the genera *Bevemovirus* and *Celavirus*, respectively.

Conclusion

In conclusion, the genome sequences of SaPlV1 and SaPlV2, novel members of the family *Potyviridae*, were identified from the transcriptome data of purple witchweed. Sequence comparisons and phylogenetic analyses suggested that SaPlV1 and SaPlV2 may be novel species from the genera *Bevemovirus* and *Celavirus*, respectively. The genome sequences of SaPlV1 and SaPlV2 may be useful for studying the evolution of potyvirid genome organizations.

Acknowledgments. This work was supported by the National Research Foundation of Korea (NRF) funded by the Government of Korea (grant number 2020R1A2C1013403) and the Chung-Ang University Research Scholarship Grants in 2021.

Supplementary information is available in the online version of the paper.

References

Adams MJ, Antoniw JF, Beaudoin F (2005): Overview and analysis of the polyprotein cleavage sites in the family Potyviridae. Mol. Plant Pathol. 6, 471–487. https://doi.org/10.1111/j.1364-3703.2005.00296.x

Bejerman N, Debat H, Dietzgen RG (2020): The plant negative-sense RNA virosphere: virus discovery through new eyes. Front. Microbiol. 11, 588427. https://doi.org/10.3389/fmicb.2020.588427

Bos L, Diaz-Ruiz JR, Maat DZ (1978): Further characterization of celery latent virus. Neth. J. Plant Pathol. 84, 61–79. https://doi.org/10.1007/BF01976409

Bushmanova E, Antipov D, Lapidus A, Prjibelski AD (2019): rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. Gigascience 8, giz100. https://doi.org/10.1093/gigascience/giz100

Capella-Gutierrez S, Silla-Martinez JM, Gabaldon T (2009): trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 25, 1972–1973. https://doi.org/10.1093/bioinformatics/btp348

Chung BY, Miller WA, Atkins JF, Firth AE (2008): An overlapping essential gene in the Potyviridae. Proc. Natl. Acad. Sci. USA 105, 5897–5902. https://doi.org/10.1073/pnas.0800468105

Crooks GE, Hon G, Chandonia JM, Brenner SE (2004): WebLogo: a sequence logo generator. Genome Res. 14, 1188–1190. https://doi.org/10.1101/gr.849004

Elangovan S, Srikakulam N, Pandi G, Jacob T, Ramakrishnan U, Madhugiri Narayanarao V, Tennyson J (2019): The first complete genomic sequence of cardamom mosaic virus, a member of the genus Macluravirus (family Potyviridae). Arch. Virol. 164, 1723–1726. https://doi.org/10.1007/s00705-019-04203-2

Gibbs AJ, Hajizadeh M, Ohshima K, Jones RAC (2020): The potyviruses: an evolutionary synthesis is emerging. Viruses 12, 132. https://doi.org/10.3390/v12020132

Goh CJ, Hahn Y (2021): Analysis of proteolytic processing sites in potyvirus polyproteins revealed differential amino acid preferences of NIa-Pro protease in each of seven cleavage sites. PLoS One 16, e0245853. https://doi.org/10.1371/journal.pone.0245853

Goh CJ, Park D, Hahn Y (2021): A novel tepovirus, Agave virus T, identified by the analysis of the transcriptome data of blue agave (Agave tequilana). Acta Virol. 65, 68–71. https://doi.org/10.4149/av_2021_107

Kondo T, Fujita T (2012): Complete nucleotide sequence and construction of an infectious clone of Chinese yam necrotic mosaic virus suggest that macluraviruses have the smallest genome among members of the family Potyviridae. Arch. Virol. 157, 2299–2307. https://doi.org/10.1007/s00705-012-1429-1

Mbanzibwa DR, Tian Y, Mukasa SB, Valkonen JP (2009): Cassava brown streak virus (Potyviridae) encodes a putative Maf/HAM1 pyrophosphatase implicated in reduction of mutations and a P1 proteinase that suppresses RNA silencing but contains no HC-Pro. J. Virol. 83, 6934–6940. https://doi.org/10.1128/JVI.00537-09

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020): IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. Mol. Biol. Evol. 37, 1530–1534. https://doi.org/10.1093/molbev/msaa015

Nakamura T, Yamada KD, Tomii K, Katoh K (2018): Parallelization of MAFFT for large-scale multiple sequence alignments. Bioinformatics 34, 2490–2492. https://doi.org/10.1093/bioinformatics/bty121

Olspert A, Chung BY, Atkins JF, Carr JP, Firth AE (2015): Transcriptional slippage in the positive-sense RNA virus family Potyviridae. EMBO Rep. 16, 995–1004. https://doi.org/10.15252/embr.201540509

Palani SN, Sankaranarayanan R, Tennyson J (2021): Comparative study of potyvirid NIa proteases and their cleavage sites. Arch. Virol. 166, 1141–1149. https://doi.org/10.1007/s00705-021-04997-0

Park D, Goh CJ, Hahn Y (2021): Two novel closteroviruses, fig virus A and fig virus B, identified by the analysis of the high-throughput RNA-sequencing data of fig (Ficus carica) latex. Acta Virol. 65, 42–48. https://doi.org/10.4149/av_2021_104

Park D, Goh CJ, Kim H, Hahn Y (2018): Identification of two novel amalgaviruses in the common eelgrass (Zostera marina) and in silico analysis of the amalgavirus +1 programmed ribosomal frameshifting sites. Plant Pathol. J. 34, 150–156. https://doi.org/10.5423/PPJ.NT.11.2017.0243

Park D, Hahn Y (2021): Identification of genome sequences of novel partitiviruses in the quinoa (Chenopodium quinoa) transcriptome datasets. J. Gen. Plant Path. 87, 236–241. https://doi.org/10.1007/s10327-021-01002-z

Revers F, Garcia JA (2015): Molecular biology of potyviruses. Adv. Virus Res. 92, 101–199. https://doi.org/10.1016/bs.aivir.2014.11.006. https://doi.org/10.1016/bs.aivir.2014.11.006

Rodamilans B, Valli A, Mingot A, San Leon D, Baulcombe D, Lopez-Moya JJ, Garcia JA (2015): RNA polymerase slippage as a mechanism for the production of frameshift gene products in plant viruses of the Potyviridae family. J. Virol. 89, 6965–6967. https://doi.org/10.1128/JVI.00337-15

Rose H, Doring I, Vetten HJ, Menzel W, Richert-Poggeler KR, Maiss E (2019): Complete genome sequence and construction of an infectious full-length cDNA clone of celery latent virus - an unusual member of a putative new genus within the Potyviridae. J. Gen. Virol. 100, 308–320. https://doi.org/10.1099/jgv.0.001207

Seo JK, Kwak HR, Kim MK, Kim JS, Choi HS (2017): The complete genome sequence of a novel virus, bellflower veinal mottle virus, suggests the existence of a new genus within the family Potyviridae. Arch. Virol. 162, 2457–2461. https://doi.org/10.1007/s00705-017-3374-5

Shen W, Shi Y, Dai Z, Wang A (2020): The RNA-dependent RNA polymerase NIb of potyviruses plays multifunctional, contrasting roles during viral infection. Viruses 12, 77. https://doi.org/10.3390/v12010077

Spallek T, Mutuku M, Shirasu K (2013): The genus Striga: a witch profile. Mol. Plant Pathol. 14, 861–869. https://doi.org/10.1111/mpp.12058

Valli A, Lopez-Moya JJ, Garcia JA (2007): Recombination and gene duplication in the evolutionary diversification of P1 proteins in the family Potyviridae. J. Gen. Virol. 88, 1016–1028. https://doi.org/10.1099/vir.0.82402-0

White KA (2015): The polymerase slips and PIPO exists. EMBO Rep. 16, 885–886. https://doi.org/10.15252/embr.201540871

Wylie SJ, Tran TT, Nguyen DQ, Koh SH, Chakraborty A, Xu W, Jones MGK, Li H (2019): A virome from ornamental flowers in an Australian rural town. Arch. Virol. 164, 2255–2263. https://doi.org/10.1007/s00705-019-04317-7. https://doi.org/10.1007/s00705-019-04317-7

Yoshida S, Kim S, Wafula EK, Tanskanen J, Kim YM, Honaas L, Yang Z, Spallek T, Conn CE, Ichihashi Y, Cheong K, Cui S, Der JP, Gundlach H, Jiao Y, Hori C, Ishida JK, Kasahara H, Kiba T, Kim MS, Koo N, Laohavisit A, Lee YH, Lumba S, McCourt P, Mortimer JC, Mutuku JM, Nomura T, Sasaki-Sekimoto Y, Seto Y, Wang Y, Wakatake T, Sakakibara H, Demura T, Yamaguchi S, Yoneyama K, Manabe RI, Nelson DC, Schulman AH, Timko MP, dePamphilis CW, Choi D, Shirasu K (2019): Genome sequence of Striga asiatica provides insight into the evolution of plant parasitism. Curr. Biol. 29, 3041–3052. e3044. https://doi.org/10.1016/j.cub.2019.07.086

Acta virologica **65**: 365 – 372, 2021 doi: 10.4149/av_2021_402

Two novel poty-like viruses identified from the transcriptome data of purple witchweed (*Striga hermonthica*)

Dongjin Choi[1], Chaerim Shin[1], Ken Shirasu[2,3], Yoonsoo Hahn[1*]

[1]Department of Life Science, Chung-Ang University, Seoul 06974, South Korea; [2]RIKEN Center for Sustainable Resource Science, Yokohama, Kanagawa 230-0045, Japan; [3]Graduate School of Science, The University of Tokyo, Bunkyo, Tokyo 113-0033, Japan

Received May 12, 2021; accepted June 3, 2021

---

[*]Corresponding author. E-mail: hahny@cau.ac.kr; phone: +82-2-820-5812.

Fig. S1. Alignment of the polyprotein sequences of SaPlV1 and related viruses

Putative cleavage sites are marked by vertical bars (|) and highlighted in yellow.

```
Striga-associated poty-like virus 1                    ----------------MDYLALTRI-VANRQTIDMP----RVLELAIKEVYGTYNRELNSA---IDFKGEQLETTPAT---TDPLDVFIK    63
Bellflower veinal mottle virus (YP_009508455.1)        ----------------MDPLFLKRF-NMDGGKLQIC----APISDALKAAYNNHGVDIKSSYAVTAPCGTVISVENST---NEVLKDFVE    66
Artichoke latent virus (YP_009129267.1)                MATVKA-NV-NFKVDNVDTLNTHLMQLMSGSALKIQPLTAAALMRMVDRHFEANAMIKGSEFIMVDGGGKTLATFNTSMRNNANLETFMK    88
Narcissus latent virus (QDC21212.1)                    MATVKS-SV-NFKVENVDTLNTHLMQLMSGNPLNVPPATARALLELANKRFETNKMAKGSEFLMVDGDGKTVATFNKAARNNADLRTFMD    88
Broad-leafed dock virus A (YP_009507671.1)             MAKSSN-DV-AFKVENVDTFNTHMLQLITKNELGILPETLKVLTAIIERRYEVCSMKDPRDFMMVDGKGKLLARFSQLRGREMTLKEFLS    88
Crow-dipper mosaic virus (QGV12925.1)                  MASASKLEV-NFKVDNVDTLNTHVLQILSGKSLTMPEKTKEALIECVNKKFETFNGDTSKDFLMVDGKGVVLGKFQNFDARNINLKTFLE    89
Alpinia oxyphylla mosaic virus (AWO77093.1)            MASNSK-IVSNFKVEVVDFLNTHAAQITTGKNLNIEDKTRSKVVAFVRKQYINNELKDGKDFVMIDGKGKTVANFPTTVRGTTKLKDFLT    89
Cardamom mosaic virus (YP_009508901.1)                 MASGKK-QLGNFKVEVLDVLNTHMAQMLMGKTLSVEERTREVLVQIVKKHYRKNEMKEGGDFVMVDGKGKTVASFPTLLKGKPTLKDFVD    89
Yam chlorotic necrosis virus (AZQ00683.1)              MATVKP-DV-NFKVELVEFLSTHNIQMMTGNPLTIPDKTRAKLVDFVKRFYEINKGEQAKDFVMLDSKGKTIASMPMAVTSSTKFKTFLE    88
Chinese yam necrotic mosaic virus (YP_006590058.1)     MATVKS-DI-NFKVENVDILSTHSMQMLTGKPLTIPDRTRALLVEIVGKRYQNNDGNTSADFVMLDGKGAMIANMCMAITKGMKFKDYKD    88
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   MATVKS-DV-NFKIENVDILSTHSMQMLTGRPLTIPDKTRAQLIDIVARRYQENGGTNSSDFVMLDGKGVLIANMCMAITKQTKFKDYKD    88
                                                                       :: :            : :       :       :                 *  :            :  :

Striga-associated poty-like virus 1                    NELKEINDAA-GDCGKIA-CVR--PRTLPEGFYATMSYAMGGLKGVIPGPVSKRRCFRDGYCYMNIFVAIAPHVYDEDALVYAKFLNDCP   149
Bellflower veinal mottle virus (YP_009508455.1)        AGMKFNDDVA-GECPKGQ-CNEASKGRSSWFLNCSPTLAVGGRSATFIMPMSPRRVFSSGYCYLNLAVAMSPYIFDEDAIKFAEFLHDLP   154
Artichoke latent virus (YP_009129267.1)                GEIKFPAQQSFELCDKIVKCTKMHQQHVAHTRLPAAGYTFGGYSKLCPIPLYQGHVAKQGHCFKTLMLAISYFVTKEFDGVFAGIMDEVT   178
Narcissus latent virus (QDC21212.1)                    SKIAFPAQQSFELCDKIIKCTKMHQQHTAHARLPSVNYAFGGYSKLCPIPLFKDKVAKQGHCFGTLLLALSYFVTKEFDDEYAKIINEIV   178
Broad-leafed dock virus A (YP_009507671.1)             QSFSVPAQTSFTACDKVVKCVKGHQQQLAHLRVPSVDYVFGGLSRVCAIPLIKNRVAKQGNCFFNALIAISYFIRQEDDIMFANIVKELD   178
Crow-dipper mosaic virus (QGV12925.1)                  KTTPVPAQESFKKCDKIIKCTKVHQQQMAHMRMPSMNFVHGGISKVCAIPLIVNKIARQGNCIYNALMAMSYFVREEDDELYASIVKEVL   179
Alpinia oxyphylla mosaic virus (AWO77093.1)            AKFEIPDEQSFERCDKIIKCVKAHQQQMAHMRTISNDYAFGGLSKICPIPMIKGMVPNQGMCFLTLLISTSYFITPELDEQFSLVIDEVL   179
Cardamom mosaic virus (YP_009508901.1)                 KEFQIPAQQPFNTCDSVTKCIKAHRQQLAHMRTISSDYTFGGISKICPIPLIQGMVPVQGMCFFTMVVSLSYFIPPELDDKFAQLLEEIL   179
Yam chlorotic necrosis virus (AZQ00683.1)              AGLRLPAQASFLGCDKVVKCIKTQQQHLAHIRLASNDYVFGGISKSCPIPMIKGMVPKPGFCFLNIIVALSYFVTAEFDQVFESTIDDVM   178
Chinese yam necrotic mosaic virus (YP_006590058.1)     GMVNMPQQTSFAECDKVVKCVKVQQQHLLHARLPTNDYVFGGMSKSNAIPMIKNMVPKSGSCFLSAIVAMSYFVTPEFDEIFMQTINDVL   178
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   GNISMPQQGSFADCDKAIKCVKVQQQHLLHTRLPANDYVFGGMSKSNAIPMIKNMVPKSGSCFLSVIVAMSYFVTPEFDEIFVETVKDVL   178
                                                              : .   * .   * .            :   . ** .     *:        * *  .  :: : .:  *    :   :.:

                                                                                                                    HC-Pro|P3
Striga-associated poty-like virus 1                    LVLGSWPTMNSLAKAMIWIGQKIPNLYNKAVPAVSISHTAEACHVVDQRGPVKGWHILDAPTFRDVILFSL--KSDLSEYIIG|G-DPVT   235
Bellflower veinal mottle virus (YP_009508455.1)        IVLGKWPAMVKVARSFAWLLQHMPYLCDRHIPHISINHNLNAAHVSDQRGPMIGCHILNAYTLKDFVLTGM--DTLNANTMLG|GMDALT   241
Artichoke latent virus (YP_009129267.1)                SNIKSWPSLKDVSKICQYIISKVPILGPVPIPVVAVDHAKKLIHICDQRGIPDGWHQLKMGTLAELANAGLLSQSSLHTFFVG|GDAQQP   267
Narcissus latent virus (QDC21212.1)                    SFLGAWPKLAQIAKICQYIIMRVPILAPVPIPVVAVNHEKSLMHICDQRGIPDEWHQLKMGTLAELANAGLLSSSKLCSYYVG|GTDE--   265
Broad-leafed dock virus A (YP_009507671.1)             AVITSWPKLSDVSVYLQYLIAKLPYLGAMPIPAVAVSHERKLIHFCDQRGVPHGWHVMKMGILAEAANAGFMKGSGIPNYYVG|GTHE--   265
Crow-dipper mosaic virus (QGV12925.1)                  ADGTAWPKLERVSKMMHYIIMKLPYLAAAPMPAIAVDHERSLIHICDQRGVPQQWHVLKIGTAAELANAGLMKSSNLINYFVG|GTNQ--   266
Alpinia oxyphylla mosaic virus (AWO77093.1)            SEMKPWLTLQTASKIVQYIICKIPVLAHVPIPAVAVDHMKSLIHVCDQRGVPSGWHVLKIGTLAEFANIGIIENSKLTSYFVG|GSEKND   268
Cardamom mosaic virus (YP_009508901.1)                 QLLKAWPTFETVAKIAQFIIYRIPILAHVPIPALAVDHENGLMHFCDQRGVPAGWHVLKIGMLAELANAGTMTTSKLNKYYVG|GSNEGQ   268
Yam chlorotic necrosis virus (AZQ00683.1)              RELGPWPKLEAVSKAVQFIIAKVPILGPVPVPSIAVNHEDKLIHICDQRGVPNGWHVLKVGTASELANAGLIKGSSISNNFVG|VFGDAP   267
Chinese yam necrotic mosaic virus (YP_006590058.1)     GELGSWPTLQNVSKAMQFILAKVPTLSMVPLPVIAVTHEKKLIHICDQRGVPNGWHILKIGTVAELANAGFIKHTKLNGYFVG|APESIT   267
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   HELGSWPTLKNVSKAMQFILAKVPILGMAPLPVVAISHEKKLIHVCDQRGVPNGWHILKIGTASELANAGLIKNSKISDHFVG|STEDVR   267
                                                            *  :   :    ::  ::* *    :* ::: *     *. ****     * :.     :    .    :      :*

Striga-associated poty-like virus 1                    AAYMHLSKCIRHANNTRQPWVT---FNKMVLEDSALAATLVLSPATLIKLESWFEDREEFRRLVATIESGVGDALTRIIVIKRAIEGVKI   322
Bellflower veinal mottle virus (YP_009508455.1)        SAYQSLDKAIMQANKSFQPWLT---FYRMICADSMLAATLIMSPATLQKLESWFEDDEGFRRVVATLETTVSDALLRMVIIKRAIHGVKM   328
Artichoke latent virus (YP_009129267.1)                EE-MLYLRGLSKVKANLRTWVTKGTMVDDLARDIDLAAFMMLSPVMLSRLRTLIEREEASAMKAIVMDSSCNNKLVVASALRTAVQGVLV   356
Narcissus latent virus (QDC21212.1)                    DKTELYRRGLSKVKANLTRWMSKGTMIDDCTRDLDLAAFIMLSPNMLSRLRSLVERDDDAAMKAILMDASCPNKLVVASAIKTAIQGVLV   355
Broad-leafed dock virus A (YP_009507671.1)             TTVQLYSNQLAKVQGKLKGWIRSGGLFEDLVKDTQLAAFVILSPALLSRLQNLIESEASAVVSIEKLEAAHENKVVAMTAVRTALTGVRI   355
Crow-dipper mosaic virus (QGV12925.1)                  EIVELYSTQINKAKQLLPKWIKGGDIFDDITKDVNLAAFMMMSPSMLSKLQNVIHTTASEALNLEKLETSHENKIVAINAIQAALAGIRV   356
Alpinia oxyphylla mosaic virus (AWO77093.1)            DELQIYVDQLTKIKKNFKEWVLKGNLFETLKNDMLLTAFLVLSPAHLSKLHNFLESNANEALQICELDTVNKNKILAATIISTGLKGVRI   358
Cardamom mosaic virus (YP_009508901.1)                 DDLDFYVEQIHKIKKNFSRWLTSGTLFSDLANDVHLTAFLALSPAHLAKLHHYLEISAEEAQKIVQLDAVNKNKIMAAAVIQTALKGIRI   358
Yam chlorotic necrosis virus (AZQ00683.1)              EERVFYVENLTKVKHALTKWRKPEAFLNALTQDINLMSFLLLSPSLLVKLQRTLEKGANEALMLDVIERSTSDKIVTANLIKAALEGITV   357
Chinese yam necrotic mosaic virus (YP_006590058.1)     DDKMFYTRNINKVKNLMTLWRSPERFVEAMANDIELTAFILLSPSLLSKLYNLLSIGSSEALKIEALERANSNKIVVASLINIALQGVRV   357
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   EDKMFYNRNINKVKSLMQLWKSPERFVDGMANDIELAVFIIMSPSLLAKLYNLLSKGASEALRLEALERANNNKIVVASLINAALQGIRI   357
                                                                : : :     *     :      *  *   : :**  * :*   .            ::    : :     :  .: *: :

Striga-associated poty-like virus 1                    HFLDNDIETATAALHQRVLEYIRNADD--GGALNAAATRFSNLVTEKKEQFYYFEKRIHSLSDFRWRREHDFGVISIGESCCTGAIHMLR   410
Bellflower veinal mottle virus (YP_009508455.1)        HFRTDNVERSTNELHRAIIAYIDSQDDQSAKDLGDAARRFETMALEKKMQFVYLESSIAHCSDYRWRRERGFSYISCGESLCTLLLSKLG   418
Artichoke latent virus (YP_009129267.1)                HTGETRIERIWLQVNNVLQDHLNSEGKEIEVALSRALHRLHNHLMSEKKLIFSYERRLNLLTHDQFKLEFGCSHGWGSKFYYMLAGRNGE   446
Narcissus latent virus (QDC21212.1)                    HTNETKLEKIWTNVNNVLQDHLAAGGREIDRELSRALHKLHSYLLHEKKTIFSYERRLYALTATQFRQEFGCSCGWGGKLLAMAFKQNGS   445
Broad-leafed dock virus A (YP_009507671.1)             KSGDKDIEKIWHHIHTLMMGIYDGEESHYKGEMRQAVTNLYTTLVAEKKYVTACERALYSATEEEFAKSFGCQPTWYDKFSFTAWRESRR   445
Crow-dipper mosaic virus (QGV12925.1)                  RAGCSDIEKVWLHIHSIMMNHFDEEENKFKAEMRLAVTRLYAAMIAEKKYVTSCERAIYRTTKEEFLKNFGLQQGFVSKLSFTHWRNRRS   446
Alpinia oxyphylla mosaic virus (AWO77093.1)            KWRETSCEKLWLHLLKTIEAVLEADDTQQATNLRSACERMYEVMCANKKFVYCCEKRIYYLTDAEFQTTLGFSPTWFGALQARLGFTRAS   448
Cardamom mosaic virus (YP_009508901.1)                 KLRETDIEKVWLHLHKTLDHILQDDDSDASARLREACTRMYNVLCANKKFVYQCEKHTYSRDNATLREMFGCSSTWLSRLQRKLHILSGE   448
Yam chlorotic necrosis virus (AZQ00683.1)              KLGETQLEKVWLHLLEVVRVQLDYDECQRNKDIIDACGMVYNQLCKEKKSIYHYEKQIYHMDEREFQRTFYYSPLSLGEAVSGFINTKFG   447
Chinese yam necrotic mosaic virus (YP_006590058.1)     KMGETSLEKVWLHLLNVLTANLSIEESRRNTDILQACNAVYNELIKEKNYMYHCEKQIYNLTDKQFEDMFGCSRTWHSKLCDKLSHLNVA   447
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   KMGETSLEKVWLHLLNVLTANLSIEESQRNNDILKACNMVYHEFVKEKNYMYHCEKQIYQLTDKQFEDMFCCSHTWQEEFCRKLSHLNII   447
                                                       :      *     :   :              :  *   .      :*  .   *

Striga-associated poty-like virus 1                    NTL--PYLEKLEAKEK----------------FFQFAAAWRCLFVFVYLLAETIALALVGWFSIKRAMLFVLKVLARHYLGQNHMHHLWL   482
Bellflower veinal mottle virus (YP_009508455.1)        SCI--PAIQLQEQRERLP----------------EFIRAARYTWVTIYWFVQAASLMLLGWFSIKNFMLFLLRAVTKYYLGHHYAHHIWT   490
Artichoke latent virus (YP_009129267.1)                TDVGKSSISYKIFNDGITHRTIEAINAYFIISTVCVINTLNALFGLVQFAFYIMLMCF-GFMSLTKFMFHCAKALLIRRLATNWER---M   532
Narcissus latent virus (QDC21212.1)                    VDVGRSAISLRAFDDGITHRTIEAVNLFFLISTFHIFRALSYIFVITRILFYIFLTAF-GCMSLSKLLFHLAKAMLIRRLAHNWER---L   531
Broad-leafed dock virus A (YP_009507671.1)             GYVGAPRIKLQSLEDGLTGVACQFLSSLGIQMVLGLINTGCKCYSLAKFICYIFLLIW-GSLSLSKFMLFCMKQLIVRKFSNNYKK---L   531
Crow-dipper mosaic virus (QGV12925.1)                  SGLGYSNIKLKYLEDPINSAFANHMSRVVMLLMLGVVKTGSQLFSVTQFFFYIFLVMW-GSMSLSNFIFYMFKSVVISRLSGNYKK---L   532
Alpinia oxyphylla mosaic virus (AWO77093.1)            DSLTVSKIRLSCFSDNIVYRTLPYVNAFFLYFTIQLFATMSYLFSVARIIFY-CIFVWHGIFSISSLVLMLVKSLIVSRLSRNYNK---L   534
Cardamom mosaic virus (YP_009508901.1)                 RQLVVSNIKLACFSDGIIHRTIPYVNAFYLYFTINLFAFLSNIYSLARLFF-LFIFAWYGCVSLTSIVFHLIKMLVLSRLSRNYNK---V   534
Yam chlorotic necrosis virus (AZQ00683.1)              NLLAKPRLRLNCFSDGIDRYSFGPFLNIMNITIIKLLLFAGRMYNLFRVFFCLCAFCW-GFMSLGNLAYIAFKTAVLRRLSGNYEK---L   533
Chinese yam necrotic mosaic virus (YP_006590058.1)     KSVQQSSVKLSCFSDGITHRTIQAVTHHFIMCFIRLLIFAQHAYSILRFFFLLAACCW-GFMSITNLVFMAFKAVVMRKLATNYEK---L   533
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   KSVQQPSVKLRCFDDGITHKTIQLVTQHFIICFVRLLIFAQHTYSIMRFFFCLCACCW-GFMSITNLVFMAFKAVVMRKLATNYEK---L   533
                                                         :  . :      :                    .       :               * .*:        :      :. :  :
```

```
                                                                                         P3|6K1
Striga-associated poty-like virus 1                    MAVMGITTLIAARTYIKALHP-----------TKLQ|AS--ANEKRMTGLMAFVILVVHVFDVDLALMLSSSLRSINQLAVMLTEETNGL   558
Bellflower veinal mottle virus (YP_009508455.1)        LLISTIALLVSAWTYMKATKP-----------TQLQ|AT--TNEKKVTGLIAFIVLAVHIFDADLAIMLSSSLHTISRTASMLTDETRNI   566
Artichoke latent virus (YP_009129267.1)                MIITSIFLIYELSRFIMKKKAEREKLNEGRS-EELQ|ASVKSSEKQMMAAMAMMTLVVHAFDIDLAITMSGALNHVARLANMLTDTTSGW   620
Narcissus latent virus (QDC21212.1)                    MIVTSIFLVYELARFIIGRKATRQKNVHSKD-QELQ|GPHKSSEKQMMAAMAMITLIVHAFDMDLAITMSSALNHVSRLANMLTDTTSGW   619
Broad-leafed dock virus A (YP_009507671.1)             VLFGTLFVIYELATYVARKMKQRKEKGDG---QELQ|LNSKENEKKMMAAMAMITLFVHAIDMDLALVMTSSLNHVARLVGLLTDSTTGW   617
Crow-dipper mosaic virus (QGV12925.1)                  MLLGSVFVIYELAMYIKRELAKKRDGK-----QTLQ|FKGKESEKKMMAAMAMATLAVHAFDIDLAIMMSNSLHHVSRLVSLLSDSTTGW   616
Alpinia oxyphylla mosaic virus (AWO77093.1)            LICGTVFCVFELGRYIIKQKQRKNQIQP----HELQ|AGLKTSEKQMMSAMAMLTLLVHAFDMDLAVMMSNSLNHVARLANMLTDTTSGW   619
Cardamom mosaic virus (YP_009508901.1)                 LFCGFVFCMFELGRYIAWKKSQRKENQP----QELQ|ASIKSSEKQMMSVMAMITLLVHAFDIDLAITMSNSLNHVARMANMLTDTTAGW   619
Yam chlorotic necrosis virus (AZQ00683.1)              LIFGCVFALYEVGSFIIKKRKERQQKLQTKEGEILQ|AYGKSSEKKMMSAMAMITLIVHAFDMDLALMMSNSLNHVARLANMLTDTTSGW   622
Chinese yam necrotic mosaic virus (YP_006590058.1)     LIFASIFCLYEVGRFIIKKRKANKDKAAGRT-TELQ|AYGKSSEKQMMAAMAMVTLFVHAFDMDLALMMSNSLNHVARLANMLTDTTTGW   621
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   LIFACIFCLYEVGCFIIRHKKKSKELGTGKT-QDLQ|AYGKSSEKQMMAAMAMITLFVHAFDMDLALMMSNSLNHVARLANMLTDTTTGW   621
                                                       :    :  :     ::                  **      .**:: . :*:  * ** :* ***: ::.:*. : : . :*:: * .

                                                               6K1|CI
Striga-associated poty-like virus 1                    LPKLIG-TRLQ|FDESDLA-DLELEMDPEEVRNETLQEKCMTFGMWLETKVASYVDYTRELQYGGPEVHYRISPLKQQEIAEDMTQTKRA   645
Bellflower veinal mottle virus (YP_009508455.1)        LPRIINGTVLQ|GDIGEI-MELDVEIDPEIAQHEELRTKHKTFQAWIDEKVCSLEQYTRELQYGGSSVHFVVHSSNHDDISDDMLATKRE   654
Artichoke latent virus (YP_009129267.1)                LVGGTATEELQ|MHIFDVALEVDEQQKMEGEMMASTSSSLDTFSAWVNESVATGVDNTRPLTYGSVDNVYKLDSENGAEVGASMTNTKKA   709
Narcissus latent virus (QDC21212.1)                    LMGGTATEELQ|MHLFDVALEVDKQQQIENEMAASSSNLADTFSAWINENVAYGTDNTRPLTYGDVENVYKLDSKNGSNVGATMVNTKKA   708
Broad-leafed dock virus A (YP_009507671.1)             LVGG-GRQELQ|MKIFDLALEVDDTMKADEEVAATTSNHQDTFSAWVNEQLVLGNDNTRPLSYGRTDSLFTLTSDNATEVGQNMVDTKRA   705
Crow-dipper mosaic virus (QGV12925.1)                  LVRGGSHQELQ|MKFFELALEVDDKVKQENELEAQTSTSMDTFASWINEQIAMGNDNTRPLVYGRNDEIYKLNKENASEVGATLTQTKRA   705
Alpinia oxyphylla mosaic virus (AWO77093.1)            MMGGTGTQELQ|MELFDLVLEADEKIQSDLEEAVTSHRTCETFASWMSEQSLTESNNTRPLSYGRPESYVCVDRENAVEIGQNLVDTTNA   708
Cardamom mosaic virus (YP_009508901.1)                 VMRGNDSQELQ|MQLFDLALEADDTIRNELDEASTSHTTYETFSSWMAEQTLFENDKTRPLSYGRVESLVEIDRDNAVESGQALVDTTNA   708
Yam chlorotic necrosis virus (AZQ00683.1)              LIGGANTQELQ|MRLFDVVLEVDEVMEKEIQQTSVYEGGTETFSSWINEQIALGNDNTRPLAYGRDESVFFVDRENAIQVGQDMVETRNA   711
Chinese yam necrotic mosaic virus (YP_006590058.1)     LTSGGGTQELQ|MKLFDVALEVDETMTHEMDQQAAMDCSNETFAAWINEQVLLGNDNTRPLAYGRDDSVFYVTRDNAIDVGQDMCDTKNA   710
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   LTSGGGTQQLQ|MKLFDVALEVDETMSNEMEQQAVHDCSNETFASWINEQILVGNDNTRPLAYGRDDSVFYVTRDNAIEVGQDMCDTKNA   710
                                                       :        **     ::  : :     :            **  *:  .     : ** * **  .    :   :  : .  :  * .

Striga-associated poty-like virus 1                    WNSVTGGTGSGKSTRIPVFYYQRLKQMADRNKRILVCEPSRATVVNVAAGISSFLGEQVYYKHRTKEQAGNMGIQVMTYGSALMRAVGDS   735
Bellflower veinal mottle virus (YP_009508455.1)        WNSVVGGTGSGKSTRIPVHYYNKLQKAIGRQHKILICEPSRATTANVAMGITHFFGQQVYYKHRTREQVGHMGIQVMTYGSALMRSLRDP   744
Artichoke latent virus (YP_009129267.1)                WSHVVGKTGSGKSTRVPLGYYNALQTMAARRRNILICEPTQATTQNVANALSHFHGKSVFYKHEGKEQMGDMSIQVMTYGSAFFRSVHNP   799
Narcissus latent virus (QDC21212.1)                    WSHVVGMTGSGKSTRVPLGYHGALQTIAARKRNILICEPTQATTQNVAAALSRFHGKQVYFKHEGREQLGDMSIQVMTYGSAFFRSVNNP   798
Broad-leafed dock virus A (YP_009507671.1)             WSLVVGQTGSGKSTKVPIAYYNKLQIQAGRRKNILVCEPTQATTQNVASALSHFHGKSVYFKHEGKEQHGDSSIQVMTYGSAFFKSVNNP   795
Crow-dipper mosaic virus (QGV12925.1)                  WSQVVGQTGSGKSTKVPMSYYNTLQTIAGRRKNILICEPTQATTQNVAAALSHFHGKSVYFKHEGKEQHGDTSIQVMTYGSAFFRSINNP   795
Alpinia oxyphylla mosaic virus (AWO77093.1)            WTQVIGQTGSGKSTRVPIAYYNRLQHLPARRRSILVCEPTQATTQNVSYALSHQHGKQVFYQHEGKTQNGDSSIQVMTYGTAFFKAMNSN   798
Cardamom mosaic virus (YP_009508901.1)                 WTQVVGQTGSGKSTRLPIAYYNRLRHVAARKRAILICEPTQATTQNVAYSLSHQHGKQVYYQHEGKIQNGDMSIQVMTYGTAFFKAMSAD   798
Yam chlorotic necrosis virus (AZQ00683.1)              WSQVVGQTGSGKSTRVPLAYYNKLQTMPGRARSILICEPTKATTQNVASAISHQHGKQVYFKHEGKEQTGDPTIQVMTYGTAFFRACNNP   801
Chinese yam necrotic mosaic virus (YP_006590058.1)     WSQVIGQTGSGKSTRVPLSYYNKIQTLPGRNRSILICEPTKATTQNVAAALSTQHGKQVFFKHEGKEQAGDPTIQVMTYGSAFYRSCNNP   800
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   WSQVIGQTGSGKSTRVPLSYYNKLQTISGRCRNILICEPTKATAQNVAAALSTQHGKQVFYKHEGKEQAGDPTIQVMTYGSAFYRSCNNP   800
                                                       *. * * *******::*: *:  ::    * : **:***::**. **: .::   *:.*:::*. : * *.  *******:*: ::

Striga-associated poty-like virus 1                    NFLNSFDAVFLDESHIVSEHGLTLEALLDGYRHVRKFYVSATPRAGPFEDNGHKRFQTQRVDVENSDPNYWLKEQGRGTAYDVTKRGPVV   825
Bellflower veinal mottle virus (YP_009508455.1)        HFIMQFDAIFFDEAHFVSAHALTLESLSKQYPEVRKFYMSATPRVGVTPHQAKGRFNTEVREVENTDPNFWLKEQGTGSRYDVTSLGPVI   834
Artichoke latent virus (YP_009129267.1)                TFLDDFDAVFLDESHLITPHSLALESLLNKHTKVRKFYLSATPRNGISCDDVARRFQIYEHTVEKCSVDEFIAQLDKGTATDPMKYGDKV   889
Narcissus latent virus (QDC21212.1)                    TFLDDFDAVFLDESHLISPHSLALESLLNKHTRVRKFYLSATPRNGILCDDVKRRFEIHEHAVEACDLEQFIMQLGKGTATDPMQFGDKV   888
Broad-leafed dock virus A (YP_009507671.1)             SFLSSFDAVFLDESHLISPHSLSMEGLLNKHTEVRKFYLTATPRDRTLQQTVNRRFQIFEHQVEKADVAEFIAALNGKTNLDALQYGERV   885
Crow-dipper mosaic virus (QGV12925.1)                  GFVDGFDAVFLDESHLVTSHSLAMEAILNKHTTVRKFYLSATPRIPVDVTHQDRRFQIYEHTVEKADVSDFIAALNGKTILDALEYGDKV   885
Alpinia oxyphylla mosaic virus (AWO77093.1)            EFIEKFDAVFLDESHLISAHSLAFESYLNKCTTVRKFYLSATPRTSCSMPDASRRFEIYEHSLPETDINTFVASIGKGDSLDALNYGEKV   888
Cardamom mosaic virus (YP_009508901.1)                 TFIQQFDAVFLDESHLITAHSLALESYLNKCVSVRKFYLSATPRNHVPTNAIVRRFQIFEHAQPEVSIEAFISSIGKGDSLDALNYGEKV   888
Yam chlorotic necrosis virus (AZQ00683.1)              VFLDGFDAVFLDESHLISAHALALESLLNKQTHTRKFYVSATPRRQVNQPQGTRRFQIFEHHVETADLNDFISSLGKNGNLDATQFGDKV   891
Chinese yam necrotic mosaic virus (YP_006590058.1)     AFLSNFDAVFLDESHLVSAHALALESLLNKNNRVRKFYLSATPRKQFPEMTGSRRFEIFEHQVESGDVNDLISAIGKGTIMDATKFGEKV   890
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   AFLSNFDAVFLDESHLISAHALSLESLLNKNNRVRKFYLSATPRKSFPQQTGTRRFEIFEHQVESGDVSDLISAIGTGSILDATKFGDKT   890
                                                        *:  ***:*:**:*::: *.*::*.  .    .****::****          **:         .    :   .     *  . *

Striga-associated poty-like virus 1                    LCFVQGRGQADKLAAKVNNSSIRDEKGEKFTGYSLHSENFDDNYPKVIKASNEGETCFIFCTNILETGVTLSADCVVDFGSTMRPELDIM   915
Bellflower veinal mottle virus (YP_009508455.1)        LCFVQGKRQADTLASKVNASG-----KIQFKGISLHSDNFDNNYNLVVKATNEGEECMIFCTNILETGVTLNADCVVDFGFTMRPSLSVA   919
Artichoke latent virus (YP_009129267.1)                LVFLAGKGECDKAASKVMSTN------LGIKAVSLHKSNFKTNYVKVMNSVDGGDRVIIFATNILETGVTLNVDVVVDFGFTNSPVLDLT   973
Narcissus latent virus (QDC21212.1)                    LVFLASKSECDQAASRVMSMN------LDVKAMSLHKDNFKTNYLKVVAAMDESAKVMVFSTNILETGVTLNVDVVVDFGWTNRPHLDLT   972
Broad-leafed dock virus A (YP_009507671.1)             LVFLSGKNECDRAAAKVAGGV------RGVKSVSLHKDNFKANYQKIIDQLERDEQFVIFTTNILETGVTLNVDVVVDFGYTNSPVLNLV   969
Crow-dipper mosaic virus (QGV12925.1)                  LVFLSGKNECDKAAAKVNGGV------KGVSAISLHKDNFKINYAKVCQQLEMDGKYMIFATNILETGVTLNVDVVVDFGYTNVPDLNLS   969
Alpinia oxyphylla mosaic virus (AWO77093.1)            LIFLSGREQCNKAAHKTASTQ------YGITAFSLHKENFSVNYSKILQALSQPGRVYIYSTNILETGVTLNVDVVVDFGYTNQPHLDLN   972
Cardamom mosaic virus (YP_009508901.1)                 LIFLSGREQCNRAAMKTAATQ------YGIRAFSLHKENFPSNYPKILDALSAPGRCYIYATNILETGVTLNVDVVVDFGFTNQPKLNLT   972
Yam chlorotic necrosis virus (AZQ00683.1)              LVFLSGKKECDRAAARVCAEV------SSLKAISLHSQNFETNYERICDQLNQPGKLIIFCTNILETGVTLNVDVVVDFGFTNTPSLNTV   975
Chinese yam necrotic mosaic virus (YP_006590058.1)     LVFLSGKKECDRAATKVNSTN------SGVKAISLHRDNFSANYNRLCHDLTQPGKIYIFATNILETGVTLNVDVVVDFGFTNTPVLNTS   974
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   LVFLSGKKECDRAAAKVNSTN------TRVKAVSLHRDNFSTNYNRVCDELNQPGKCYIFATNILETGVTLNVDVVVDFGFTNAPTLNTT   974
                                                       * *: .: :.:  * :.            . . *** .**  **  :           :: **********..* ***** *  * *.

Striga-associated poty-like virus 1                    TKRLSLNAHRVTQFERHQRIGRVGRVKDGFALCCGKAVHGRPRTPPEVVYGAALYSFVYDLDLFADESLDTSWLANITKKQAEVMLSFDL  1005
Bellflower veinal mottle virus (YP_009508455.1)        EKRCLLTSSRVTQHERLQRIGRVGRVKDGVALTCGKCLPGRPPISPDVVYEAALYAFLYDLDLYADSTLDTNYLGNITRQQAEVMLNFDI  1009
Artichoke latent virus (YP_009129267.1)                GKTFLLERRRVTQAERKQRIGRAGRLRDGHAIVIGKVGRTEELVSADVVYEAALISFVYNIDIYINSHFDHVWIGNVTRQQAKTMINFRL  1063
Narcissus latent virus (QDC21212.1)                    EKTFLLHRQRVTKAERKQRIGRAGRLKEGHAIVVGTVSHNVELAPADVVYEAALLSFVYNLDIYVNSHFDSVWVSNITRAQARTMLNFRI  1062
Broad-leafed dock virus A (YP_009507671.1)             EKTLLLRKRRVTDAERRQRIGRAGRLRDGHAIVVGKTVQATELVAADVVYEAALLSFVYNLDVYINAHFDHSWLAGITRAQAKTMLAFRM  1059
Crow-dipper mosaic virus (QGV12925.1)                  DKTLLLRKRRVTKAERQQRIGRAGRLRDGHAIVIGKTTEPMEIIPANVVYEAALLSFIYNLDIYINTHFDHTWLSSITRAQAKTMANFRV  1059
Alpinia oxyphylla mosaic virus (AWO77093.1)            ERTLLLQKRRVTESERKQRIGRAGRLKHGHAIVLGKTSRAIEVVTADVVFDAALLSFVYNLEVYVNTHLDSTWLAKITREQARTMLSFRL  1062
Cardamom mosaic virus (YP_009508901.1)                 ERTLLLEKRRVTEAERKQRIGRAGRLRDGHAIVLGKTCQAIEMVTPDVVFDAALLSFVYNLEIYVNAHLDCEWLATITREQARTMLNFRL  1062
Yam chlorotic necrosis virus (AZQ00683.1)              DKTLLLHKRRVTKSERQQRIGRAGRLRNGHAIVIGKVSEPIETVSAEIVFEAALISFVYNLDVYVNSHFDAAWLGSITKEQARTMLSFRV  1065
Chinese yam necrotic mosaic virus (YP_006590058.1)     DKTLLLNKRRVTQAERKQRIGRAGRLREGHAIVIGKTSTPFETVSADVVFEAALLSFIHNLDVYVNAHFDQAWLSSITRDQAKTMMAFKI  1064
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   DKTLLLTKRRVTQAERKQRIGRAGRLKDGHAIIIGKTSTPFEVVSADVVFEAALLSFIYNLDVYVNAHFDQAWLSSITRDQAKTMMAFKI  1064
                                                        :   *   ***. ** *****.**::.* *:  *.        ..::*: *** :*::::::  :  :*  ::. :*: **..*  * :

Striga-associated poty-like virus 1                    PIFVLRDLVGKDGAMRGEMITALKKNLLRDMHIVSRDISVASDRWQSWPRAHDQILNMTHGDVPEELEKYKNSRIPFVSFTLNKVSIVEF  1095
Bellflower veinal mottle virus (YP_009508455.1)        PMYVLRDLVDKDGSMQPIMVSLLKNHVVGDTQITTRDVRVSADKWASWPNAHDLIMLCLRGSEDEEMMKLAKEKIPFCAYQLLDVDLKSF  1099
Artichoke latent virus (YP_009129267.1)                PSFAMKDVVFPDGSVRDEFLRAVKDRTNRSANIKTLQGCTINPVYEGWPVLGTYAQKFGIAFEDSRYNNLSKMRVPFIFHDMNELDIEAY  1153
Narcissus latent virus (QDC21212.1)                    PSFAMKDVVFHDGSVRTEFLEQMKSYTQRSANIKTTTHCTINHVYDTWPLLGTYAQKFGISFDDARYRKFSKLKVPFIYHEMGSMDLEGY  1152
Broad-leafed dock virus A (YP_009507671.1)             NSFFMRDLVFSNGSVRPELLQALKNNVQRSSNIKTATMQCVSHVYESWPMLGAHA------PVDNLDEKLVKSRVPFITHDLFEMQVEEL  1143
Crow-dipper mosaic virus (QGV12925.1)                  SPFVMRDLVFADGSVRPEVLSLFKKETMNSTSIKTRSATHVSHITEAWPKLGAHI------PQGETFNPLSDKRVSFITHDLLEMDLDEV  1143
Alpinia oxyphylla mosaic virus (AWO77093.1)            STFFMRDLVNSQGHIRPELLDALKNKTWRSLKAHTTMFQARNSEYQQWQRLDHYSFSTLVLNNERILSEVGHVKIPFITHDMMDFDIIEI  1152
Cardamom mosaic virus (YP_009508901.1)                 SVFFMRDLVNKQGNIRSELLQAVKNKTWKSLKVHTTNFQANNREYQQWNRLDHYTLTNFCAENSQAFGEISHIRVPFITHDMLDFDLVEI  1152
Yam chlorotic necrosis virus (AZQ00683.1)              SPFIMRDLVFPSGHVRQEMLNCLKNKLQRSASIKTANYTCVNHIFESWPKMDHPFISTIVQNEPNSLERLSKLRTPFVTHDMGELNLEEF  1155
Chinese yam necrotic mosaic virus (YP_006590058.1)     SPFIMKDLVFANGHIRSEMLEFLKPHLHHSANIKTTNYQCVNHIYESWPRLDHHSLIDSMQNNEEKTKKIHKMRTPFITHDLNQLDLEMF  1154
Yam chlorotic necrotic mosaic virus (YP_009507672.1)   SPFIMKDLVFANGHMRGEMLDFLKPHLHHSANIKATNYQCVNHIYESWPRLDHHSLFLDSQAHDSEVKRLSKMRVPFITHDITQLNLEQF  1154
                                                         : ::*:*  .* ::  .:  .*     .    :            *                       . : .*  . : ...:
```

```
Striga-associated poty-like virus 1                   VEAAATYEPKLSFKTTKLGPPTRRVLMRIDPDNINQCHQIAVCLREHLKGMLNALVEARVRVQESKLLCMF--PASKRLLSDQEKRIAVM  1183
Bellflower veinal mottle virus (YP_009508455.1)       TECCAKYEPYRAFQTITAKSMNKKVLLRVDPENINICHSVASALLKQQNDVLSSLLNMQTACRDSKLLSCF--RQTRRFMSDHQNRIEAT  1187
Artichoke latent virus (YP_009129267.1)               AEAAASYKPSMLTRWAKPAKEVSNVILHVNQKNVCEAIGVVRSLIASTKSLIQSKKHNQNLHRESPLACLFTKRTTLELESKLGEQIKLG  1243
Narcissus latent virus (QDC21212.1)                   AEAVSSYKPSMITQWAKPAKEVANVILHVNNQNVHEAINVVRSLIVSTQAQILSKRHAQNLHRESPLACFFAKSTTMELEARLGEQIKLG  1242
Broad-leafed dock virus A (YP_009507671.1)            AKAAQAYRSTVKSRWGKPVKEAANVIMHANQSNIHDAIRVAQSLRNEAQRQIQEKERVQNLHRESPLACLFSKDTVRGLDXKIGEQIQMA  1233
Crow-dipper mosaic virus (QGV12925.1)                 TKALAAYQSTVKERWGKPIKEAMNVIMHVNQENIYETLAVARVMRSEAVKSMQQRQNTIKLHRNSPLSCLFGKKTIQQLEEKLGQQVRLA  1233
Alpinia oxyphylla mosaic virus (AWO77093.1)           VKAVANYKPNMLTVFGQPKPRNIGLIMRVDETNVFNTMRMARLLKSDYEQQILNKKAALQAQKESPMAYFLSTRVVDSLASKLSQQISQA  1242
Cardamom mosaic virus (YP_009508901.1)                AKAVAHYKPNMMTVFGSKPAKGVSLVMKVDETNVFDTLRVARLLKRDYENQISSKKTAINTQRESPISYLLSTRIVDDLTAKLTQQIQRA  1242
Yam chlorotic necrosis virus (AZQ00683.1)             LRCADLYKPSVLTRWGRPVKQSTNVLMHVNSNNVHETIRVATLLRHDYSQQIHMKQHAQQLHQNSPFAYFFSKKTVDELSTNIGKQIAIA  1245
Chinese yam necrotic mosaic virus (YP_006590058.1)    ANCVEKYRPNVLTRWGRPVEQTTNVLMHVNQENIHATIRIANLLRYDYQQQIQQKKQAQQLHKDSPFAYFFSSKVVDELASNIGKQVAMA  1244
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  TNCVEKYRPSVLTRWGRPVEQTTNVLMHVNQENIHSTIRIVNLLRFDYQQQILQKKQAQQLHKDSPFAYFFSTKVVNELENNIGKQIAMA  1244
                                                       ..   *..               :::: :  *:     :.  :       :          ::* :   :       :     :::

                                                                                                 CI|6K2
Striga-associated poty-like virus 1                   KRNIQEVDKHIGKLTMYDTFVRDCNVPESFDMAEFQKVHQHMELQ|ARGNNNETELKKVLDMKHSDELKVRDVLVHHSGKIALGMVAMSG  1272
Bellflower veinal mottle virus (YP_009508455.1)       KRNVSKIRDHLAKLERYDTFVRDKEINGEFSHADFGSVFDHMSLQ|MRGEANNNEVRKILQLEDNAQVNVSDLFIHNGDKIAIGLLATTG  1276
Artichoke latent virus (YP_009129267.1)               ERNLVKLTKLLGNLELFMNLDEMKDEEPELSSGDMEEIGRVLELQ|MQTTCNEDHIATVLHLEELPSTTFREAIVIGRKRVACALVLMCI  1332
Narcissus latent virus (QDC21212.1)                   ERNLSKLKKFASNLELFANINVMQDTELELTSSDMEEIGKVLELQ|QETTCNEGHVQKVLHLEDMPSTSFREAIVVGRKRVAVALTLMCI  1331
Broad-leafed dock virus A (YP_009507671.1)            RRNIEKLDKFISTLEIFAASQEVGGE-MEITSEDLSDIGRCMELQ|MDTTCSNEHIQEVLGLEELPSVTFKDAIILGRQRVATAMMILCV  1321
Crow-dipper mosaic virus (QGV12925.1)                 QRNLTKIDKFIGSLEMFATVNEHTDEGFEVTPEEMDNIGACMELQ|MNTTCNEEILQKVLKLEELPSVSFRDAIIVGREKVMVATMILCV  1322
Alpinia oxyphylla mosaic virus (AWO77093.1)           ERNIVKLTTFITNLEIFMNTANSNVE-QDMQTDDLEEIGRSMQLQ|MDGNLTRHALTNILKLEDIPNVSFREAILIGNKRSLIALSFLVC  1330
Cardamom mosaic virus (YP_009508901.1)                ERNIRKLDGFITNLEVYANAPLPNEP-AVMGHGDYEEIGRCMQLQ|MEGKLTRESMIESLQLEDIPNASLKDAILLGNRRSILALSFLAC  1330
Yam chlorotic necrosis virus (AZQ00683.1)             QRNIQKLDRFISNLEIFVTMNEVDGD-IELTQQDMHEIGQSLDLQ|ADGKFSRDTLCDTLNLESLPSTTFRDAVVIGRKKAIWAIMILCC  1333
Chinese yam necrotic mosaic virus (YP_006590058.1)    QRNVSKLDKFISRLEMFATMNEMAGD-VEVTQQEMHEIGQCLDLQ|AEGTFSKDNMNVILSLETLPQTTFRDAIIIGRKKAIWGIMILCC  1332
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  QRNVAKLDKFISRLEMFATMNEMADD-VEVTQQEMHEIGQCIDLQ|AEGSFNKENVNVILNLERLPQTTFRDAIVIGRKKAIWAVMILCC  1332
                                                      .**: ::      *  :            .   :  .:   :.**      ..  :   * ::   . .. : .:    :   .

                                                                                       6K2|VPg
Striga-associated poty-like virus 1                   AYLLSSLLHAL-------------RSKEPDAVYTLE|GKGKPY-NRSKRSEAVALNQAFDM----------FEELKQRKEKRVHHKERPS  1337
Bellflower veinal mottle virus (YP_009508455.1)       AYILGQIYAML-------------RTTETITASSLE|GKGKPIRNRDKRSEARAVNESFNFIE-RMRAESETQTVKKRRDKGK---QQSD  1348
Artichoke latent virus (YP_009129267.1)               AAFGGLAWYYLWDDDTGLDNKWNKKNKKAVLKDVLE|MKGKSF-NRDKRSA--TAYEKILKDSYEGEDNYNLDEFRTRRKGRA--DADKT  1416
Narcissus latent virus (QDC21212.1)                   AAFGGLAWYYLWDDDEGLDNKWNKDNKRAVLKDVLE|MKGKAF-NRDKRNP--AAYEKILHDDFAGDSLEDLRPFQKMKGKKK--GKPQT  1415
Broad-leafed dock virus A (YP_009507671.1)            AAFSGLAWWYMWSDEDGLDNDYNKKNKKQVYEEILE|MKGKSF-NRDKRMP--AMQEHKDMADDYIENNPDIEKFKSKRETKHR-SDGGA  1406
Crow-dipper mosaic virus (QGV12925.1)                 AAFSGLAWWLMWDEDGGLDNEYNKEQHESVYTKVLE|MKGKAF-NRDKRSE--ASLLAYEKADVYGENLQDVQMFKSKRGKSKKMHDDSK  1408
Alpinia oxyphylla mosaic virus (AWO77093.1)           SAFAGLAWYLTWDFDEGLENSYNKRQRVAVHNKVLE|MKGKGL-NRDKRNV--AMQETYDEAYTSIRDDEDFDRVRSRRQRAK--ETDIA  1414
Cardamom mosaic virus (YP_009508901.1)                GAFAGLAWYLTWDDNEGLNNKWNKKQRVAVHKEVLE|MKGKHL-NRDKRNV--ALQDTFDEAYTAIRGDEDFERVRSRRKGAK--EKDIA  1414
Yam chlorotic necrosis virus (AZQ00683.1)             AAFGGLVWWLMWDDDDGLNNEENKQRRKAVCDEVLE|MKGKSF-NRDRRNP--MMQDTIDMADFYMRDNEDFVKLKKKNNNARDDSHKG  1419
Chinese yam necrotic mosaic virus (YP_006590058.1)    AAFGGLAWWLLWDDDEGLNNDENKDRRNEVCSKVLE|MKGKSF-NRDRRNP--MMQDHFDAADFYMRDVEDFASLRSRRKVSR-VDDAVS  1417
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  AAFAGLAWWLLWDDDEGLNNTENKERRDEICNHVLE|MKGKAF-NRDRRNP--AMQDHFDTADFYMRDDEDFQTLRSRRKTSSGPNDAIS  1418
                                                      . : .                             **  ***   **.:*                         .:  :

Striga-associated poty-like virus 1                   VVSNLLKKTNP-FVNFYDIADDSAVTEAVFKMLDGSVVHKTTTPIADIPNLGRIIAEREMDDSQPVLSWADEAERVDPDQLICEVTLKDG  1426
Bellflower veinal mottle virus (YP_009508455.1)       AVSRLLTKTNP-FVNFYDIA-DADVETAIFSTLKGKVIHETATPVSDVKRL-DLISTNVDGDGEPIN-LSDE------DDLMCYITLKDG  1428
Artichoke latent virus (YP_009129267.1)               PFENLMTKAAP-FITMYDITSDENVVNAVFMDHNKQAFYETADPLKNMGEVKKHLEQMKLKQPV-FK-WGDEAD----DDVFCDVTTRDG  1499
Narcissus latent virus (QDC21212.1)                   VFENLMTKKGP-FVTMYDVTSDENVVNAVFLDTNKQAFYETGNPLANMKNVRSHLEDHLHNKST-GL-WSEIDD----DEIFCDVTKKDG  1498
Broad-leafed dock virus A (YP_009507671.1)            PLDRFMSKGPMVFKNFYDIASDEEVAKAIFSDENNHVFYETANPLKHMKEVEKHLNAHKATSNL-LA-WGDEAN----DLIYCTVTKNDG  1490
Crow-dipper mosaic virus (QGV12925.1)                 PLNKFLNAEPP-FISLYDITTDDNIVSAVFQDTNRQAFYETANPLAHMKEVEEHLQKHIEKGEL-IQ-WADAAD----DTVYCVITKNDG  1491
Alpinia oxyphylla mosaic virus (AWO77093.1)           PVMRHMRSEKP-FITLYDLTLDSDITHAVFSDHNSQAFYETANPLANLDKVKQHLEEHRQGEKI-IF-WSDMTD----DTIFMTITKKDG  1497
Cardamom mosaic virus (YP_009508901.1)                PVMRYAQQKRP-FLTLYDLTLDEDITHAVFADHNNQAFYETANPLANLKDVETHLQSHKDKGGV-VF-WSDYAD----DTIFMTITKRDG  1497
Yam chlorotic necrosis virus (AZQ00683.1)             LVQRMMSQSKP-FITLYDINNDADIVNAVFMDHNKQAFYETANPLKNMEQVRQHLDDHKAKEGGQIF-WGDDAD----YTLFCNITKRDG  1503
Chinese yam necrotic mosaic virus (YP_006590058.1)    PVLRYAAKSRP-FITLYDINVDSEVATAVFQDHNGQAFYETANPLKNMDLVREHLNKHKAKDGTQIF-WSDESD----FDIFCKITKTDG  1501
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  PAMRYAMKSRP-FITLYDINVDSEVASAEFQDHNGQAFYETANPLKNMNLVRKHLEEHKQKNGTQLF-WSDESD----FDIFCKITKTDG  1502
                                                         .        * .:**:  *  :  * *   .  ..::*  *: .:  :   :              .:         :   :*  **

                                                                                                   VPg|NIa-Pro
Striga-associated poty-like virus 1                   RRVHVDMTKHKSRMMTRTGGLAGYENKDGQFRQVG--------STRLE|VASSVPFSKINIALGRMVGTIADGSRVRLNAILYGDFIICP  1507
Bellflower veinal mottle virus (YP_009508455.1)       RDVMVRLDRHRSRQLTRTGGLMGYPNRDGEFRQVG--------TTKIE|MKGPIPFTNISTKCVNMVGLIYANGRPVMNCVLYGDFIVCP  1509
Artichoke latent virus (YP_009129267.1)               TTIRVRLTPHSSQRLTSTHGVQGYAQDEGRYRQTGDAEVLKMPTQHLE|VDTRLADNMVNLDVGNMIGLVSVKGG-NANCLLYKDWVIMP  1587
Narcissus latent virus (QDC21212.1)                   MVIRIRLTPHKSMRLTSTSGRQGYSEHDGDFRQTGDAEILKQPDQILE|VDTRLSNNHVSVEAGAMIGITTLQAG-SMNCILYKDWIILP  1586
Broad-leafed dock virus A (YP_009507671.1)            SVYRVRLTPHNPHRLTKHHGVQGFENKFGIFRQSGQTEVLQRPQQELE|IATHLQTSQVNLDVAKMIGTVTVDGG-LICCILYKDFLVMP  1578
Crow-dipper mosaic virus (QGV12925.1)                 TVMRVKLTPHQPNRVTNTFGTMGYHNKAGQYRQTGPTEILKHPPHSLE|IATHLQTNQINLDVGSMIGIAEAGGG-QINCILYKDFIILP  1579
Alpinia oxyphylla mosaic virus (AWO77093.1)           SQQRVKLTPHASQRKTKTGGVQGYASHEGEYRQTGDVEILKQPTQVLE|IGTQLTNNQANLDILNMIGHVNIETG-RLHCILYKDFIIMP  1585
Cardamom mosaic virus (YP_009508901.1)                TVQKVRLTPHSSERTTRHGGQQGFKEHEGQYRQTGDVEILKQPQQTLE|IDTRLSNNNTNLEIMNMIGHIQIGEG-RLHCLLYKDFIIMP  1585
Yam chlorotic necrosis virus (AZQ00683.1)             SVLRVKLTPHIPSKSTTSGGAQGFQNKADCYRQTGETEVLVQPTQALE|IDTRLPVNNINLDVANMIGKVRMANG-TLHCILYKEFVILP  1591
Chinese yam necrotic mosaic virus (YP_006590058.1)    TIMKVKLTPHEPLRMARR-GTQGFVEKEDCYRQTGQAEILQHPGVNLE|MATRLPENKLNLQVADMIGKVSMSEG-TIHCILYKDFILMP  1588
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  TVMKVKLTPHEPTKRSKH-GTQGFSNMEDCYRQTGQAEILHHPTQALE|MATRLPDNKTNLQIADMVGRVTMSEG-TIHCILYKDFIIMP  1589
                                                          : :  * .   :   *  *: .  . :** *           :* :   :  .  .     *:*           .:** :::: *

Striga-associated poty-like virus 1                   AHTQVLSLPITFRFEHATCTVDHV-EAMKFEKCDLILIKRPNSIAPVKVVSKATTITEPTLIQIIYRDLGSFSCHVSASDLAVPFDNGRF  1596
Bellflower veinal mottle virus (YP_009508455.1)       AHIKLVGPELKFRFQHATCTF-VVDEYMAFTQCDLILIKRPREIAPVAVIAKCGVLTEPSYVQLAYRNQQNLDGTLSASDICTPFDNGRW  1598
Artichoke latent virus (YP_009129267.1)               AHVMMCKLPITLTFKHYTVTLSTLPECYSFVGFDLLAIKRPSTLAPVRCSATLESAKSGMTVQMLYKKPVINKTLMTVTDVAYKTKEHRW  1677
Narcissus latent virus (QDC21212.1)                   AHIMMRPLPLTFAFKHYTCTISELPECYSFIGYDLLVIRRPRNLAPVRCYATLDFAKDGMTIQMMHKKPVVNKVLMTVTAEAYRTPEHRW  1676
Broad-leafed dock virus A (YP_009507671.1)            AHVMMKKLPMRISFSHCTVVVTELPEMYSFIGYDLVLVRRPSELAPIKCQAHCGTAHDGMLVQMIYKKPVTNKVVPTITAPIHQTKEHRW  1668
Crow-dipper mosaic virus (QGV12925.1)                 AHVMLKSLPIKFTFKHAHVIVSELPQAYSFPGFDIIVVKRPTTLPPVKCVAYCGIAHENMVVQMLYKKLVSHKLVTTITAPIHQTKEHRW  1669
Alpinia oxyphylla mosaic virus (AWO77093.1)           AHVMQKELPITLSFKHYTVKVEELGEVYAFVGFDLILMKRPHQLAPVKCVASISQAQEAMIVQMVHKKFVTLKPVITITAAIHQTKEMRW  1675
Cardamom mosaic virus (YP_009508901.1)                AHVMQKPLPLTISFKHYTVKIPELQEAYAFEGFDLLCIKRPPQLAPIKCSASLATAQEGMIVQMLHKKFLTNKPIITVTAPIHETSELRW  1675
Yam chlorotic necrosis virus (AZQ00683.1)             AHAMMSKLPIDLVFKHKTITISEFPEAYCFPGFDIMLIKRPTSLAPVACRATVAQASDGMIVQIVHKKHVTEKTVLTVTAPTHQRDDFRW  1681
Chinese yam necrotic mosaic virus (YP_006590058.1)    AHAMIKQLPMEISFKHFTITIDTLPEAYCFPGFDIVLIKRPAKLAPVRCHATLAQATDGMIVQMVHKKSVSDKTVLTITAPIHQRDDWRW  1678
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  AHAMITKLPMEITFKHYTIKIGTLPEAYCFPGFDVMLIKRPTNLAPTRCHATLATATDGMIVQMLHKKSVSDKTTLTITAPIHQRPDWRW  1679
                                                      **       : : *.*    .  . :   *   *:: ::**  :.*    :      .   :*: ::.    .   : :       : *:

                                                                                                                                      NIa-Pro|NIb
Striga-associated poty-like virus 1                   SYSVSTKDGMCGAAIVDVKTGMITGIHVSANDLIKRNFMEPFSTSMVDVLQKKAPFVRDE-------VWYFDSIASGYAPHELDRLQ|S-  1677
Bellflower veinal mottle virus (YP_009508455.1)       TYTISTKKGMCGAAVIELKTGKFVGIHVSANEVIRRNFMEPISESMVQVLQKKEDFIPSR-------DWTFTSTECGYMPGEISGLQ|AN  1680
Artichoke latent virus (YP_009129267.1)               EHQIPTIYGMCGAPMLDVSSGKIVGIHILGDTARKCNTFEGFPPDMLKLVNSNDPKVRNLFVRERVKTWEFVPEMHGHNSARIKNLQ|I-  1765
Narcissus latent virus (QDC21212.1)                   EHQIPTAAGMCGSPVFDVASGKIVGIHILGDIMRKRNTFEAFPGDMMKLVNSNDPKIKDLYIKNRLREWNFEAEVHGHDSRRLINLQ|G-  1764
Broad-leafed dock virus A (YP_009507671.1)            AHQIPTHNGMCGCPVLDVVTGKIVGIHVMGDLAKKHNVFEAFPSEAITIMGTNDRKVHASYFRNKVNMWVFQPEMHGYLAKNLVNLQ|M-  1756
Crow-dipper mosaic virus (QGV12925.1)                 AHQIPTENGMCGCPVLDVATGKIVGIHVMGDHRMKHNVFETLPPEVLTLIQTNDKKVHQTFHRNQLKAWVFQPEMHGYLSKNLTNLQ|MN  1758
Alpinia oxyphylla mosaic virus (AWO77093.1)           AHQIPTIVGMCGAPVLDTQTGKIVGIHVMGDTLKKHNVFETFPSEALEILGTNDKKVHQRYFNNRLKAWKFQPEVHGYDPRKIQGLQ|N-  1763
Cardamom mosaic virus (YP_009508901.1)                AHQIPTVVGMCGAPVVDTQTGKIVGIHVMGDSFKKHNVFETFPSDALEILNTNDKKIHQRYISQKIKIWTFIPETHGYDPRKIQGLQ|M-  1763
Yam chlorotic necrosis virus (AZQ00683.1)             AHQIPTVAGMCGAPVLEVATGKIVGIHVMGDTFMKHNVFETFNNDIMTLMNTNDKKIISTFQRSKLTSWTFMPEVHGYDPKKLKNLQ|H-  1769
Chinese yam necrotic mosaic virus (YP_006590058.1)    AHQIPTVSGMCGAPVIDVASGKIVGIHVLADSLKMHNVFETFPSQLLEIINTNDKKVHQRYHQARVNDWTFLPEAHGYFPSELVGLQ|M-  1766
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  AHQIPTVSGMCGAPVIDVASGKIVGIHVMADSLKMHNVFETFSPDMMEILNTNDKKVHAKFHQARLMDWVFLPEAHGYEPSKIKGLQ|M-  1767
                                                       : :.*  ****..:.:  :* :.***: .:     * :* :  . : :: .:   :           * * .   *: . .:  **
```

```
Striga-associated poty-like virus 1                   YE-----------------------WA-L------------------EF--DPLRYSVEKMNESAGAWGMFNNYHRVSEAQRPVTFSLSG  1723
Bellflower veinal mottle virus (YP_009508455.1)       YQ-----------------------WD-L------------------EF--DDSRYTIGNMNETASAWGFIKNHHQVEPCSESLNLSLHG  1726
Artichoke latent virus (YP_009129267.1)               DT-----------------------IEFR------------------QFTRDTSIYTVENLTRSAAAGGLFK--PREVMEKRSLPPTVSA  1812
Narcissus latent virus (QDC21212.1)                   DS-----------------------LPIS------------------KFSRDVSIYSVENITRSAMAGGLFK--PREVSEPRNLPPTVST  1811
Broad-leafed dock virus A (YP_009507671.1)            -------------------------MELK------------------TFSRNIEIYTKEKFEKSANCGGLFK--HREIFGPRDSEFLHQF  1801
Crow-dipper mosaic virus (QGV12925.1)                 DTSIKEEIDEMIKNAQLNERLRTMRFDLLFQIDRAHCGVIDNNVVIKTFSRDTSIYKIENFRRSAECGGLFK--PREITKAISNKIIDES  1846
Alpinia oxyphylla mosaic virus (AWO77093.1)           ED-----------------------FSLE------------------TVPNDVSMYTIENIMEDAAAGGLFK--PREVRDAERLPIGIVA  1810
Cardamom mosaic virus (YP_009508901.1)                LK-----------------------VESL------------------RVPKDTSMYTIENFVQEAQAGGLFK--CREISAPRPLPIGVSA  1810
Yam chlorotic necrosis virus (AZQ00683.1)             EQ-----------------------FEFL------------------EFSRDTSIYTVENMNADARAGGLFV--PRVLENPRSLPPSVSA  1816
Chinese yam necrotic mosaic virus (YP_006590058.1)    ES-----------------------FEFI------------------EFSRDTTMYTVDNFNRDATAGGLLK--SRVVEESKTLPVGVSA  1813
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  EI-----------------------FNFL------------------SFPRDISMYTIENFNADATAGGLLK--ARKVEEPKEMPLGVSA  1814
                                                                                                      .  :   *.  ::   * . *::    :

Striga-associated poty-like virus 1                   GGFEILGEATSNLCNKHKIVGESVYWKEFKQCCPDLVEGIEEYEDAYCPSALNREAYYKDVGKYDR--HLRCRADINLLIKARNMVKDDL  1811
Bellflower veinal mottle virus (YP_009508455.1)       -GFEMLGKSVSHLCSKHKIVGLSPYWQEFKQLCPDLVEGIEELEDQYAPSALNRDAYYKDISKYNR--DLACKCDIQRLEKAREMVAHDL  1813
Artichoke latent virus (YP_009129267.1)               IHMHNLAYSNGLLNTRHIFEGENPYWKQFKLCNEWVDPIVERYEDNYMPSALNREAYWKDLLKYNR-PQHLCKVDDVALKSSVAQLVREL  1901
Narcissus latent virus (QDC21212.1)                   LHMTNVAYANGLLNTRHIFEGENPYWKQFKLCNPHLTDAVSEYEDKYLPSALNREAYWKDLLKYNR-PLHQIKPNEAALHASMVKLIRVL  1900
Broad-leafed dock virus A (YP_009507671.1)            EHFDNLAYAHALLNTRHTYVGESPYWLEFKRNHQSLVRGIEEYEDAYLPSRLTHTAYWKDLSKYNR-AYKGVDHDEKILLSAADCLIHML  1890
Crow-dipper mosaic virus (QGV12925.1)                 EHMDNMAYSHAILNTKHVYVGENPYWIQFKANHKQLVQGIEKFEDNYLPSELTYNAYWKDLLKYNR-PLKSSKHDEKALLMAIKKVVTVL  1935
Alpinia oxyphylla mosaic virus (AWO77093.1)           QDMTNLAFANALLNKRHVYIGESPYWTEFKRRHAQHVKGIHEFEDEYAPSILSYDAYWKDLLKFNRQSNATPQFDKRILNLAAQAVIRNL  1900
Cardamom mosaic virus (YP_009508901.1)                QHMQNVAFANAILNKRHTYVGESPYWREFKRIHSEHVRGISAFEDFYAPSALTFDAYWKDLLKFNRTSASDPTWNEKALKHSMLATIQAL  1900
Yam chlorotic necrosis virus (AZQ00683.1)             LHMDNLAYMNGLLNPRHVITGESPYWLEFKRFHPRQVRGIEEFENKYAPSVLNYDAYWKDLLKFNRLENANLQYDKEILKCAALAVVNQL  1906
Chinese yam necrotic mosaic virus (YP_006590058.1)    THMSNVAYMNGLLNPRHTITGESPFWREFKRCHPKQTKGIEEFENAYAPSVLSYDAYWKDLLKFNRAEFKADKIDKDILKCATLALVKQL  1903
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  INMKNVAYMNGLLNPKHTVTGESPYWKEFKRCHPRQVKGIEEFEDAYAPSVLSYDAYWKDLLKFNRVEHSKSGLNEEILRHATLCLVRQL  1904
                                                        :  :.   . *  :*   * . :* :**         :   *: * ** *.  **:**: *::*        :   *  :       *

Striga-associated poty-like virus 1                   KKAGLFATRLMTAAEVLGDLDVNTAAGALYACKKKLLFTGMTDDQVVQLANCCYDKLVKGESVGIWNGSLKDELRPVEKVLENKTRVFTA  1901
Bellflower veinal mottle virus (YP_009508455.1)       KVAGMRPTRVMDAEEVLGDLDVSTAAGALYACKKKVVFAGWDDEMLINFATLCKSKLISGENVGVWNGSLKDELRPIEKVVANKTRVFTA  1903
Artichoke latent virus (YP_009129267.1)               ERAGMTKTKIRTTDQVLEDIQWGKAAGPLYGMKKKELCKNLTMEELTSLALHCRSELNKGKNAGLWNGSLKAELRPKIKVEANKTRVFTA  1991
Narcissus latent virus (QDC21212.1)                   RESGMTSTRIRTCNEVLEDIQWNKAAGPLYGMKKEELCKNMTMEDLTALAIHCRTELRRGKNAGVWNGSLKAELRPKEKVELNKTRVFTA  1990
Broad-leafed dock virus A (YP_009507671.1)            ESAGMTPTRIRTPEEVLSDIQWNKAAGPMYGMKKRELCQHLTEEELIAMAIHCRRELVRGENAGIWNGSLKAELRPLEKVEQDKTRVFTA  1980
Crow-dipper mosaic virus (QGV12925.1)                 EQAGMRKTRIKTPIEVLSDVQWNKAAGPMYGVKKRELCMNMTEEELITMVIHSRNELVKGQNAGIWNGSLKAELRPIEKVNQHKTRVFTA  2025
Alpinia oxyphylla mosaic virus (AWO77093.1)           QQAGLTATKIRTTNQVLDDVQWTTAAGPLYAMKKKELCKDLTEEELQSLAIHVRQRLIAGKNCGVWNGSMKAELRSIEKVQQAKTRVFTA  1990
Cardamom mosaic virus (YP_009508901.1)                KDAGMVPTRVRTTFEVLSDIQWSTAAGPLYAMKKKELCKDLSTEELDALAIHVKTRLIKGENCGVWNGSMKAELRPIEKVQANKTRVFTA  1990
Yam chlorotic necrosis virus (AZQ00683.1)             KRAGMTETRIRTSEEVLGDLQWGKAAGPMYAMKKNELCKNLTDEELTTLTIHCKKQLIEGRNCGVWNGSLKAELRTKEKVSQNKTRVFTA  1996
Chinese yam necrotic mosaic virus (YP_006590058.1)    KDSGMQQTKIRTVEEVLDDVQWGKAAGPMYAMKKLELCKDLSEEDLTALAIHCRTQLLKGKNCGIWNGSMKAELRVVEKVLQKKTRVFTA  1993
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  KEAGFKPTRIRTVEEVLSDVQWGKAAGPMYAMKKLELCKDLTEEELVSLAIRCRTQLKRGHNCGVWNGSMKAELRTIEKVLQKKTRVFTA  1994
                                                      . :*:  *::    :** *::  .***.:*. **  :      : :  :.     .*  *.. *:****:* ***   **   *******

Striga-associated poty-like virus 1                   APLTTLIGGKFVVDDFNKQFYGTHLNARHTVGINPWAGGWHRLAQFLGGQDMPYYVSGDGSRFDSSLDPILFDQVLKLRLELM--PDVNG  1989
Bellflower veinal mottle virus (YP_009508455.1)       APITTLVGAKFFVDDFNKQFYTTHLKARHTVGINPWEGGWNRLADFLGGSQMPLYVSGDGSRFDSSIDPLLFDQVLKLRLQFS--DQSDD  1991
Artichoke latent virus (YP_009129267.1)               APITTLIGSKFFVDDFNKQFYASHLKAPHTVGINKFSNGWAKVHDKLNREGW-LHGSGDGSRFDSSIDPFLFDMIYTIRCHFMCDDDRRE  2080
Narcissus latent virus (QDC21212.1)                   APITTLIGAKFYVDDFNKQFYATHLKAPHTVGINKFQNGWARVHDKLNHPGW-LHGSGDGSRFDSSIDPFLFDIIYTIRCHFMRDEDRGE  2079
Broad-leafed dock virus A (YP_009507671.1)            APITTLVGAKAYVDDFNKQFYATHLHAPHTVGINKFQRGWERVHRYLDEPGW-LHGSGDGSRFDASIDPFLFDVIYSIRCHFMAPECKEE  2069
Crow-dipper mosaic virus (QGV12925.1)                 APITTLLGSKCFVDDSNKQFYNTHLKAPHTVGINKFQKGWERVHDYLNTPGW-LHGSGDGSRFDASIDPFLFDAIYSIRLHFMDERDQGE  2114
Alpinia oxyphylla mosaic virus (AWO77093.1)           APITTLIASKFFVDDFNKQFYETHLKANHTVGINKFSRGWERLYNFLDRPGW-KHGSGDGSRFDSSIDAFWFDYLLTIRLSFFTNDERAI  2079
Cardamom mosaic virus (YP_009508901.1)                APLTTLIASKFFVDDFNKQFYATHLKAPHTVGINKFARGWEQLYTYLHKDGW-LHGSGDGSRFDSSIDDFWFDKLYTIRAHFFHEDDKSV  2079
Yam chlorotic necrosis virus (AZQ00683.1)             APITTLVAAKHFVDDFNKQFYSTHLKANHTVGINKFQRGWEDLYKFLDRPGW-LHGSGDGTRFDSSLDPFWFDLLYSIRYHFFTHDDQEV  2085
Chinese yam necrotic mosaic virus (YP_006590058.1)    APITTLIGSKFFVDDFNKQFYGTHLKASHTVGINKFQRGWEKLYNFLNVDGW-LHGSGDGTRFDSSLDPFWFDILYSIRSNFFCEEDRQD  2082
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  APITTLIGSKFYVDDFNKQFYGTHLKANHTVGINKFQRGWEKLYTFLNKDGW-LHGSGDGTRFDSSLDQFWFDLLYSIRVETFADEDKDE  2083
                                                      **:***:..*  *** ***** :**:* ****** :  **  :   *       : ****:***:*:* : ** : .:*

Striga-associated poty-like virus 1                   SHAALKNLYHEIVFTPILLENGQIVMKKVGNNSGQPSTVVDNTIILMMCFYYACLRKTNDE--DWIRSNFLFVCNGDDQKCAMTQDFLDK  2077
Bellflower veinal mottle virus (YP_009508455.1)       IKQALKHLYHEIVYTPILLENGHIVMKKVGNNSGQPSTVVDNTLVLMMCFYYCALAVSDDP--SWIRNNFLFVCNGDDQKCAMTQEFIDA  2079
Artichoke latent virus (YP_009129267.1)               ATRAMSNMFREFVFTPIHTISGNILVKNVGNNSGQPSTVVDNTLVLMLSFYYAYAVKTKDYAFDHIDDRFVFVCNGDDNKFAVSPAFVKE  2170
Narcissus latent virus (QDC21212.1)                   ASMAMSHMFREFVFTPIHTINGNILIKRVGNNSGQPSTVVDNTLVLMLSFYYAYARKTNDLTFDRIDEDFCFVCNGDDNKFSLSPDFVAK  2169
Broad-leafed dock virus A (YP_009507671.1)            AEAALSHMYREFVFTPVHTIAGNIIMKRLGNNSGQPSTVVDNTLVLILSFLYAYISKTGDTTCSQLHERMRFVCNGDDNKFSISREFEHE  2159
Crow-dipper mosaic virus (QGV12925.1)                 AEQALSHMYREFVFTPIHTVTGNIIMKKLGNNSGQPSTVVDNTLVLMLSFYYAYIRKTGDFECEEIENRFKFVCNGDDNKFSISPEFAQM  2204
Alpinia oxyphylla mosaic virus (AWO77093.1)           AIQALKNMYREFLYTPIHTVSGNILVKQVGNNSGQPSTVVDNTLILMMSFFYAYICKTGDDNCEFINERFRFVCNGDDNKFSVSPQFASE  2169
Cardamom mosaic virus (YP_009508901.1)                AQQALGNMYREFLYTPIHTTSGNILVKQVGNNSGQPSTVVDNTLILMMSFYYAYIMKTQDFNCECLNDCMRFVCNGDDNKFSLAPDFVKK  2169
Yam chlorotic necrosis virus (AZQ00683.1)             AKDALSHMYREFVFTPIHTTTGQVLMKKVGNNSGQPSTVVDNTLILMMAFTYAYIKKTDDRTCERMDECFRFVCNGDDNKYSISKEFNEK  2175
Chinese yam necrotic mosaic virus (YP_006590058.1)    AKTAMAHMYREFVYTPIHTITGQVLVKKLGNNSGQPSTVVDNTLILMLSFLYAYIRKTNDRTCAQINQRFKFVCNGDDNKYSVSPEFHEE  2172
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  ARVALGHMYREFVFTPIHTITGQVLVKTLGNNSGQPSTVVDNTLILMLSFLYAYIRKTGDTTCQHIDSRFKFVCNGDDNKYSVSQDFHAT  2173
                                                         *: ::::*:::**:    *::::* :**************::*::.* *.    : *     : . : *******:* :::  *

Striga-associated poty-like virus 1                   GCFDFDRMLSECGLTYEFDELTSDIKEYPYMSLTMVESETGHIGFMLDQRRIVAINQWMTKKGVLGVAQRAFPAMLHAYNDPWLFTIMHA  2167
Bellflower veinal mottle virus (YP_009508455.1)       GGLNFENQLRQCGLNYEFDEPTTNIAEYPYMSLTMVPQGNGVFGFILNPERIVAINQWMPKKGILGVAQRAFAAMLHSYNDKWLFAIMHS  2169
Artichoke latent virus (YP_009129267.1)               FGGVFTNEIAQLGLNYEFDALTPDITANPYMSLTMISVCGR-IGFQLNPERILGIVQWIKKGGVVHASQAAFAAMIESFNDPDLFSVMHS  2259
Narcissus latent virus (QDC21212.1)                   HGGSFENEINELGLTYEFDDLTPDIMKNPYMSLTIVQVGER-IGFQLNPERIVGIVQWIKKGGVLHAAQAAFAAMVEAFNDPSLFTVMHS  2258
Broad-leafed dock virus A (YP_009507671.1)            FGGDFSNEIGELGLSYEFDILTDNIMENPYMSLTMVQHPSG-VGFQLNPRRIVGIVQWIKKGGVVHAAQAAFAATIEAYNDPWLFGIMNL  2248
Crow-dipper mosaic virus (QGV12925.1)                 FGGDFSQEITELGLKYEFDELTKDITENPYMSLTMIRTKSG-IGFQLNPERIVAIVQWAKKGGLIHAAQSAFAALVESYNGPWLFSIMNL  2293
Alpinia oxyphylla mosaic virus (AWO77093.1)           FGTDFSGEIKQLGLNYIFDAITDDITENPYMSLTMVRTHEG-IGFTLHPSRIIAITQWMKKGNLIQATQAAFAAMVEAYNDPWLFGILHL  2258
Cardamom mosaic virus (YP_009508901.1)                YGGEFTTEIKQLGLTYEFDDLTEDITENPYMSLTMVRTCSG-IGFSLHPSRVVAIVQWIKKGDIIQATQAAFAAMVEAYNDPWLFSILHL  2258
Yam chlorotic necrosis virus (AZQ00683.1)             YSGDFSKEIGELELVYEFDDLTDDITLNPYMSLVMVRTKQG-IGFQLHPERIVAIVQWIKRGDILQATQAALAATIEAFNDPWLFGIMHL  2264
Chinese yam necrotic mosaic virus (YP_006590058.1)    FSGDFSREIAELGLTYEFDDLTADITQNPYMSLVMVRTPGG-IGFQLNPERIIAIVQWIKRGDVLQASQAAFAAMIEAFNDPWLFGVLHL  2261
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  FGGDFSKEIAELGLTYEFDDLTEDITLNPYMSLVMMRTPGG-IGFQLNPARIVSIVQWIKRGDVLQAAQAAFAAMIESFNDPWLFGILHL  2262
                                                          *   : :  * * **  * :*   *****.::      .** *.  *::.* **  : .:: .:* *:.* :.::*.  ** :::

                                                                                                                               NIb|CP
Striga-associated poty-like virus 1                   YLVWLLVNYEDEILYQMRQTGERVSYLSPAYVKMLHYGG---------------------------------------THLQ|VDS----  2213
Bellflower veinal mottle virus (YP_009508455.1)       YLYWLLLSYEQELLWAIEQTGESVSYIPPYAVHVMHYGG---------------------------------------TVLQ|IDT----  2215
Artichoke latent virus (YP_009129267.1)               YLIWLLVTYRQELRYAMHNDLVSVVYMDPAQVFALHYNDATD-------------HHTWFSDDLDEPSSDDDDDDVQTQELQ|MNR----  2331
Narcissus latent virus (QDC21212.1)                   YLVWLLVTYKDVLLYAQENDLGSVCYMDPCQVFALHYGSSEG-------------LESVDFESDNESANDADDDVTPSLELQ|MDV----  2330
Broad-leafed dock virus A (YP_009507671.1)            YLIWLLCEYKDALVYANEHELATICYMDPLQIHALHYEVHSE--------------------------------EGTQELQ|MDL----  2300
Crow-dipper mosaic virus (QGV12925.1)                 YMVWLLSEYKDAFIYAEENGIATICYMDPCQIHALHYARAEDSGTPYYAILDRAEYIKEPNEATYEQQQLQMKSDEAFQTLQ|MDFNKKE  2382
Alpinia oxyphylla mosaic virus (AWO77093.1)           YLVWLIIEFRDELEFAKDNDVLGVTYMDPCQVHALHYGINEA---------------QIQEEDEDWTDDEDENLISQTQHFQ|MDL----  2328
Cardamom mosaic virus (YP_009508901.1)                YLVWLIIEYKDALNFARVNGIFGVVYMDPCQVHALHYGIPTA------------NELKEDEDYDDDSDEDLEIVEFCSQQFQ|MDL----  2331
Yam chlorotic necrosis virus (AZQ00683.1)             YLVWLICENSELLAFACRQEMQSICYMDAYQIYSLHYDKQDD------SLKPLLDEAIEENRYMNGKGYVSFDEAEGSQVLE|MDL----  2343
Chinese yam necrotic mosaic virus (YP_006590058.1)    YFVWLLCQYREEIRYAMDHDLGAVCYMDAYQVYALHYDTRDD-----------INDLQIDSASCEIEKTVVVAGSTQHISLQ|MDL----  2335
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  YLVWLICQYKDEIRYAMDNNLGAVCYMDAYQVYALHYDTQED----------IEHDKIETHDAAQGFDEIQVDHVAPYINLQ|MDL----  2337
                                                      *: **:    : : :   :    : *: .  :  :**                                           :: ::
```

```
Striga-associated poty-like virus 1                   -------------GSDDDKSEKQE---------KEKTVPNNNDELAG--VSR--------------------------------WIVPKM  2247
Bellflower veinal mottle virus (YP_009508455.1)       --------DDEGKAKDTNNKKDTG---------KGIEGSGTQAELLG--GIQT-------------------------------WVLPNL  2255
Artichoke latent virus (YP_009129267.1)               -EEIEAAARKEQEEKDAAAKEESERKEAEEARGIRERTRKGKDEIPG--PTATPSSSDSSLE-KGNENISEPQGDPEEKEEDVKWVMPAL  2417
Narcissus latent virus (QDC21212.1)                   ---ESLISEKGKNAKNTNKDEQSKRTDATAQGESSSPLKSSTEEAAN--RGDTNPPQGDPLV----------------DDEIVEWVIPKM  2399
Broad-leafed dock virus A (YP_009507671.1)            ----EKKKKEEEQAKALEAAELQAEKERAALKAKAALEAKGKKKMED--PPSPPPPAKGTDN------VTDPPGTNSDDEEEIQWKMPAI  2378
Crow-dipper mosaic virus (QGV12925.1)                 QEEKEKKEREEKEGKEKAEAARKAEQDRLAAERREMQERGKQKKADE--TRTESSRRNNKDNIDELPAPTPDQDPVDEDGPDIQWALPAV  2470
Alpinia oxyphylla mosaic virus (AWO77093.1)           --------TAPTQRTPLVPTTSTP----AVTPPNNQQLVPSTPMDGA--STSQQQPLNQNRE--VIEQPPQATPDSNNDENEIEWRIPPI  2402
Cardamom mosaic virus (YP_009508901.1)                ----VGTPTAPRQGSTIASASTSGTASTNLPGSGGTRTAPLAPITGQQHAENPPQPVESFDA-----QQQDFAPSGGDDDTDIQWRIPPT  2412
Yam chlorotic necrosis virus (AZQ00683.1)             ----TLAPTEQTTQKDKGKQHEQR--------REGRPGPSTQPIETG--DNNNNQPIEQLGD---------------MHDEEIEWRIPAV  2404
Chinese yam necrotic mosaic virus (YP_006590058.1)    --------STPVQLPTKKPSVEDK--------GKALATPSTTATLPD--SSQGHQPVEEPNN-----------NPDTVDEEDIEWRIPAI  2396
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  --------TAPAPSTTPETSKSKG--------KEKVTEVFGQQQTGG--TNQGTQPVEEPSN-----------EPDTVDADDIEWRIPAI  2398
                                                                                                                                          * :*

Striga-associated poty-like virus 1                   TTTARSLGFRSIRGTT-FKPETFKNIPRDITAIMRNDCATDAQYIQWESEVRADYDIATEGEWNTVFTAWLLYCANNGTTDKYNPLDVIP  2336
Bellflower veinal mottle virus (YP_009508455.1)       NKFERSSGFRKIGGRFVTTKQAIKSIPRDVRSLMRNDVATDNQFMAWETEVRDEYSVANDEAWQTLLMAWALFCAHNGTTNKFRHTDVMP  2345
Artichoke latent virus (YP_009129267.1)               NPNRGGVVIPTINGKKLWKRGILKHVPKQ-QYDATTTKATQTQLTNWVEAVKKDLRLKDDNAWALVLTAWCIWCADNGTSPEVDTNQELE  2506
Narcissus latent virus (QDC21212.1)                   SSNIVTSPVPVVNGKKLWKRGILKNMPKI-MFSTTSTMATQVQLTSWVEEVKKSLALNTDDAWTVVITNWCIWCANNGTSSEIDTSQNME  2488
Broad-leafed dock virus A (YP_009507671.1)            QKSSLSQLVPTIKGKKIWNHRVLKFIPDE-QFDVNAARAKDEEYSAWVDDIRSSLKIRSETDFQIVLTAWCLYCANSGTSSEMDVNQHFE  2467
Crow-dipper mosaic virus (QGV12925.1)                 QRLSLGRLTPKIDGRRIWNAKVLNGIPRE-QFRVSSALADDESYKNWEKEVKDALKIRSERDYQTVLTAWCLWCANNGTSSEVDTTQDLE  2559
Alpinia oxyphylla mosaic virus (AWO77093.1)           PKTASHFNNPVVKGKRLWNSRIAKNIDPE-QFEQTSQKATTLQFERWVEKVKKNLGNPSEQHFQIYLTSWCLWCANNGTSSKVATNQMME  2491
Cardamom mosaic virus (YP_009508901.1)                PRRLSHFNNPRVKGKRIWNRRIINSIAKE-QFTQSSQLATTLQFERWAEDVRKSLGTPNEDDFQIYLTSWCLWCANNGTSSEVDVNQTME  2501
Yam chlorotic necrosis virus (AZQ00683.1)             AKSLRHISIPRVKGKAVWNQKILKKISKE-QYYETTQMATSENFEKWMEAIRKNLGTTTEADFQICLTSWCLWTANNGTSPELDPSQVME  2493
Chinese yam necrotic mosaic virus (YP_006590058.1)    QKGFGHYKIPKVKGKRIWNPKILKKIAHE-QFTTTSQMVTTDKLEKWTEEVKRDLVVTNETDFQICLTSWCLWCANNGTSSELDASQFME  2485
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  GKGVERYQIPRVKGKNVWNPRIIKKIARE-QFTTTSQMVTQNQLEKWIEDVKRDLATTSNSDFYICLSSWCLWCANNGTSPELDTSQFME  2487
                                                                 : *    .    : :            .   .   *   ::       :  :   :  * :: *..**: :    : :

Striga-associated poty-like virus 1                   MPDGRGGTVDRQIGGFIRASSKV-GLRKLMRKFSRETSQMLLELGQMTKWGLKRGFQDRGMIPYAFDFYVFDEMTPPWVREQLSSAKHSA  2425
Bellflower veinal mottle virus (YP_009508455.1)       MPTGQGTTTDVQIGGFVKASQQV-GLRKIMRKLSRETSQMLNELGEMTKWGMGHGIHDNWMIPYAFDFYLEDEYTPPPVHDRLAAAKHAA  2434
Artichoke latent virus (YP_009129267.1)               IHDGLGKVQAVKIDTFVDPAIENGGLRKIMRHFSGITQEILAKGGRMSAYGIKRGFTDNIMIPYAFDFMVANKRTPKIVREQLAQAKIAA  2596
Narcissus latent virus (QDC21212.1)                   IRDGFGKVQEVPIEIFVNPAVENGGLRKIMRHFSGITYEILKVGKQMTAWGNKRGFTEKSMIPYAFDYYVVTNTTPKTVREQLAQSKAAA  2578
Broad-leafed dock virus A (YP_009507671.1)            VHDGNGKVGLLPAKIMIDSAVKNGGLRRIMRRLSEPTSQMLAKGGRLTTWGIKRGITRREMIPYAFDFYVATSSTPKTIREQLAQAKIAA  2557
Crow-dipper mosaic virus (QGV12925.1)                 VFSGDGKVLKIPIRVFTEPAVEQGGLRKIMRRLSEPTTLMLKKGNVMTAWGTKRGFTQKSMIPYAFDFYVQTTTTPKTVREQLNQAKAAA  2649
Alpinia oxyphylla mosaic virus (AWO77093.1)           IHAT-GQFASIPISIFVDPAIEFGGLRKIMRHLSDVTSKILEQGGKMTAWGKKRGFTQLAMIPYAFDFCVQSLKMPKTVREQLNQSKAAA  2580
Cardamom mosaic virus (YP_009508901.1)                IHSG-GKYSTIPIAIFVEPAVQNGGLRKIMRHLSDITSQILAKGGKMTAWGTKRGYTQLAMIPYAFDFCVQTNGMPKTVREQLNQGKAAA  2590
Yam chlorotic necrosis virus (AZQ00683.1)             VHAN-GQIIEVPISIFIEPAATLGGLRKIMRRLSGVTSKILEEGGVMTAWGKKRGFTQRTMIPYAFDAYMQTDSTPKIVREQLNQSKAAA  2582
Chinese yam necrotic mosaic virus (YP_006590058.1)    VHAN-GQIMGIPIQIFVEPAIQHGGLRKVMRHFSGITSKMLSEGGKMTAWGRKRGFTQRSMIPYAFDFFVPTDTTPKTIREQLSQSKAAA  2574
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  IHAN-GQVTGVPIQIFVEPAILHGGLRKVMRRFSKMTSRMLAEGGRMTSWGIKRGFTDRALIPYAFDFFVQTETTPRTIREQLNQGKAAA  2576
                                                      :    *         :  .:    ***::**::*  *  :*     :: :*  :*     :******  :     *  ::::*  .* :*

Striga-associated poty-like virus 1                   LGRGVRDTLLLDDKHHDASAQI-RSRNDQRESF---------KAPEY  2462
Bellflower veinal mottle virus (YP_009508455.1)       LGAGEVDAMLMEKKHHDLQTIV-RPRTAQTERF---------RAPEV  2471
Artichoke latent virus (YP_009129267.1)               IGHGIRRSLVTDGSVNGSKTSYERHTDQDQDEFEHGHDV-DRRPHLT  2642
Narcissus latent virus (QDC21212.1)                   IGSGTVRKMILDGNIQGSHASYERHVDTDNSEYEHGSSV-DQRPYLT  2624
Broad-leafed dock virus A (YP_009507671.1)            IGSGVHRVMVTDGKLQRARTSYERHTDDDVTEHEHGDHG-DERAYLD  2603
Crow-dipper mosaic virus (QGV12925.1)                 IGKGVQRVMLLDGKIQGSRTSYERHVDTDKDEYSHGDGGEDTHPHLY  2696
Alpinia oxyphylla mosaic virus (AWO77093.1)           IGSGHQRVMLMDGKIQRSKTSYERHVDTDVDEFEHGGAI-EPRATLY  2626
Cardamom mosaic virus (YP_009508901.1)                IGSGYQRVMLLDGKVQRSKTSYERHVDTDVDEFEHGSMG-EPRATLY  2636
Yam chlorotic necrosis virus (AZQ00683.1)             IGSGIQRALLLDGKLHRSKVSYERHTDEDRDEYEHSDNG-DQRPSLY  2628
Chinese yam necrotic mosaic virus (YP_006590058.1)    IGRGVQRVMLLDGKVHGSRTSYERHTDNDQDEYEHGGAE-DQRPALY  2620
Yam chlorotic necrotic mosaic virus (YP_009507672.1)  IGRGTRRVMLLDGKIHGSRTSYERHTDGDQDEFEHGSLD-DQRPALY  2622
                                                      :* *    :: : . :   .   *    :   .         :.
```

Fig. S2. Alignment of the “small” polyprotein sequences of SaPlV1 and BVMoV

The PIPO segment is highlighted in cyan.

```
Striga-associated poty-like virus 1         MDYLALTRIVANRQTIDMPRVLELAIKEVYGTYNRELNSAIDFK---GEQLETTPATTDPLDVFIKNELKEINDAAGDCGKIACVRPRTL    87
Bellflower veinal mottle virus (NC_039002)  MDPLFLKRFNMDGGKLQICAPISDALKAAYNNHGVDIKSSYAVTAPCGTVISVENSTNEVLKDFVEAGMKFNDDVAGECPKGQCNEASKG    90
                                            ** * *.*:  :  .:::   :. *:* .*..:. :::*:  ..   *  :..  :*.: *. *::  :*  :*.**:* *  * .. .

Striga-associated poty-like virus 1         PEGFYATMS--YAMGGLKGVIPGPVSKRRCFRDGYCYMNIFVAIAPHVYDEDALVYAKFLNDCPLVLGSWPTMNSLAKAMIWIGQKIPNL   175
Bellflower veinal mottle virus (NC_039002)  RSSWFLNCSPTLAVGGRSATFIMPMSPRRVFSSGYCYLNLAVAMSPYIFDEDAIKFAEFLHDLPIVLGKWPAMVKVARSFAWLLQHMPYL   180
                                             ..:: . *   *:** ...:  *:* ** * .****:*: **::*:::****: :*:**:* *:***.**:* .:*::: *: *::* *

Striga-associated poty-like virus 1         YNKAVPAVSISHTAEACHVVDQRGPVKGWHILDAPTFRDVILFSLKSDLSEYIIGG-DPVTAAYMHLSKCIRHANNTRQPWVTFNKMVLE   264
Bellflower veinal mottle virus (NC_039002)  CDRHIPHISINHNLNAAHVSDQRGPMIGCHILNAYTLKDFVLTGMDTLNANTMLGGMDALTSAYQSLDKAIMQANKSFQPWLTFYRMICA   270
                                             :: :* :**.*. :*.** *****: * ***:* *::*.:* .:.:  :: ::** *.:*:**  *.*.* :**:: ***:** :*:

Striga-associated poty-like virus 1         DSALAATLVLSPATLIKLESWFEDREEFRRLVATIESGVGDALTRIIVIKRAIEGVKIHFLDNDIETATAALHQRVLEYIRNADDGGA--   352
Bellflower veinal mottle virus (NC_039002)  DSMLAATLIMSPATLQKLESWFEDDEGFRRVVATLETTVSDALLRMVIIKRAIHGVKMHFRTDNVERSTNELHRAIIAYIDSQDDQSAKD   360
                                            ** *****::***** ******** * ***:***:*: *.*** *:::*****.***:**  :::* :*  **: :: ** . ** .*

Striga-associated poty-like virus 1         LNAAATRFSNLVTEKKRAVLLFRKTDSLTFRFSLATRARFWCYIYRRKLLYWSYSHVAKHFTISRKTRS---------------------   421
Bellflower veinal mottle virus (NC_039002)  LGDAARRFETMALEKKDAIRVLRKFNSPLFGLSLASRARFQLYIMWRKFVYFAAIKARKLYTCNSAPRAEGTAARIHTRGQIHMGNHLLV   450
                                            *. ** **..:. *** *: ::** :*  * :***:****  **  **::*::  :. * :* .  .*:

Striga-associated poty-like virus 1         --------------   421
Bellflower veinal mottle virus (NC_039002)  RASSKPHVAGVVFN   464
```

Fig. S3. Alignment of the polyprotein sequences of SaPlV2 and CeLV

Putative cleavage sites are marked by vertical bars (|) and highlighted in yellow.

```
Striga-associated poty-like virus 2  -----------------------------------------------MAAKIATSYVETGLL---------------FGSWTPQNVWA--    26
Celery latent virus (AZJ53460.1)     MSKRIYTIIVVLCFQVCFQNLRTQPTQSSHTFSTNPAIPGTDALQFEENANLTYSTIKYNILKFNLNYKQSIMSVVSFGSITSMDFDAAC    90
                                                                                      *::: * :: .:*               *** *. :. *

Striga-associated poty-like virus 2  ----IDGPTTEVPQLPTAAPVRNQAERLVRAL------------------------------------------------------PKVQ    58
Celery latent virus (AZJ53460.1)     LAAMIETPGGSIPPTPQSPPTSPVAVKQRKILNFPIAKIRTTPDASFEMCVKFPESFIDSFCAQAQKELKYWHAAITQLKFFGGETPKTL   180
                                         *: *  .:*  * :.*.   * :  : *                                                      **.

Striga-associated poty-like virus 2  EALE-------------------------EGAKEV-------------------------------------------------------    68
Celery latent virus (AZJ53460.1)     ETLVNQGQAHTHQVILNLVKILDSAPKAIQGKKELENFFQLSPHGNNSKEPIDVSRKVYMEPCKISPRKRQVCSCDNDDDAHYHCYYCDI   270
                                     *:*                          :* **:

Striga-associated poty-like virus 2  --------------------VLSNFQWGSLSARFYNPKGVGHDI-----------------------LEKKMVLVKSTHR----------   105
Celery latent virus (AZJ53460.1)     VCSSKNLLQEHERDFCEDAQSVQAFGYKLESPNVFDPPHVTQQRSVAPSLGKTLESPVKSPEQSKPNLEKSFPLVESSTNSGMIFFGSIA   360
                                                          :. * :   *...::*  * ::                        ***.: **:*: .

Striga-associated poty-like virus 2  -----------------------------------------------------------------------------KPLLEEVVQTRFV   118
Celery latent virus (AZJ53460.1)     TMVPSHIEKYVRNCETENPIDAAASNLAMQEAKSSGAPCIVVHHKALPGGKKDFLFPHNSPQVVRTETEEPIAGTIDRPTIKRALFTRIK   450
                                                                                                                  :* ::..: **:

Striga-associated poty-like virus 2  TTEKQILVRPGANICAKTKRPLRPGEVKQLIKATGDPQHPLFCLPITKLIETTHPIYRIEIDAKEEFYVLRGDVRLLSRRQRQKLHQKRW   208
Celery latent virus (AZJ53460.1)     KKAQEICVNPGGTIQRKTKRWLRPAEVAQIVRATSDPQHPLFKVDVTQIIEVVHPVYRTERTEVVQQCITRGTYKLMSKAQQRKARAMRS   540
                                     .. ::* *.**..*  **** ***.** *:::**.******* : :*::**..**:** *     :  : **  :*:*: *::* :  *

Striga-associated poty-like virus 2  NKELVIDESDTSSWNSREHWVEKLVPKKAYTKYIKCGKLPEELEP---WTNARNSDDFELPSKNKLKKMS-TAQKLACVDKNFEHDLKGH   294
Celery latent virus (AZJ53460.1)     AGMLVITDNPTTHWVSEPQKMLVVKEKLSTTKHVKLRNVEVNAESEMFWGTKTK----EGPSKTALKRCKRNIDRLALLDPQMGESANGE   626
                                        *** :. *: * *. : :  :  * : **::*  ::  : *.   * .  :    * ***. **: . . ::** :* :: .. :*.

Striga-associated poty-like virus 2  CWRNIFTDRISFGDMKSQPKGWHEHRFGRVKGSFIPLVKFCELLQEEVARFPSLAEMLVPRPFCYREGGRLVYHVGYSKFSRGFCSLQSL   384
Celery latent virus (AZJ53460.1)     CWMNTFKHHLKVGSIDILPNKVRLPNLRSAFSRWIPLVDYVEILKFHCKSQPKLKRVVIPTPVTYLEGSRYHIHVGYSK-NCSWITVEQL   715
                                     ** * *..::..*.:.  *:  :  .:  . . :****.: *:*: .    *.* .:::* *. * **.*   ****** . .: :::.*

Striga-associated poty-like virus 2  LHPPIKSGNPKVPKSVLLEAVVGAEPTEDVETFDTIDWEFDLGVPIVDIDLASKVAGTLEVAEQIADYQTGTTYGEPNDVTACELGHCYH   474
Celery latent virus (AZJ53460.1)     IRQLQTLLTSSKYGEHFKRAIVGGEPED----------KFTPVVPIVDVE-TERAKSSLAKWTTAQQRYMGSIRTRINSQAEKHKIDSEK   794
                                     ::   .  ...   . : .*:**.** :          :*   *****:: :.:. .:*       :   *:   . *. :  .  .. :

Striga-associated poty-like virus 2  KFWWDPSLPVWKNDVNRGICIAMTRSFRENKMYLRDFLVQLEDQESMGFIPQVKVVATPFIYCLKGRLYMHVGDHPEGANCGRNDALRYI   564
Celery latent virus (AZJ53460.1)     KIW----IPMRHDTMD----MLTPPYLFENG--LRNNEVQQVGQVLGDSVDRAGNSSGQSSQCQQQNVAL--------ASEGNNDNV--I   864
                                     *:*    :*: :: ::    :  .  : **   **:  **  .*   . : :.   :     * : .: :        *. *.** :  *

Striga-associated poty-like virus 2  HEFSRRLPYHLWKEVIVGASPIKKKKWFQVTNSGEELSGEELVTVNRKELLKLLRHQQKLSSVASGLVGENCVRPSGSESSSELFEMLNS   654
Celery latent virus (AZJ53460.1)     NESVRSI-----QNLVTANMQLQEQCKLLLASHEQAI----MDSVEHGN-LEIQKHDVEVSQ-----------KPSTRKSDSQ------R   927
                                     :*  * :     ::::..   ::::  : ::.  : :    : :*:: : *:: :*: ::*.           :**  :*.*:

Striga-associated poty-like virus 2  ELSRSAMNCGNASSLLKRTELNGNKQHGKSLKFWESKWMPILGPLLGVSSLEILHQMQMREGGSWLDLGISNKLFQMTSTVAIRSMQTYF   744
Celery latent virus (AZJ53460.1)     NLQKFSLKKIVASEEMSRTLGRG----------WRKSVTSIGVPIVSASIAEALNQVVQRGNTSWLDVGISGTLLKQCTLFATRTFQAYC  1007
                                     :*.: :::   **. :.**  .*          *...  .*  *::..*  * *:*:  * . ****:***..*::  : .* *::*:*

Striga-associated poty-like virus 2  TAKMIKGIWNLSKSEVHMHVMKQVHSLHESAGAETLRVKAWYANLPASVKILFIGAIFMGSVHFVRKLFRVKVVNTDGNRADGNFSEVVR   834
Celery latent virus (AZJ53460.1)     SYKLARNVLTLTVGELYDNVKSYINSIMGSTDPEVTGFLSQVRSAPSMVKMAILLTMFAISVKLMRKFFKVKNNGTSFTVSGENVSASQL  1097
                                     : *: :.: .*: .*:: :* . ::*:  *:..*.  . :   . *: **: :: ::*  **:::**:*:**  .*. . :. *.*

Striga-associated poty-like virus 2  VSVSQRQALPHTQPSKQVKLFMTAAGMIATVSMFCDVRTARYIKEWMDLWWYAVTSATQMGSFTDLIMSPREYLKSIMDPQLGEQHAFNQ   924
Celery latent virus (AZJ53460.1)     RISAQAQARSTDNMTPTVKKLCSILGMIGLVCCCYDRTTWAYQKDWMDAWITSITYAGASDSIWESISHPFETLHNIAVSGGDRSPETTA  1187
                                        :* ** .  : :  ** : :  ***. *.   *  *  * *:*** *  ::* *   .*: : *  * * *:.*  .  ...   .

Striga-associated poty-like virus 2  RFLTLIRDAEQQQNGIENNSELTKTYMKNREALGMENPMSEVQGFLLHEILDQVQEAPFTYMGALKGLNEILVSHGTMYQIAKDLAEGFL  1014
Celery latent virus (AZJ53460.1)     RLERILAGA-----GLNAQAQALDEF----------GASSSVMGQTLQNILDEVESTNVSIVSEMKALPHYHRNATTFNQAARDLVTEPD  1262
                                     *:  :: .*     *:: :::  . :          .. *.* *  *::***:*:.: .: :. :*.* .   .  *: * *:**.

Striga-associated poty-like virus 2  KEKFNLLNAPTGSGKSTIFPAYVSARTKKRILILVPLVAATMGIYSRLNEKLPNQVGYHADKTSANVHAKIIVSTYGHIAHQLMQGMDPY  1104
Celery latent virus (AZJ53460.1)     ATYQMLLTAATGTGKSTLFPVHLRSQSQKRVLLLIPLVAATHGVYQRLKSQRVNDIGYHADSISENPNAKLIISTYGHMCVKLLGGQNPF  1352
                                          **.*.**:****:**.:: ::::**:*:*:****** *:*.**:.:  *::*****. * * :**:*:*****:. :*: * :*:

Striga-associated poty-like virus 2  ENYGIILADECHVSTLETAVVITDLLARKRNMQQSVMFMTATPFKHLTLESVATEQDVQQVRTSKFQSVKTFINYCREGGEQRVLQTAEN  1194
Celery latent virus (AZJ53460.1)     DQFDYILADECHVVTLETVTVISHLLQQREMATWKTVFMTATPFNNITLNSVETEQPVIMQQTEHFHNPKSFVDFLKAGGTERVQTYAKG  1442
                                     :::. ******** ****..**:.** ::.    ..:*******:::**:** *** *   :*.:*:. *:*::: : ** :**   *:.

Striga-associated poty-like virus 2  GCIIFCATHKEVVELASFLNSPSHPAIAYHSGLRSPLGEFIEKNKDRLGKFPYFVCATNALESGVTIPARTCIDFSTKIVSQVEGDRNTV  1284
Celery latent virus (AZJ53460.1)     GCIVFCSTQKETEESAKALKASGVIALFYHASNRLEWDSFAKKNERSMGQLNFYLFATNALESGVTIPMKSCVDFVTKMHPVVGGDRKTI  1532
                                     ***:**:*:**. * *. *::..  *: **:. *   ..* :**:  :*:: ::: ************ ::*:** **: . * ***:*:

Striga-associated poty-like virus 2  SMARQTITMPEQIQRRGRIARTQPGIYLYTHAGEQNQVRLDPDSSVKYLLNCWVNRTVCCKEICDLPDESTVRITRAMVPMVWCHDTPPL  1374
Celery latent virus (AZJ53460.1)     TMAPTSISIQEQLQRRGRVGRTCPGGYLYTSVGTPLMYKLDPDSSIKYLLYCWKSGIKCYKEALNIPDECTITFTKEKIGAIWTHDTPPV  1622
                                     :**  :*:: **:*****:.** ** **** .*     :******:**** **  .   * **  ::***.*: :*:  :  :* *****:

Striga-associated poty-like virus 2  VQCSLMDHLGCIFQNAIEFCGAFQSVPGQMPATTTMLDSTQVAKFHVMTVTLTNSDEVQDLKVPQPHHWFNEPRVVALWNNLLKSSSFEL  1464
Celery latent virus (AZJ53460.1)     VTAALVDNFGAVYRNANFFLASHRRNYVEIPHTTDMILPSTLSTWENFELDGNEVSDGTRMRVPQNHFFFRNERVQESWLKLQAAILTEL  1712
                                     * .:*:*::*.:::**  * .:.:    ::* ** *: .: ::.:. : :  .: .:   ::*** *.:*.: **   * :*  :   **

Striga-associated poty-like virus 2  TPGECSERKNNMLARLESQVAYNSTSTDLDLASLLAKFYENIKVFRQQISAMQSFTANTLEKTAFLDSFSLLSFANKNIRLRSEKRIKEI  1554
Celery latent virus (AZJ53460.1)     TEAEATKKRDIVIENLMARRVSGHPASKLEIARMIMAKQQVVQQARDTKRVRETLSESISDYSGIFSNFSGIFSVQERLKKASIKANEEL  1802
                                     * .*.::::: :: .* :: . . .::.*::* ::    : ::  *:   . :::: .  : :.::..** :  .::.::  * *  :*:

Striga-associated poty-like virus 2  EQDIADTEACILFLEARLTGQCDANLAIEKTEQDKIKEYLACLMDMGYAKGSFQSCFFIRETTWRRFRDFVDLLPDGTYRQKSFTKRILE  1644
Celery latent virus (AZJ53460.1)     DMVIQENESHILFLQDMIKETPEIIPDMALEEQIQHMEYAKAILENGWISGNPQAKLLIMRTTHKNFHDLVTKTKDGTYRMKSYVQRMFD  1892
                                     :  * :.*: ****:  :.   :    :   ** :  **  .::: *: .*. *: ::* .** :.*:*:*    ***** **:.:*:::
```

```
Striga-associated poty-like virus 2  TARSHPWIGLSVCSAGVAICCYALFSTLKKSEDKGMKSIGNLETKSNVFHAHEVVYLPESMPYAGTLVKGIAISGASFLITRKISDLITD  1734
Celery latent virus (AZJ53460.1)     FVKKHPLLIFMSIMMGTSLAA-GYFMMSKDSEDD------DAIVQDKVFKRNDKAMLEWCLRGKACKCDATHFEAQYVLDSRHYRTILED  1975
                                      .:.** : :     *.::.. . *   *.***.      :  .:.:**: :: . *  .:   .   ..  :..  .* :*:   :: *

Striga-associated poty-like virus 2  -----LRNWWTGK-----------------------SKPKIIVKMDDDQRIDTVWYDIYEGDTWIAS-FETLSRIQDYDSQMMVCSEFRC  1795
Celery latent virus (AZJ53460.1)     WVKFPLRGFHNIQIVNYGTVSKYARALAFLSVCALLANPTMVYNSAAHSMAGNSEYNESVAKSLMHNILRDWNRVPLID---LLVKGIDG  2062
                                          **.: . :                       ::*.:: :   ..  ..  *:   ..: : . :.  .*:   *   :: . :

Striga-associated poty-like virus 2  ALDEYKSRFLQKAITQGYVP--------EGKGKLRAHRTKALKKKTSEDQEPRGRMKAYYDPYSEGKTRRGLKKVFRQFYNVDDADVKEI  1877
Celery latent virus (AZJ53460.1)     SDDRYDQYIHELYTSGGLIAFESDTGKFEGKMSISQYRKDAAKGQTKRSAASRSREEDHYDPRSSGRLKSGIRRAYRQFYNIEDSDVQEI  2152
                                     : *.*.. : :   : * :.        *** .:  :*..* * :*...  .*.* : :*** *.*: : *:::.:*****::*:**:**

Striga-associated poty-like virus 2  IIHGEKHEPVLVISSLDALNAEVDRVKYSDPHLYALYQDVKEKLENAEDDDPEAYLQRIKETSEKIKGNARWVDFAE-DEMTDMIYALQN  1966
Celery latent virus (AZJ53460.1)     ILTNKKGAPILKIGSLDELNQHVDLLKFSDPELYELYLHARDKLDLDEPESSSGF-------------TGKWGDYAEDDEFMKMISALDS  2229
                                     *: .:*  *:* *.*** ** .** :*:***.** ** ..::**:  * :....:             ..:* *:** **: .** **:.

Striga-associated poty-like virus 2  LVKKASEEAFIPVTVKTYDGRTIQATVANYRGK----------WQETSWPRIDNSELRQKLDDALRMLPEGFVSKIKDDCTDEQAHEIDE  2046
Celery latent virus (AZJ53460.1)     LTKQASEEAFIPVQVKLRDGRTVQANVARYWQKDYPTGKSVKQWAQTTWAPPQFTALRERVGKALELIPESRPIHLHGKVPNGTLIEFQD  2319
                                     *.*:********* **  ****:**.**.*  *          * :*:*.  : : **:::..**.::**.   :::.. .:    *:::

Striga-associated poty-like virus 2  LVKCVLHENARKQNREAVMPGTQCQTDVCDWTPRVGIIHRKDEEGNFTQVFLQCIALNNVCIYPYHGWLSDGEELQFHFPTTTFVGKMKR  2136
Celery latent virus (AZJ53460.1)     AMKDLHEKTAVKAVAEAKIGDTQFEADPSDVTSRVGVVMVKTSANAEWESWNQCVALNNIVIFPHHYTLKDGNNLRFKFSSSDFESTCHI  2409
                                      :* : .:.* *   ** : .** ::* .* *.***::  * . .   : : **:****: *:*:*  *.**::*:*:*.:: * .. :

Striga-associated poty-like virus 2  SEEFGNNDIAYTPLPKRIKGVSGGVILSKPSEKENVFHFSRIVSQKVKTEVQYQGFSITAHIDGNC-----WAHTVPTQVGSCGGPMLNM  2221
Celery latent virus (AZJ53460.1)     VDGYNGLDMAWAPINVKIRGLKKKVCLGTPRNGSYLWHFSMINQGKDLPEARLMGYSSVTKVQEESHPSFDWTHTVSTQVGNCGGPFVDK  2499
                                      : :.. *:*::*:  :*:*:.  * *..* : . ::*** * . *  .*.:  *:* .:::: :.     *:***.****.****:::

                                                                                             NIa-Pro|NIb
Striga-associated poty-like virus 2  RGHLIGYHVGTAGDFSYNDFLGFSEELIKSIRKIDVSRTARRQGMMEWRETEFYKTSNYMPPMLNRQ|DPIPEEWQAPAHKDIKRCTDAD  2310
Celery latent virus (AZJ53460.1)     HGVIVGYHTGAFQLGQFNTFLGLSAPLIAHLTKLDVKPSAQPQSKMIWREVDFYRSPNYLPPTINNQ|EPIPEEWRYPEGKSVYPCVDPG  2588
                                     :* ::***.*:    .:* ***:*  **  : *:**. :*: *. * ***.:**::.**:** :*.* :******: *  *.:  *.*..

Striga-associated poty-like virus 2  WMARELLKGPSFELLGKMTRMVDYNTKISKNQDFAIWFNLEETKRHLDEINERRALRNLEPLHISHTISAQNREAAILDTSKYNRITKYT  2400
Celery latent virus (AZJ53460.1)     WMGSRLVKGSGFRLIGKMQRHVEYSTKISLNEHFDMWMSQEKTQNELTRLNKNRVEKGLEKAFISHTIAAQNKEAAIKDTSKYARTTLGT  2678
                                     **. .*:**..*.*:*** * *:*.**** *:.* :*:. *:*:..* .:*:.*. :.**  .*****:***:**** ***** * *  *

Striga-associated poty-like virus 2  WSDDLLHKATQMVINLLEPHIQKCARQPLELVYQDMEWSTACGARYDGLKADFRTRVVGETNMMAYGEYAWARFDVPAKEYVPTIWTNSL  2490
Celery latent virus (AZJ53460.1)     YSEPLLKRATALTIQMLEEHIKLCKRQPLDLVYGDMEWNTACGAQYNGLKSAFRDQVVGIENMDAYGQYCWERFNVPTDQYKPCIWTNSL  2768
                                     :*: **::** :.*::** **: * ****:*** ****.*****:*:***: ** :***  ** ***:*.* **:**:.:* * ******

Striga-associated poty-like virus 2  KDELRPIEKVEANKTRTFTAAPIDFVVGAKQAVDQFNHQFMAKHLTLPHTVGINQWSGGWHRLYQKLEGKNFLYSSGDGSRFDSSPTSEM  2580
Celery latent virus (AZJ53460.1)     KDELRPIEKVKENKTRTFTAAPIEFVIGAKQAVDAFNHQFMDAHLKLPHTVGINQWSGGWHKLYKKLYGKNFVYSSGDGSRFDSSPCFYM  2858
                                     **********: ***********:**:******* ******  **.***************:**:** ****:*************   *

Striga-associated poty-like virus 2  FDAIYTIRCHFADKSMWQVLNNIYTEICFTPIVLHDGNIVKKDHGNNSGQCSTVIDNSLIMLILCCAAYLEHTPPSWHSVKQMNEHWHFC  2670
Celery latent virus (AZJ53460.1)     FDALYTIRTYFADPEIHQVLENIYLEVCHTPIVLHDGNVVMKNHGNNSGQCSTVVDNSLIMMILCCASYLEHTPATMHSLDAIKSHWHFC  2948
                                     ***:**** :*** .: ***:*** *:*.*********:* *:***********:******:*****:******.: **:. ::.*****

Striga-associated poty-like virus 2  VNGDDYIGGMSPQLAKLLTKERMALTFDAFQFKYEWSDYSKSLFDQEYMSLKFIKINSDDTFPTSKALIAPWREGSRQLSTLSHTTSFEP  2760
Celery latent virus (AZJ53460.1)     VNGDDYIGGMSPLLASHLTKEKMAKTFSDFQFIYEWSDYSPSLFEQDYMSLKFINIVERKGQTTGQQLIAPWREASRQLSTLAHTSSGAP  3038
                                     ************ **. ****:** **. *** ******* ***:*:*******:* . .   .*.: *******.*******:**:*  *

Striga-associated poty-like virus 2  WIKLQVALTERVKAWVDRDLFEFITSYAKWYLNHVGESCQRKEWQEVQALWWDEQHIFNHYFSRESARSQGSIELFRSMPEGEDIIWGPR  2850
Celery latent virus (AZJ53460.1)     EIKLQVALTERVKAWVDKDLFDFITEYCRWLVEYFDRFTNTQAWNEAKKLWWDEQQIFNHYFSFESICNAPYSQIVNETPD-EFFANGVR  3127
                                      ****************:***:***.*.:* :::...  : : *:*.: ******:******* **  .    ::... *: * :  * *

Striga-associated poty-like virus 2  ESFNFEV-EDGSEVRTS------LGNADSSL------------------------------ENDAHKRK------RNDDRTLSVCFQQNC  2897
Celery latent virus (AZJ53460.1)     ESRPLRILRDGIKFGVAVTAANYLGPSDHDVPMIANTMLNVAKIGLANSTAERIDRMLFGKENPEHSRADSLVVVKTEQTDATICLRTHC  3217
                                     **  :.: .** :. .:      ** :* .:                              **  *.*       :.::   ::*:: :*

                                                                                                       NIb|CP
Striga-associated poty-like virus 2  PCPSEH---AFQRRDFNQKNLLRFCTTEWIEKLESYDFYELPESLYEQQEILFHVWFHILKG----QTVQQIQ|NDLSLTRSRKMCSVAH  2979
Celery latent virus (AZJ53460.1)     KCQAQHFDGKYECWVSSPSVAIKMFATLKPRILSTTKFVGVK---FLPKILRAHVWALYLSGFSWEETMQIVQ|SHYPGEKQQRK---AD  3300
                                      * ::*    ::    . .  ::: :*   . *.: .*  :    :  : :  ***   *.*    :*:* :* .. .  :.::    *.

Striga-associated poty-like virus 2  WFSRQIIGVCICHYQNDNGKMNYKGVITILGKSSKLNTNNRQAMTTVVATPQHY---FRLTNPQGFGNDAQAANAAWNALSEADKEAWRQ  3066
Celery latent virus (AZJ53460.1)     WFLQQLLKELVLIFKVKGSKF------IELGEHAQVQGKTQLDSTQVDMDPNFNAAAYAATLRGGPHWGTHNSQGLFDAIKVLNPNA--A  3382
                                     ** :*::   :  :: ...*:        **: :::: :.:   * *   *:.    :  *   *   .:: ::. ::*:.  : :*

Striga-associated poty-like virus 2  RFEALPVHNGQRRISDQEIVPPRQRREERREEQHEQQRPPPQGGARIAHGENAKRQQSLMQKYGNILTTAEPEGFKQDVMSSKAVGLVEN  3156
Celery latent virus (AZJ53460.1)     NVDIGNARTAVQREMQRLIAADAPRQQPPPQVGGGHQQPPPAGGQTQGQPGGYTPSQAFTNKFGNIMAEPDAPLVLDSQATMREVAQIEA  3472
                                     ..:   .:.. :*  :: *..   *::    :   :*:*** **   .:  . . .*:: :*:***:: .:.  . :.  : : *. :*

Striga-associated poty-like virus 2  RWARRCGLPNGASLVNHPEFWRFIFTYVCNNGTSTSGNLEQEFMVNEEIIKISMLVDDANQHGGWRRFWRSKADDLYNFLAILKENGENM  3246
Celery latent virus (AZJ53460.1)     AWAR---LLEVQSLEGLGSFWNYMFSYVGNNGTSSGGDPRDYIPAGNGRVTLAQLKSKA-QGEQWRRYWRSHASDMRDFLRLLQASDRPL  3558
                                      ***   * :  ** .  .**.::*:** *****:.*: .: : ..:  :.:: * ..* *   ***:***:*.*: :** :*: ... :

Striga-associated poty-like virus 2  PIDWAKKNGFPPEHSHLGFDVVDYCKDLSPQEKQVLAAIKARAVPRNRGTLVGTSLKPNTGGDEETYGNVDRDIVR-DMGGGFR  3329
Celery latent virus (AZJ53460.1)     PIRWARNNGIKDANYEIAFDFADALPDLSAAQMSIILAAKNLAVRRGQGQMLNAGTKVGGRSRTETYDQAVRDAADVQFPGA--  3640
                                     ** **::**:   : .:.**..*   ***. : .:: * *  ** *.:* ::.:. * .  .  ***.:. ** .  :: *.
```

Fig. S4. Alignment of the "small" polyprotein sequences of SaPlV2 and CeLV

The PIPO segment is highlighted in cyan.

```
Striga-associated poty-like virus 2  MAAKIAT-----------------------------------------------------------------------------------     7
Celery latent virus (MH932227)       MSKRIYTIIVVLCFQVCFQNLRTQPTQSSHTFSTNPAIPGTDALQFEENANLTYSTIKYNILKFNLNYKQSIMSVVSFGSITSMDFDAAC    90
                                     *: :* *

Striga-associated poty-like virus 2  ------------------------------------------------------------------------------------------     7
Celery latent virus (MH932227)       LAAMIETPGGSIPPTPQSPPTSPVAVKQRKILNFPIAKIRTTPDASFEMCVKFPESFIDSFCAQAQKELKYWHAAITQLKFFGGETPKTL   180


Striga-associated poty-like virus 2  ------------------------------------------------------------------------------------------     7
Celery latent virus (MH932227)       ETLVNQGQAHTHQVILNLVKILDSAPKAIQGKKELENFFQLSPHGNNSKEPIDVSRKVYMEPCKISPRKRQVCSCDNDDDAHYHCYYCDI   270


Striga-associated poty-like virus 2  ----------------------------------------------------------------------------SYVETGLLF----G    17
Celery latent virus (MH932227)       VCSSKNLLQEHERDFCEDAQSVQAFGYKLESPNVFDPPHVTQQRSVAPSLGKTLESPVKSPEQSKPNLEKSFPLVESSTNSGMIFFGSIA   360
                                                                                                             * .::*::*    .

Striga-associated poty-like virus 2  SWTPQNVWAIDGPTTEVPQLPTAAPVRNQAERLVRALPKVQEALEEGAKEVVLSNFQWGSLSARFYNPKGVGHDILEKKMVLVKSTHRKP   107
Celery latent virus (MH932227)       TMVPSHI------EKYVRNCETENPIDAAASNLA-----MQEAKSSGAPCIVVHHKALPGGKKDFLFPHNSPQVVRTETEEPIAGTIDRP   439
                                     : .*.::       . * :  *  *:   *..*.     :*** ..**  :*: :    . .  *  *:.  : :  :.   : .*  :*

Striga-associated poty-like virus 2  LLEEVVQTRFVTTEKQILVRPGANICAKTKRPLRPGEVKQLIKATGDPQHPLFCLPITKLIETTHPIYRIEIDAKEEFYVLRGDVRLLSR   197
Celery latent virus (MH932227)       TIKRALFTRIKKKAQEICVNPGGTIQRKTKRWLRPAEVAQIVRATSDPQHPLFKVDVTQIIEVVHPVYRTERTEVVQQCITRGTYKLMSK   529
                                      ::..: **: .. ::* *.**..*  **** ***.** *:::**.******* : :*::**..**:** *     :  : **  :*:*:

Striga-associated poty-like virus 2  RQRQKLHQKRWNKELVIDESDTSSWNSREHWVEKLVPKKAYTKYIKCGKLPEELEP---WTNARNSDDFELPSKNKLKKMS-TAQKLACV   283
Celery latent virus (MH932227)       AQQRKARAMRSAGMLVITDNPTTHWVSEPQKMLVVKEKLSTTKHVKLRNVEVNAESEMFWGTKTK----EGPSKTALKRCKRNIDRLALL   615
                                      *::* :  *    *** :. *: * *. : :  :  * : **::*  ::  : *.   * .  :    * ***. **: . . ::** :

Striga-associated poty-like virus 2  DKNFEHDLKGHCWRNIFTDRISFGDMKSQPKGWHEHRFGRVKGSFIPLVKFCELLQEEVARFPSLAEMLVPRPFCYREGGRLVYHVGYSK   373
Celery latent virus (MH932227)       DPQMGESANGECWMNTFKHHLKVGSIDILPNKVRLPNLRSAFSRWIPLVDYVEILKFHCKSQPKLKRVVIPTPVTYLEGSRYHIHVGYSK   705
                                     * :: .. :*.** * *..::..*.:.  *:  :  .:  . . :****.: *:*: .    *.* .:::* *. * **.*   ******

Striga-associated poty-like virus 2  ------FSRGFCSLQSLLHPPIKSGNPKVPKSVLLEAVVGAEPTEDVETFDTIDWEFDLGVPIVDIDLASKVAGTLEVAEQIADYQTGTT   457
Celery latent virus (MH932227)       NCSWITVEQLIRQLQTLLTSSKYGEHFK-------RAIVGGEPED----------KFTPVVPIVDVE-------TERAKSSLAKWTTAQQ   771
                                           ..: : .**:** ..  . : *       .*:**.** :          :*   *****::       * .. ..:*.: *.

Striga-associated poty-like virus 2  YGEPNDVTACELGHCYHKFWWDPSLPVWKNDVNRGICIAMTRSFRENKMYLRDFLVQLEDQESMGFIPQVKVVATPFIYCLKGRLYMHVG   547
Celery latent virus (MH932227)       RYMGSIRTRINSQAEKHKIDSEKK-DLDTNEARHDGYVNSTISFRK----------WAEKQRSSTSRPG--------------------   829
                                         .  *  :     **:  : .  : .*:..:.  :  * ***:            *.*.*    *

Striga-associated poty-like virus 2  DHPEGANCGRNDALRYIHEFSRRLPYHLWKEVIVGAS-PIKKKKMVSGHKLRRRTVWRRVSNSKSKRVVKAVTTSAKIIFSGIRSCWRKL   636
Celery latent virus (MH932227)       --------------------SWRFCRSCWKQFRSEFSMPTTKCGACIRRKQRQRDKRERAQHSKLSYCQYAVARAMQIVARLTRTSYHGL   899
                                                         * *:    **:.    * * .*      :* *:*   .*..:** .    **: : :*:    *:.:: *

Striga-associated poty-like virus 2  RQTERIRELQRTLRDVEFRALKERNELWQRF-----ESSEAHRAEWEQTAWKIAQVLGIKMDADLGAIARRVLARNSTSNANEGRRFLA   720
Celery latent virus (MH932227)       RRTRKLGDSEARCRGLA-ETINEEKRLTEEFAKILIEENSRLRRDVENIGQRMEKICHLNRCSNCECFH----CRSFKSSRSKGKYFLA   983
                                     *:*.:: : :   *.:  .:::*.:.* :.*     *...  * : *: . :: ::  ::  ::  .:     .*. .*. .:*: ***
```