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# Complete genome sequence of Habenaria mosaic virus, a new potyvirus infecting a terrestrial orchid (*Habenaria radiata*) in Japan

Hideki Kondo<sup>1,\*</sup>, Takanori Maeda<sup>2</sup>, I Wayan Gara<sup>1</sup>, Sotaro Chiba<sup>1</sup>, Kazuyuki Maruyama<sup>1</sup>, Tetsuo Tamada<sup>1</sup> and Nobuhiro Suzuki<sup>1</sup>

<sup>1</sup>Institute of Plant Science and Resources (IPSR), Okayama University, Kurashiki 710-0046, Japan.

<sup>2</sup> College of Bioresource Sciences, Nihon University, Fujisawa 252-8510, Japan

\*Corresponding author: Hideki Kondo e-mail: hkondo@rib.okayama.u-ac.jp Tel. +81(86) 434-1232 Fax. +81(86) 434-1232

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### Abstract

The complete genomic sequence of Habenaria mosaic virus (HaMV), that infects a terrestrial orchid (*Habenaria radiata*), has been determined. The genome is composed of 9,499 nucleotides excluding the 3'-terminal poly (A) tail, encoding a large polyprotein of 3,054 amino acids with the genomic features typical of a potyvirus. Putative proteolytic cleavage sites were identified by sequence comparison to those of known potyviruses. The HaMV polyprotein showed 58% amino acid sequence identity to that encoded by the most closely related potyvirus, tobacco vein banding mosaic virus. Phylogenetic analysis of polyprotein amino acid and its coding sequences confirmed that HaMV formed a cluster with the chilli veinal mottle virus group, most of which infect solanaceous plants. These results suggest that HaMV is a distinct member of the genus *Potyvirus*.

# Introduction

Habenaria radiata (Thurnberg) K. Spreng. is a wild terrestrial orchid growing in wet grasslands in both warm and cold temperate regions in Japan. This orchid is cultivated as an ornamental plant because of its beautiful bird-shaped flower petals [18]. At present, the occurrence of two viruses, Habenaria mosaic virus (HaMV, unassigned virus) and watermelon mosaic virus (WMV, potyvirus, formerly WMV-2), has been reported from *H. radiata* plants in Japan [8, 12]. HaMV causes mosaic symptoms in *H.* radiata plants [12], whereas the symptoms of WMV are stunting in addition to leaf mosaics and distortions [8]. HaMV is sap-transmissible to some experimental plant species, but *H. radiata* is currently the only known systemic host [12]. Despite the lack of sequence information on the HaMV genome, the virus has long been believed to be a potyvirus because of its filamentous particle length of ca. 750 nm, non-persistent mode of transmission by aphids and formation of typical cylindrical inclusions in infected cells [12]. Furthermore, HaMV shows distant serological relationships to several potyviruses including WMV, and is thus suspected to be a new potyvirus species [12]. Here, we report the complete genomic sequence of HaMV. The phylogenetic relationship of HaMV with other potyviruses revealed that HaMV is sufficiently distinct

from known potyviruses and is a possible new species of the genus Potyvirus.

## Materials and methods

An original isolate of HaMV (Ha-1) was obtained from a commercially available H. radiata plant showing mosaic symptoms in Okayama Prefecture, Japan in 1974, by N. Inouye [12]. HaMV (Ha-1) had been isolated by single legion transfer using an experimental host Chenopodium quinoa. The virus was purified from mechanically inoculated leaves of C. quinoa, essentially as described by Gara et al. [8]. Viral RNA was extracted from purified virus particles using proteinase K and SDS followed by phenol extraction and ethanol precipitation. First and second cDNA strands of HaMV genome were synthesized using the TimeSaver cDNA Synthesis Kit (Amersham Pharmacia Biotech, Uppsala, Sweden) with an oligo(dT) primer or virus-specific reverse primers designed according to the newly determined sequences. Two regions (nucleotide positions at 530-3710 and 3606-5766) with some sequence ambiguity were amplified by RT-PCR using virus-specific primer sets and sequenced. PCR was performed using KOD or KOD FX DNA polymerase (Toyobo, Osaka, Japan). The 5' end of the RNA genome was determined by RACE using the 5'RACE system (Invitrogen, Carlsbad, CA, USA). All cDNA and RACE fragments were cloned into the pGEM-T or pZErO-2 vector (Invitrogen, San Diego, CA, USA) according to the manufacturer's instructions. These plasmid clones were used to transform competent Escherichia coli DH5 alpha or TOP10F' cells. The DNA sequences were determined by the dideoxynucleotide chain-termination method with a DNA sequencer, model ABI377 or ABI3100 (Applied Biosystems, Foster City, CA, USA). Sequences of the primers used in this study are available upon request.

Sequence assembly was performed using the AutoAssembler program (PE Applied Biosystems). Sequence data were analyzed using GENETYX-MAC (Software Development Co., Tokyo, Japan) or Enzyme X (version 3, Mek & Tosj). The putative translation products were compared with the corresponding regions of other potyvirus sequences available in GenBank using BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Phylogenetic tree construction was based on a maximum-likelihood (ML) method as described previously with minor modification [5, 14]. The potyviral polyproteins or their

ORF sequences were aligned with MAFFT version 7 [13] and gap-cleaned using Gblocks version 0.91b [20]. Selection of the best-fit model for the data sets was performed using jmodeltest 2 [7, 10] and ProtTest 2.4 [1] for nucleotide and amino acid sequences, respectively. ML phylogenetic trees were generated in PhyML 3.0 using the appropriate substitution mode [11]. The resulting ML-trees were visualized using Figtree version 1.3.1 (http://tree.bio.ed.ac.uk/software/figtree/).

### **Sequence properties**

The full-length genome sequence of HaMV Ha-1 is 9,499 nucleotides (nt), excluding the poly (A) tail at the 3' end (Fig. 1). The sequence has been deposited in the GenBank database as accession number AB818538. The genome organization of HaMV is typical of a potyvirus, containing a large open reading frame (ORF, 135-9,299 nt) that would encode a polyprotein of 3,054 amino acid (aa) residues with an estimated molecular weight of 345.4 kDa (Fig. 1). Nine putative protease cleavage sites were predicted, based on a multiple alignment of polyproteins encoded by closely related potyviruses (supplementary Fig. S1). The HaMV polyprotein is potentially cleaved into ten functional mature products (P1, HC-Pro, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb and CP) by the viral-encoded proteases [2, 22] (Fig. 1). In these proteins, conserved motifs of potyviruses were detected, such as the <sup>170</sup>Hx<sub>8</sub>Dx<sub>32</sub>S<sup>213</sup> (x, any amino acid residue) motif in the P1 protein, the <sup>313</sup>KITC<sup>316</sup> and <sup>442</sup>FRNK<sup>445</sup> motifs in HC-Pro, the <sup>1207</sup>GSGKSx<sub>3</sub>P<sup>1251</sup> and <sup>1293</sup>DExH<sup>1296</sup> motifs in CI and the <sup>2599</sup>GDD<sup>2601</sup> motif in the NIb [22] (supplementary Fig. S1). However, the Ha-1 isolate has <sup>2774</sup>DAT<sup>2776</sup>, instead of the DAG motif important for aphid transmission, at the N-terminus of the CP [16] (supplementary Fig. S1). A point mutation (G to T in the triplet) presumably occurred during several rounds of transfer through mechanical inoculation under green house conditions (data not shown). In addition, the presence of a small overlapping ORF (PIPO, expressed after ribosomal frameshift or transcriptional slippage at motif G<sub>1-2</sub>A<sub>6-7</sub> <sup>[2757</sup>GAAAAAA<sup>2763</sup>], Fig. 1, arrow) was also predicted within the P3 cistron [6].

A BLASTp search with the sequence of the polyprotein encoded by HaMV Ha-1 revealed that it shared significant aa sequence identity (53–58% identities; 95–96% query coverage: QC) to the polyproteins encoded by members of chilli veinal mottle virus (ChiVMV) group (subgroup 5) and their two relatives [9, 19], i.e., ChiVMV, chilli ringspot virus (ChiRSV), pepper veinal mottle virus (PVMV), tobacco vein banding mosaic virus (TVBMV), and wild tomato mosaic virus (WTMV) as the subgroup 5 members, and yam mild mosaic virus (YMMV) and christmas bell potyvirus (YMMV, an unclassified potyvirus) as the relatives. For each gene product of HaMV, aa sequence identities to the ChiVMV subgroup (subgroup 5) and two related viruses are 28-42% (37-96% QC) in P1, 61-64% (100% QC) in HC-Pro, 28-35% (95–100% QC) in P3, 32–57% (31–98% QC) in PIPO, 67–78% (96–98% QC) in 6K1, 58-62% (100% QC) in CI, 47-58% (98-100% QC) in 6K2, 59-69% (94-100% QC) in VPg, 52-58% (100% QC) in NIa, 61-70% (92-100% QC) in NIb and 61-70% (98-99% QC) in the CP region. Based on pairwise comparisons of the complete genome sequences, HaMV Ha-1 shares identities of 55-59% at the nt sequence level with ChiVMV and its related viruses. These values are far below the current species demarcation criteria (CP aa sequence identity less than about 80%; and nt sequence identity less than 76% either in the CP or over the whole genome), set by the International Committee on Taxonomy of Viruses [3, 4], which supports the designation of Habenaria mosaic virus as a novel species in the genus *Potyvirus*.

An ML phylogenic tree was constructed by PhyML with GTR+I+G as the best-fit model selected by jmodeltest 2, based on an alignment of the nucleotide sequences of polyprotein ORF from the 78 selected potyviruses (see supplementary Table S1). As shown in Fig. 2, HaMV is clustered within the ChiVMV subgroup (subgroup 5), which includes ChiRSV, ChiVMV, PVMV, TVBMV and WTMV [9]. A similar ML-tree was obtained using an alignment of the polyprotein aa sequences (supplementary Fig. S2 and Table S1). These phylogenetic analyses suggest that HaMV might have a common ancestor with the ChiVMV subgroup members, which are mainly distributed in Asian countries and whose primary hosts are solanaceous plants [19].

A search for possible recombination events using the Recombination Detection Program (RDP3) [17] revealed that no detectable recombination between HaMV and WMV, both of which could infect *H. radiate* (data not shown).

In conclusion, this is the first report of the complete nt sequence and genome organization of a potyvirus isolated from a terrestrial orchid, *H. radiata*. Sequence comparisons and phylogenetic analyses indicated that HaMV should be classified as a new member of the genus *Potyvirus*, within the previously established ChiVMV

subgroup (subgroup 5).

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#### **Figures**

Fig. 1. Schematic representation of the genome organization of HaMV Ha-1. The 5'and 3'-untranslated regions (UTRs) are shown as bold lines. Two highly conserved blocks, the potyboxes 'a' (<sup>14</sup>ACACAAaCAU<sup>25</sup>) and 'b' (<sup>42</sup>UCAAGCA<sup>49</sup>) [21], are present in the 5'-UTR. The box represents a large ORF, encoding a viral polyprotein. Six polymorphic sites at positions 297 (C/T), 736 (G/A), 1,436 (C/T), 4,995 (T/C), 6,314 (G/A), and 8,466 (T/C) were identified (data not shown). Of those, three sits 297 (P55S), 736 (G201E) and 8,466 (S2,778P) were non-synonymous substitutions, whereas the rest were synonymous. Numbers below the genome represent the first and the last nucleotide (nt) position of the ORF and the full-length genomic sequence excluding the poly (A) tail. The first initiation codon within the genome, at position 135, is within a favorable context for initiation (131AGAGAUGGC139, initiator codon underlined) as described by Kozak [15]. The polyprotein is predicted to encode ten mature proteins: P1 (first protein/protease), HC-Pro (helper component protease), P3 (third protein), 6K1 (first 6-kDa protein), CI (cytoplasmic inclusion protein), 6K2 (second 6-kDa protein), VPg (viral protein genome-linked), NIa (nuclear inclusion a protein/protease), NIb (nuclear inclusion b protein) and CP (coat protein). The numbers above the genome indicate the amino acid (aa) position of the predicted proteolytic cleavage sites by the viral proteinases. The aa residues around the cleavage site are indicated below the diagram in comparison with those of closely related potyviruses (see Supplementary Fig. S1). A small ORF created by ribosomal frameshift or transcriptional slippage is shown in the figure above the P3 region as a small box (PIPO) [6]. The position and nt sequences of the heptanucleotide motif are indicated.



**Fig. 2.** Phylogenetic relation of HaMV and other potyviruses. A maximum-likelihood (ML) tree was constructed using PhyML 3.0, based on the multiple nucleotide sequence alignment of the viral polyprotein ORF. Virus names and GenBank accession numbers of their genome sequences (presented as acronyms) are listed in Supplementary Table S1. Viruses with asterisks indicate unassigned species. RGMV, genus *Rymovirus*, is used as an outgroup. The branch support values were estimated using the approximate likelihood ratio test (aLRT) with a Shimodaira–Hasegawa-like (SH-like) algorithm (only values greater than 0.9 are shown as filled circles.

**Supplementary Table S1**. GenBank/Refseq accession numbers of sequences compared in Figs. 1 and S1.

Virus names-isolate names, abbreviation (GenBank/Refseq accession no.) Genus Potyvirus Algerian watermelon mosaic virus-Algeria: H4, AWMV-H4 (NC 010736) Apium virus Y-USA: Ce, ApVY-Ce (NC 014905) Banana bract mosaic virus-Philippines, BBrMV-PH (NC 009745) Basella rugose mosaic virus-Taiwan:AC, BaRMV-AC (NC 009741) Bean common mosaic necrosis virus-USA:NL-3, BCMNV-NL3 (AY282577) Bean common mosaic virus (=blackeye cowpea mosaic virus), BICMV (NC 003397) Bean yellow mosaic virus-MB4, BYMV-MB4 (NC 003492) Beet mosaic virus-Wa, BtMV-Wa (NC 005304) Bidens mottle virus-Taiwan:B12, BiMoV-B12 (EU250210) Brugmansia suaveolens mottle virus-Brazil, BsMoV-BR (NC 014536) Canna yellow streak virus-UK, CaYSV-UK (NC 013261) Celery mosaic virus-USA, CeMV-USA (NC 015393) Chilli ringspot virus-China:HN/14, ChiRSV-HN/14 (NC 016044) Chilli veinal mottle virus-pepper vein banding virus, ChiVMV-PVB (NC 005778) Clover yellow vein virus-30, ClYVV-30 (NC 003536) Cocksfoot streak virus-Germany, CSV-DE (NC 003742) Cowpea aphid-borne mosaic virus-Zimbabwe, CABMV-ZM (NC 004013) Daphne mosaic virus-Czech Republic, DapMV-CZ (NC 008028) Dasheen mosaic virus-China: M13, DsMV-M13(NC 003537) East Asian passiflora virus-Japan: AO, EAPV-AO (NC 007728) Freesia mosaic virus-South Korea, FreMV-KO FreMV-Kr GU214748 Fritillary virus Y-China:Pan'an, FVY-PA (NC 010954) Japanese yam mosaic virus-mild, JYMV-mild (NC 000947) Johnsongrass mosaic virus-Australia, JGMV-AU (NC 003606) Konjac mosaic virus-Japan: F, KoMV-F (NC 007913) Leek yellow stripe virus-China: Yuhang, LYSV-YH (NC 004011) Lettuce mosaic virus-E, LMV-E (NC 003605) Lily mottle virus-China:Sb, LMoV-Sb (NC 005288) Maize dwarf mosaic virus-Bulgaria, MDMV-BU (NC 003377) Moroccan watermelon mosaic virus-Tunisia:TN05-76, MWMV-TN05-76 (EF579955) Narcissus degeneration virus-China:Zhangzhou, NDV-ZZ (NC 008824) Narcissus late season yellows virus- China: Zhangzhou2, NLSYV-HZ2 (JQ326210), Narcissus yellow stripe virus-China:Zhangzhou, NYSV-ZZ (NC 011541) Onion yellow dwarf virus-China: Yuhang, OYDV-YH (NC 005029) Papaya ringspot virus-Hawaii, PRSV-HAT (X67673) Passion fruit woodiness virus-Australia:MU2, PWV-MU2 (NC 014790) Pea seed-borne mosaic virus-DPD1, PSbMV-DPD1 (NC 001671) Peanut mottle virus-M, PeMoV-M (NC 002600) Pennisetum mosaic virus-China:B, PenMV-B (NC 007147) Pepper mottle virus-California, PepMoV-Cal (NC 001517) Pepper severe mosaic virus-South Korea, PepSMV-KO (NC 008393) Pepper veinal mottle virus-P, PVMV-P (NC 011918) Pepper yellow mosaic virus-Brazil:Pi-15, PepYMV-Pi15 (NC 014327) Peru tomato mosaic virus-Peru:PPK13, PTV-PPK13 (NC 004573) Plum pox virus-NAT, PPV-NAT (NC 001445) Potato virus A-Hungary: B11, PVA-B11(NC\_004039)

Pokeweed mosaic virus-MS-FR03, PkMV-MS-FR03 (NC 008393) Potato virus V-UK:DV 42, PVV-DV42 (NC 004010) Potato virus Y-France:O, PVY-O (NC 001616) Scallion mosaic virus-China:Hangzhou, ScaMV-HZ (NC 003399) Shallot yellow stripe virus-China:ZQ2, SYSV-ZQ2 (NC 007433) Sorghum mosaic virus-China: Xiaoshan, SrMV-Xiaoshan (NC 004035) Soybean mosaic virus-N, SMV-N (NC 002634) Sugarcane mosaic virus-China:Hangzhou, SCMV-HZ (NC 003398) Sweet potato feathery mottle virus-S, SPFMV-S (NC 001841) Telosma mosaic virus-Vietnam:Hanoi, TelMV-VN (NC\_009742) Thunberg fritillary mosaic virus-China: Ningbo, TFMV-NB (NC 007180) Tobacco etch virus-HAT, EV-HAT (NC 001555) Tobacco vein banding mosaic virus-China: YND, TVBMV-YND (NC 009994) Tobacco vein mottling virus-S, TVMV-S (U38621) Turnip mosaic virus-UK1, TuMV-UK1 (NC 002509) Watermelon mosaic virus-Fr, WMV-Fr (NC 006262) Wild potato mosaic virus-Peru, WPMV-Peru (NC 004426) Wild tomato mosaic virus-Vietnam: Laichau, WTMV-VN (NC 009744) Wisteria vein mosaic virus-China:Beijing, WVMV-BJ (NC\_007216) Yam mild mosaic virus-Brazil, YMMV-Brazil (NC 019412) Yam mosaic virus-Ivory Coast, YMV-IC (NC 004752) Zantedeschia mild mosaic virus-Taiwan, ZaMMV-TW (NC 011560) Zucchini yellow mosaic virus-Taiwan:TN3, ZYMV-TN3 (NC\_00322) Unassigned related viruses Arracacha mottle virus- Brazil:C-17, AMoV-C-17 (NC 018176) Calla lily latent virus-Taiwan:m19, CLLV-m19 (EF105297)

Christmas bell potyvirus-Taiwan:CB, CBPV-CB (EF427894) Keunjorong mosaic virus-South Korea:Cheongwon, KjMV-CW (NC\_016159) Lupin mosaic virus-Czech Republic:Lu2, LuMV-Lu2 (NC\_014898) Panax virus Y-China:2, PnVY-2 (NC\_014252) Sunflower chlorotic mottle virus-Argentina:Common SCMoV-C (NC\_014038) Sweet potato virus C-Peru:C1, SPVC-C1 (NC\_014742) Verbena virus Y-USA:Michigan, VerVY-Michigan (NC\_010735)

Rymoviruses (outgroup):

Ryegrass mosaic virus, RGMV (NC\_001814).

**Supplementary Fig. S1.** Multiple amino acid sequence alignment of the polyprotein of HaMV and closely related potyviruses (ChiVMV subgroup and their two relatives). The putative catalytic residues, cleavage sites and other conserved motifs of potyviral polyproteins are highlighted in blue, green and red, respectively.

#### CLUSTAL format alignment by MAFFT $^{\circ}\,v7\,.\,029b)$

HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	MAIQFGTITSDMLAACKVKQHL MAA-QVIFSYLKSGSGVTTDAC-RAQAMQFTFGSFTFGKVNWNTLSSAMIE MAI-RVSFPCFYNTHNSTLSEC-KSVTMSICFGSLKPKQIDWNEASNNLLK MAT-TVTFPWSANFE-IKQGIC-RSRGFTLQFGSFEPVAIDWVQEGANILQ MAT-TVTFUGLVNKIAITGC-KIERVKIVTPI-PFIQFGTIERRMLNFNDYSDKIIE MSMFNITYLLGKQVSQQSCNRVTVASSVMAPNIQFGTITSDVLVNGDSKPRITE MAAVAMSTTLPKVIFPIEVESIGKYGGVNFIFGSFTTEETSAKITK MAG-MITFGSFAPVPIAGCTHPEMLKVAKPRVAKQVLTTRLGTNLSANRSAGRALIK *:
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	-THDEILDRAMIEKYGVAKVSRK EYETRQESFELACEKFRKERTDMRIVRK 
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	-VLPYIKSLNEQIPKPRIRKVWRVESTGFGETQIVESIVDTDNNNVIKMDDTPSVK ETFQYSPKTKYQL-KGARRKE-RKEEQERKFLASSDTIVARIVFPEAMKVEAPVEPI GVYKYAPKTRAQL-RKERKHN-RILEERAEFLNGKDSIITGMVFPVEARKAQTEEAPF GYLKYAPKTPTML-RKERRA-RLERERKDFLNAPDQVVTEICFPPEAPK-RMETPSI GTLIYKKMGVMKAEKLERRQQRRLDAEK-AFQSGDPYIITEINNAMHCNIKACEPEKR GTLKYKRMTHAKYARKVRRNE-RLDKERQAFLNADPYVITSLKIAFGDREAGVDCAPK GT-KYLKEYSARFKKECAIREKNLREEIDWFKNHEPFLVDKIKFESDDREAHIEAGET GVRSVQQKTPKVCKTFDGFDSVVTHIVIPSTTRVENDKSLQV 
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	GRVVATSFKTRSAKIARPIVQSLGEKNSLLHKVCAVAFKRGIPVTFIGKRTERVRAAR RFPPVVVRKVRKQPRPNITRVSTGSFSLFIKELVNTCDDRQIPLEMIANKRERVHVRI KYPPIVQRKPRKTPHMNYVTLNDTQFDQFTRELINACEATSQPMEIIGKRKVRVQARV RFPPVVVRKKRVAPQRQSVAISHAGFDNLLRELTVVCREMNKPLEFVGSARGLVRANI GLIFCTRSQKVRKNVKNVVHLRHTTTLDLAMNICSSFVKEGKPIEIIGKGKRRAIKCR GRIHTTPSTKRKKALKKVLKLKRMSVMDLANSICKPFIDSGKPIEIIGRRNKHIAHCR KKVFFTRSKRVRHGIKR-THLSQEQVQSLISSVIKITPMNCVIELKHKGAPSVLT KHPAVVYRKRKTPPRQNYVTLDERGLSQVILLDRQVMQILQAGKRKPITISRC 
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	H D S HV-TSNFSCMAIATHHHAGKTRNVDVPHMGSLRDTIVSVAHATWKGGKIHERNIKGDSG RRFTPSHRCAQVKTIHHRGTYQNVDFECPIALKSLFGLIAQHAWKGQDVDELKISIGDSG TRLFSNTRCLQVVTKHHKGKLCEIDVPNMRGIENSLGHLAQAAWKGGFVNEERLGYGTSG VKPSFPESRLVCVTKHHEGIQSIDVHVPNTVRAIFTRIAQLAWKGFIIBDDCKIGDSG SIHADNRVLKVNTAHERRVKRSIDFKMDPSVSLVLEFLAIHTWKGRIISDQQVKKGMSG KQYFKGRRILKVQTCHEKGEHKVPDYVENTRAIASLQTFPDTFWRGKPLHERQITRGCSG NVGPYTTLHVTKHELGKMAPIDLSLDEDSESILQSFANTLPTTLDIREEDFRPGTSG
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	P1/HC-Pro CIIPREMIEGTVHCEKDDVF-IVRGRYGNLLLDAQSYLPKKIISRINHYSAGELFWKGFD LCIPHGKLIGRVLSGDSDFF-IVRGRYGSLLIDSQAYLPKKIISRINHYSAGELFWKGFD CCIPHGLLKGRTFDGFDFF-IVRGRYGPLLMDSTRYTPKQVLADLQHYSAGDKFWSGFD VCIPKGKLKSPSRTINENLF-IVRGAYRNELQDAQQALPLYKYMRWHFSAGEKFWSGFN FVIPLASFTADIPEASNSVF-IVRGRUGDDLVDAREIVPRHEIDSIEHYSAAEQEWKGFD FVIPKSRI-PDLKTADNYKFLVVRGRWRKTLVDARVHISPEILEGINHYSIANKFWDGFE FIISRAFLNGYYCTGTHMIVRGRHKNLLCDSASYLPASYLNEITHYSVAETFWKGFD AIIRRDCLDNVAHKVPDSDYFIVRGRFAGSLLDARETFNISHRFYLRQYSVADQFWKGFD * : *** **: ::::::::::::::::::::::::::
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRsV-HN/14 YMMV-Brazil* CBPV-CB*	MAFRANRGNQLIHEPGE-KLDVEQCGAVAAILHQSLLPCCKITCTTCSKILEESSAEETR REFKTHRTTPVIHAGMN-TNNVEECGSVAAIVCQALMPCCRITCTVCAKANVDQGTSGLQ QAFRAHRTTPVIHAGMN-TLDVTQCGEVAAIMCQSLMPCCRITCTVCATTNADITQLELR KGFLTHRTTPTVHAGSN-TIDVVECGFVAAIMCQSLMPCCRITCTVCAKQVDDSSSEIA ETFRSFRTTTKMHERKNNVLDVVQCGEVAGIICQSLMPCCRITCIQCANEYATKSVDEVR QAFIKHRSNPVIHERDDSTLDVKQCGSVSGVVCQALMPCCRITCGKCADUYAQMSSTEIR EGFRTNRHIPQIHEGKN-TLPVEVGKVAGIVCQSLVPCRITCTECAAKHLQASEVEAR TEFRQQRGRTIHEGMN-TLSVEATGSVAAIACQALYPCCRITCTCGRIVDRMSETQLS * * ;* ; * * * *:: *: ** **:*** *.
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	QRIGQTARKGAQLIRRNFRGFEHVYQLLMNHANMLDCVNGNREACGKVQYIIGERTEAPF ERLIHSLETGIKELEDRYKSFPHAAQLLKGHLSSYKKPNPHHEATSKVQFLIGDRKEQPF ERIAHSIKGSISELSEKYPAFPHAVRFLKDYLISLNNLNPNREASGKVHFLIGDRKEQPF TRIEHSLADGINEIESKYPSFKHAVKFLKDYRQSLHKSNPHEASGKVQFLIGERRDQPF THIEDTLNKGISGIQQKYPNFPHTVALLETYKTMLNSVNTNREACGKVHFLIGDRTEQPF NHITSTLSNGIKILKQQHPDFPHNIAMLESYKTMLNSVNTNREACGKIHFLIGDRTEQPF NELTQTLSIGARKIREEHPDFEHVANSLKKIEHLISLRNDNREASGKIQFLIGERTEAPF DHVQAGLRAGIETLRNRFPEFHHVQDILERYSTSFNNSGNNSEAHGRIKFSIGDINEPPF .: * * * * * * * ** * **

FRNK SHVLRINETLIKGNQATASELSAASAHLLEIARYLKNRTENIQKGSLRS<mark>FRNK</mark>VSAKAHL HaMV' SYILEVNEVLIRGGRATSEEFSRASDCLLELARFHKNRVESLKKGSLHL<mark>FRNK</mark>VTSKSHI SHILAVNETLIKGGRATSDEFAHASDELLQLARFHKNRVESLKKGSLHL<mark>FRNK</mark>AASKAHI ChiVMV-PVB PVMV-P WTMV-VN MHILNINEVLMRGGRASSEEFARASDDLLELARHHKNRVESLKKGSLHLFRNKVASKAHL TVBMV-YND ChiRSV-HN/14 IHVLRVNEILIKGNRATNSELNMASNELLEIARYLRNRTDNIKKGSLATFRNKVSAKAHIIHVLRVNEVLIKGNRATSGELEGASNELLEVARYLKNRTDNIKQGSLTTFRNKVSAKAHLYMMV-Brazil\* THILSINECLLRGTKNTSTDFSRATDHLLELARWMRNRTENIRKGSIEN<mark>FRNK</mark>ISGKAHI CBPV-CB\* TYIHQISNTIFKGGRASKVEFETAMNLLLETTRWLRNRHDRIAKDPLSAFRNKVSGKALL \*\*: :\* : \* \* HaMV\* NPQLLCDNQLDADGNFIWGDRAYHAKRFFSNFFEEINPEHGYDKYIVRKFPNGSRKLA-I ChiVMV-PVB NPSLMCDNQLDANGNFIWGKRGYHAKRFFSNYFELIQPTDGYDKYVIRKFPNGTRKLATI PVMV-P NPSLMCDNOLDANGNFVWGKRGYHAKRFFANYFDRIEPTSGYDKYVIRKFPNGSRKLA-I WTMV-VN NPSLMCDNQLDVNGNFVWGKRGYHAKRFFSNFFELIQPSDGYDKYIVRRNPNGSRKLA-I TVBMV-YND ChiRSV-HN/14 NPSLMCDNQLDANGNFVWGKRGYHAKRFFANYFDVIQPADGYDKYIMRKFPNGSRKLA-I NPSI\_MCDNOL\_DVNGNFVWGKRGYHAKRFFSNYFDVTVPSDGYDKYATRRFPNGTRKLA-T YMMV-Brazil\* NPSLMCDNQLDSNGNFKWGRRGYHAKRFFSNYFDLIEPEHGYEKFKERKHPHGIRKLA-I CBPV-CB\* NPTLMCDNQRDVNGNFIWGKRGYHAKRFFSNYFSVIEPQHGYDAYVTRTFPNGTRKLA-I HaMV\* GQLILSTNLDRLREQLIGEPIKPEPLTDACVSRIHETFIYPCSCVTYDDGTPVLSEMKAP GNLILSTNLDQLRKQLEGESIEAMPLTQQCVSKRYESFIHPCCCVTYDDGSPVLSEFKAP ChiVMV-PVB PVMV-P GNLILSTNLDELRKQLQGESIQTYPLTQQCVSKRNETFIYPCCCVTYDDGSPMLSEYKAP WTMV-VN GNLILSTNLESLRKQLEGEPIETLPLTEQCIGKRHESFIHPTCCVTYDDGTPLLSEFKAP QNLILPRNLDTLMKQLEGESIELQPLTQSCISKRHERNIYPCCCVTLEDGTPEYSEFKAP TVBMV-YND QNLILPRDLGQLHRQIEGESIELQPLSTKCISKRHERNIYPCCCVTLEDGTPEYSEFKAP GNLILSTSFDVLRTQLEGESIERLPVTIQCVSKRHESFVYPCCCVTYDDGTPVYSTVKTP ChiRSV-HN/14 YMMV-Brazil\* CBPV-CB\* GSLILSTNLDELKAQLEGESIHKEPLSIKCTSEKNNSYVYPCCCVTNDVGVPIYSGLKTP \*\*\* TSNHLVLGNAGDSKYLDLPTGKGDRMYITKEGYCYMNIFLAMLVNVEKDKAKDFTKWVRD TKNHLVLGNTGDSKYLDLPAEISENLYIAKEGYCYVNIFLAMLVDVDEKDAKDFTKWVRD HaMV\* ChiVMV-PVB TKNHLVLGNSGDFKYLDLPTEISENLYIAKEGYCYINIFLSMLVEVDENEAKDYTKWVRD PVMV-P TKNHLVLGNSGDSKYLDLPTEISENLYIAQEGYCVVNIFLAMLVEVDEKDAKDFTKWVRD TKNHIVLGNSGDSKYLDMPADISENLYIAKEGYCVINIFLAMLVNVDEKDAKDYTKWVRD WTMV-VN TVBMV-YND ChiRSV-HN/14 TKNHIVLGNSGDSKYLDMPADISENLYIAKEGYCYINIFLAMLVNVDEKDAKDYTKWVRD TRNHLVIGTTGDSKYLDLPTEISEKLYIAKEGYCYINIFLAMLVEVDEDEAKDYTKWVRD YMMV-Brazil\* CBPV-CB\* TIVTQLGQWPTITDVAIACFQLSIMFPRVRDAELPRILVDHHTKTLHVLDSYGSLTTGFH HaMV\* IIVQQLGQWPTMTDVALACYQLSVLFPSTRSAELPRILVDHKTMTMHVIDSFGSLTTGYH IVVQQLGQWPTMTDVALACYQLSVLFPSTRSAELPRILVDHKTKTMHVIDSFGSLTTGYH ChiVMV-PVB PVMV-P WTMV-VN IIVRQLNKWPTMTDVALACYQLSVLFPSTRSAELPRILVDHKTKTMHVIDSFGSLTTGYH TVBMV-YND VVTEOLKEWPTMIOVALACYOLSVLFPSVKSAELPRILVDHKTOTMHVIDSYGSATTGYH ChiRSV-HN/14 vvseqlgqwptmldialacyqlsvlfpsvksaelprilvdhktqtm<mark>h</mark>vidsfgsattgyh YMMV-Brazil\* CBPV-CB\* HC-Pro/P3 ILKMNTVDQLIKIANETLESEIKHYRVGGTNYNGTDFHTRSLKQ-VIRGVYRPNELRSIL HaMV\* VLKANTTSQLILFASDTLESEMKMYRVGGE-ETQSIP---GFKTRLMRSVYRPSVFEQLM ILKANTVSQLLMFASDTLESEMRMYRVGGS-DPRTLT---DYRKRLFOSVYKPAVFKQLM ChiVMV-PVB PVMV-P WTMV-VN ILKANTVSQLILFASDTLESEMKLYCVGGS-PTDFSTETEGYKRRLFRSVYRPKEFKNLM ILKANTVSQLEKFASDTLESEMKHYRVGGL-IEDNVGHHAAVKL-LIQSVYKPKVLRTLL ILKANTVTQLEKFASDTLDSEMKYYRVGGL-IDGSETDVAALQT-VIKTVCRPKLLKELL TVBMV-YND ChiRSV-HN/14 ILKAQTVSQLIDFAHDTLESEMKHYRVGGI-MNATTVNAETIKL-LIKAVYRPKILKEII YMMV-Brazil\* CBPV-CB\* ILKANTVEQLIEFASDALKSEMKHYRVGGD-MTNNLMLHSSLRT-LIKSIYRPELMHSIL HaMV\* SHDPYILTMALLSPAILTSLFTTGSLYOATLSLIPEDTSARHLVCLLTSLAGRVSRLEDL ChiVMV-PVB IDEPLTLTLALASPTLLNEFYTNGSLYEAMEFVGHTQMPVRVAVTKILELAQKVNRAESI LEEPVILTLAIASPTLLSEFYHNVSLHRAMGLVGQAÈMPVRIAVTHIVELAKKVTRAESL LEEPIIITLALMSPTLIHEMYWSGGLHRAMQIVNKSDMNIKMVVSTILDMSKKVVKADDL PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 MEEPYLIILSIISPSVLIALYKSGSLYRAVQLLHNKEPTLRMVLSLLTMLATKVSRADDM MDHPYLIVFSIMSPSVLLAMFRSGSLHRALLSVRGQEHTLKVLVSLLTLLATKLSRSDTI ENEPYILTLCIVSPAIMREMYRNGAFKLALLSQVKCDMNIKLLSSLLESLSLKVTRAQQY YMMV-Brazil\* CBPV-CB\* MDEPYLITLSILSPSVVIEMCKSGCLFEAFKHIKTKEMPLRMIINILHGLAARISRAESY HDQVNIIEENLGAFLEILSVGDRCSYARAFMQRTIEARLESISADEELDASGFRTLRWKS YEQASLISNHLSELHGIIDQMPCRSASICCVLEFLLTSQLDTECDGELNAIGFRTLKHKS HaMV\* ChiVMV-PVB PVMV-P WTMV-VN YEQSAIIESNAQELYAILDSVPYKTEALEHILAYLLTVVLDADSDATLEDIGFRTLKYKS FNQAAIINAYTDSLLEIIKNAPHQSLAKDIVLEFLLVHQSTNEIDGDLSALGFRTLKFRS YSQYQLIQDHAERFREVLNGGDKHSISRRLAEQFIEVQIAVAESNYDTESLGFRTTKLKG TVBMV-YND ChiRSV-HN/14 FKRFDIIQNHVHKFRDVVLDGDVHSMSRKLAERYLEVQVSIIESQNETEALGFRTTRFKG IEQMAIINKDVHVIRDVLSNGSMLNHSRSQALRYVETIIAMQQMNQNLLRDGYYTTQSIQ YMMV-Brazil\* VEQVAIIDGELAQFQHVLTNADRCNISRCLAYRYIQTRMSLAVVNQRLEANGYYEGQMVS CBPV-CB\* · \* .

HaMV' VRVLEKIYTEDLEASWRELQFVEKCYIMLQRLRWRRRIIVELSQESAISFKKVFEHCSTG ChiVMV-PVB LHIMEKIYKEDLRALWCELSWSEKLRFKLHVLRSRKQYIRDSREIISGTLKEALHCSTRF LSVLEKICRDDLDAQWRDLSLSAKSRITWQSLRSRKSCTGGLRDTACSIFKKVFESSTAY PVMV-P WTMV-VN LHLMEKIYKADLEAQWCELSWLERSYVIYYTFKSRIQCMRDLSQDKSQILKQTFKCSTAF TVBMV-YND LALIEKIYOODLEELWOGLPLLEKCSCILWOLRHRRKLOVELGENGTODLSKALVTFKHY ChiRSV-HN/14 FHLVEKIYQEDLEAQWRELPLFQKLYFTAWQLRHRRALEVMLGEKDTKEHCKLLHSLKRN YMMV-Brazil\* CBPV-CB\* NSLTEKIVEELKASWRELTLSEKLLSTCRSLQVCERFGRKCREERQETLRNVSKSVTQY NQFVEKIYQDELAMCWDELPLSSKLSATIVRYKWRAYIENFSKTIDKGTLSTPCKLYMKP LHLAARPIVKIAKCCTDKFSAIVRSTHTRLLSGFIYGFRCVFRDLFTFVQVLAICNIFLT HaMV\* ChiVMV-PVB VOEKTVI.TPTPI.RYVSGKTGCGTAKVRKNVWSTTYGRAVHNFRDALRFTHTLATI.STLI.T PVMV-P VQGKAQKIPAPFMYMLSKASKSASYIRSSVLNRMYSYIAYSFHDAFQFIHTLAILSVLLT VQDRMKVIPNSVQSVCSKSVCIAKSIRHRVYKRLYRCAVNTFSDAFQFLQTMAIISILLS AQDNFDRILSPIHKRSHYVTGAPMRILRGVRCKVVGTFSYLFSDLLRFVQVLAILSVLLA WTMV-VN TVBMV-YND ASHCLRKTLVPFKAGYSKCTQVPGFVHKRMRCKLLHSLSYFFSDALRFIQVLAVISILMS LCGGLTKMKTGVKVSTEKCTYKVVSMSLRTVGGAFNILNYVTPEFLRTARVVAILSLFLS ChiRSV-HN/14 YMMV-Brazil\* CBPV-CB\* LYMAKEKFKQAAQRGRNRMSTYREMFKQRYFMQSFSMLRYIAPELSTLVRTITIFSTLIG HaMV\* ILDSLLRLRSAYIANAROVOYMRERONRDKLEKLYNILKCKLGVEPTFEEYKEFVAGVNP VYTNIVDIKNKHKKMNLLHIEEQEMKIQSRINKHYNDLTLLHNSPPSEVEFIQYVREHDP ChiVMV-PVB PVMV-P IYTNILNIRNLNKKRALLLVKEADRLKSERIERCFEEISKKLNGAPTEQQFVQFIQEKDP VFANLIDIKNKYRNSVRISDKEKMDELDKSIFKHYTDLKIKNGVKPSEDEFSEYLKERDP WTMV-VN TVBMV-YND IFNNIYAFTCQYREFKMMEASREEEKKLESLDKLYAHLSYKLGESPTFEEFRQFVSACNP ChiRSV-HN/14 TLOOLYDSMVKYRSYKTLATROEDSKKDEALERLHSHLYYKLGVLPTYDEFCKFVOEOSP YMMV-Brazil\* VFSKLQRIVNEQLHQRALLRDVQLATNWKKIETHYETLTKKLQNTPTIDEFAQYLKESNA CBPV-CB\* MLNAAKMVVVQIQQHKGRMAQQKEEEQFAALEKLYHIYCGKIGDQPTYEEFYEFVKGTNS P3/6K1 ELAKOLESSEE-LEVKHOANKRESETRLEOIVAFIALVLMVFDNERSDCVYRVMNKLKNV HaMV\* ChiVMV-PVB SALAYWSTQE--KSVDHQASKRPSEAKLEQIVAFVALMMMVFDTDRSDCVYKVLNKLRNV PVMV-P OALOYYSEON--DGVKHOASKRPAEAKLEOIVAFVALMMMVFDTDRSDCVYKVLNKLKNV WTMV-VN DAFVHWFGKD--LKVQHQASKRPSEAKLEQIVAFIALLMMVFDGDRGDCVYKVLNKLRNV QLVEFLEVSYA-PVVEHQAVKRASEVRLEQIVAFIALVMMIFDNDRSDCVYRVLNKFKNI ELLDHMGGYHGNEVVEHQA-KRESEVRLEQIVAFMALVMMIFDNDRSDCVYRVLNKFKNI ELYKEFVEYEQLPVEHQA-KRESEQRLEQIIAFIALVMMVFDNERSDCYYKVLNKLKNL TVBMV-YND ChiRSV-HN/14 YMMV-Brazil\* CBPV-CB\* SLLCILESFSS-EFVGHQDFKSENK-RIEQILAFVVLIMMLIDAERSDCVYKILNKFKGV ::\*\*\*:\*\* 6K1/CT HaMV\* MSVAEQD-VNHQSMDDEMEAFDD-NATISFELECEDPVRAYPSSSTLEQWWDNQLALNRT ChiVMV-PVB PVMV-P MGVVDNDAVNHQSLDTILENFDERDEMIEFEITAPDAKSIAYKSSTFQVWWDNQLALNNV MGVVDNDAVNHQSIDTILDDFESKNEMIEFELTAPDAKSLAYKSSTFQKWWDNQISTNNV WTMV-VN MGSVDNEAVNHQSLDTIVENFEETNEMIEFEITAPDAKSLSYKSSTFQTWWDNQITMNNV TVBMV-YND VGVADQEVI-HQSLDDIKTNFDESNETIDFELVTGETAPTPYKSTVFSDWWSNQLNMGRT ChiRSV-HN/14 VSTAEQDVV-HQSLDDIQTNFEERNETIDFELTTEDTPATPFKSATFESWWDKQLEMGHT YMMV-Brazil\* MNTAEP--VAHOSTODIIPTEEK-EOLIDEELDTHDSISYAYKSSTESKWWDNOLOMNHV IRSIEP--VGHOSLDIAPDFEF-NETIEFSLDTEGLPEPLHKLTTFSGWWNAQLIANNT : : : \*\*\*:\* \*: \* \*: \* \*: CBPV-CB' \*.\*.: GSGKS IPHYRTEGYFMEFTRANCAQVINEIVHNEHKDILLRGAVGSGKSTGLPAGLSTRGKVLLL ISHYRTEGHFVEFTRDTSAQVASDIANSDMKDFLVRGAVGSGKSTGLPSALCKRGRVLLL HaMV\* ChiVMV-PVB PVMV-P ISHYRTEGHFIQFTRETSAQVASDISSSEIRDFLIRGPV<mark>GSGKS</mark>TGL<mark>P</mark>SLLCKKGRVLLL ISHYRTEGRFIEFSRDRAAQVANEISTSDIRDYLIRGAV<mark>GSGKS</mark>TGL<mark>P</mark>HHLCKKGKVLLL IPHYRTEGHFMEFTRDAVATVVSNIIQSEKRDFLIRGAV<mark>GSGKS</mark>TGL<mark>P</mark>AQLAKKGKVLIV WTMV-VN TVBMV-YND ChiRSV-HN/14 VPHYRTEGHFMEFSRDTVVSVVQNIVLSEKRDFLIRGAV<mark>GSGKS</mark>TGL<mark>PA</mark>QLAKKGKVLIV IPHYRNEGHFMGFTRSGAAGTASEIACSDHKDILLRGAV<mark>GSGKS</mark>TSL<mark>P</mark>FLLSKHGHVLLV YMMV-Brazil\* CBPV-CB, TSHYRTEGHFLEFTRATCASVANQIITSEHTNFLIRGAVGSGKSTGLPNMLARDGRVLLL HaMV\* ESTKPLSRNVFNQLRQDPFHLSPSLMMRDSTTFGSTPITIMTSGYAFHYFANNARKLHDY EPTRPLAENVHAQLSASPFHLNPTLMMRNKSVFGSTPITVMTSGYALHYLANDAQRLKEF ChiVMV-PVB  $\label{eq:eprelaenv} EPTRPLAENVHAQLSSAPFHLNPTLMMRNKSVFGSTPISVMTSGYALHYLANNAHRLKEF EPTRPLAENVHSQLSQQPFHHNPTLMMRNKSVFGSTPITIMTSGYALHYLANNSHRLQEF$ PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 EPTRPLSENVFTQLRSQPFHLSPTLLMRNSSHFGSTPISIMTSGYALHYLANSGTALSTF EPTRPLSONVFNOLRSOPFHLSPTLMMRNSSHFGSTPISIMTSGFALHYLANSGTALSTF YMMV-Brazil\* EPTRPLVENVYTQLRGAPFHASPTMMMRHATSFGSPPVTIMTSGFVIHYLANNRSKISSY CBPV-CB\* ESTRPLAENVFTQLQCSPFHLNPTLMMRDVSSFGASPITVMTSGFALHYFANNYNKLQDF \*\*:.\*:::\*\*\*\*:.: \*:::\*\*. QFIMIDECHVLDANAMAFRSLLEEHEYQGKIIKVSATPPGREVEFTTQHKVEIRIEDSLS HaMV\* SFILFDECHVLDASAMAFKSLLVDREFEGKILKVSATPPGRETEFSTQYPVQLKTEEHLS SFIIFDECHVLDASAMAFRSLLADRAFEGKILKVSATPPGRETEFTTQFPVKLRTEDHLS ChiVMV-PVB PVMV-P WTMV-VN AFIMFDECHVLDASAMAFRSLLADRAYEGKILKVSATPPGRETEFKTQYPVTLKTEETLS DFIIMDECHVLDANAMALYSLLHDREYTGKILKVSATPPGREVEFKTQFPVKLKIEESLS DYVILDECHVLDSNAMALYSLLLERDFNGKILKVSATPPGREVEFSTQFPVELRVEESLS TVBMV-YND ChiRSV-HN/14 YMMV-Brazil\* CBPV-CB\*

HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChIRSV-HN/14 YMMV-Brazil* CBPV-CB*	FQQFVAALGTGGNADVTSKADNILVYVASYNDVDKLSKMLQEKSYLVTKVDGRTMKNGV FQQFVDAQGTGVNADVTSIADNILVYVSSYNEVDQLSKLLTDKKFKVTKVDGRTMKSGA FQQFVDAQGTGTNADVTSDADNILVYVSSYNEVDQLSKMLVERHHKVTKVDGRTMKSGA FQQFVDAQGTGTNSDVTDEADNILVYVSSYNEVDQLSKMLGKGYKVTKVDGRTMKNGS FQQFVDAQGTGTNSDVTDEADNILVYVSSYNEVDQLSKMLGKGYKVTKVDGRTMKNGS FQQFVDAQGTGTNSDVTDEADNILVYVSSYNEVDQLSKMLGKGYKVTKVDGRTMKNGS FQQFVDAQGTGTNSDVTDEADNILVYVSSYNEVDQLSKMLGANFKVTKVDGRTMKNGS FQQFVDAQGTGNNDVTXNNILVYVSSYNEVDQLSKMLAANFKVTKVDGRTMKNGS FKQFVDLGSCSNSDITTKGDNILVYVASYNEVDALAKLLVEAKFLVTKVDGRTMKNGS *:*** *: *:
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	DVVTKGTHTKKHFIVATNIIENGVTLDIEAVVDFGTKVVPTLDIDSRRITYCQTAISYG EIKTVGSKHRKHFIVATNIIENGVTIDIEAVVDFGLKVSAVVDADLRMVRILKVH-SIME EIKTVGTKQRKHFIVATNIIENGVTLDIEAVVDFGQKVGADVRSDENMICTKKGAINYGE SIKTYGTKTKKHFIVATNIIENGVTLDIEAVVDFGLKNADDIDICDKNIRYAKGSINYGE NISTSGTTKKKHFIVATNIIENGVTLDIEAVVDFGKVVPSLDVDGRSIRYSKVCINYGE GIQTHGTAKRKHFIVATNIIENGVTLDIECVVDFGVVVPSLDIDQRRVIYKKVPVSYGE NIETKGTEALKHFIVATNIIENGVTLDIECVVDFGVKVVPSLEIDQRRVIYKKVPVSYGE : * *: *******************************
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	RIQRLGRVGRFKPGVALRIGHTQKGICAIPSIIATEAAFLCFIYGLPVMTSQVSTSLLR KNSALGRVGRTKPGCALRIGHTNKGVEAIPTMIANEAAFLCLIYGLPVMTAQVSTSLIS RVQRLGRVGRTKPGVALRIGHTNKGIEAIPTVIANEAAFLCFYYGLPVMTAQVSTSLLS RIQRLGRVGRVKPGVALRIGSTQKGIEAIPNIIATEAAFLCFVYGLPVMTSQVSTSLLS RIQRLGRVGRVKPGVALRIGYTQKGIEAIPNIIATEAAFLCFVYGLPVMTSQVSTSLLG RIQRLGRVGRKKGTALRIGYTQKGIEAIPNIIATEAAFLCFVYGLPVMTSQVSTSLLG RIQRLGRVGRHKAGTALRIGYTIREVIPLNTIVATEAAFLSFVYGLPVMTSQVSTSLLG RIQRLGRVGRHKSGTALRIGHSEKNLTPIPEMIATEAAFLSFYYGLPVMTSQVNTMLS : . ****** *.* ***** : : : : :::***** .::***** *:***
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	CTVQQARVMKLFELPTYFMLDLVRHDGTMHPDVHRLLAKYKLRESEIVLNRMAIPHART) CTVQQARTMALFELPFYFTQDYVSADGSLHPAIHALL-RIQLRESEILLNNFQYHTQQS7 CTVQQARTMALFELPFYFLQDFVAADGSMHPAVHALVKKFKLRESEILLNKLAIPHAAV CTVQQAKTMALFELPIYFMMDFVASDGTMHPAIHALKKYKLRESEILLTKLAIPHAAV CTVQQARTMALFELPYFMINFIDANGSMHPHVHEVLKKFKLRESEILLTKLAIPHAVY CTVQQARTAKLFELPYFMINFIDSNGSMHPQIHELLKKYKLRESELQLNKMAIPYAVT CTVQQARTMKQFELPTHFMVDLVCYDGTMHPQIHELLKKYKLRESEILNKKAIPYAVT CTVQQARTMLFELPYFMINFIDSNGSMHPQIHELLKKYKLRESEILNKKAIPYAVT CTVQQARTMKLFELPYFMINFIDSNGSMHPQIHELLKKYKLRESEVILNKKAIPHSVX CTVPQARTMLFELPYFMNLVHYDGTMHPAVYAQVKKYRLRESEVILNKKAIPHSVX
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	HWMDVRTYNACGTNIALDPDVKIPFFCKDLPEQLLANLWNIIQKNKGDAGFRTLKSHDAA SGCQCASTTNAPKQLDMDPDVKLSFYVKEVPEELYEKLWHCVQENKGDAGFKKLRTHNAA KWMSVREYNQCSKQMDLDPDIKLSFLVKEVPEELYEKLWHCVQSHRGDAGFKKIATHNAA QWLTVTEYNRSGSSLQIAPECRIPFLVKEIPELYEKLWQVVLNHKGDAGFKRITHNAA KWISVRDYNRSGHULQMDPDCKIAFLKEIPDTLYEKLWKTTNDCRGDAGFKRLATYNAA SWHKVRDYDNDAQLVNMAPNDKIPFLCKDIPDAYEKIWKTVDCHKSDAGFKNLTSVNAA SWISVKEYSQCGVVLALEPNVKLPFFVKDIPDKLYSSLWEVVVKHKSDAGFKNLTSVNAA SWISVKEYSQCGVVLALEPNVKLPFFVKDIPDKLYSSLWEVVVKHKSDAGFKPLKSSNAA :: *::::* *::*
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChIRSV-HN/14 YMMV-Brazil* CBPV-CB*	KIAYKLHTDEHSVQRTVA-IIDALIVEEQTKKAYFDSLVVNTCSNASFSLQSISNRIRAH KIAHKLRTDDMAIQRTIL-LIDQLIANEMQKKEHFDSLVNANTSSLSFTLQSVSNLIRS KIAHKLRADNASIQRTVCSSIND-AAEMQKKEHFDSLVNANTSLSFSLQSISNNIRS RIAHKLRTDDMAIQRTIC-YIDQLIASEMQKKEHFDSLVNAGTSSLSFTLQSVSNMIRS RVAYKLRTDEHSLQKTIG-IINQLIIAEREKQAHFESLAGFSLGSQCYSLQSICNAYKSI KISYKLRTDHSIQRTIR-IIEQLITAEREKQAHFESLTSFSLSSQCYSLQSICNAYKSI KIAYKLKTDPQSIPRTIR-VIDELIKMEMEKKAHLDTVSSFTCSSNMSLHSIGLIQSI KIAYUKTDPLSITRTCA-HIDELIRIEMQKATFDSLANYSVHSFFSLESITRAIRSI :::: *::* :: * :: * :: * :: : * :: :: ::
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	CI/6K YKQNNTTENISVLAAAKAQLLDFQHSCYEDSIIINPSSKRVVDKIMDNGALETVLHOSR HARIFGA-NFSVLHAARAQLVEFNNLHSDEIHEVCHQYMPLRDHIIDCGAMETVHHOST YAKDYSVQNLSILHEARAQLVEFNNLYSEDIISGAASIWTMRDSIVECGAMETVHHOST YAKDYSVQNLSILHAARAQLVEFSNLHNEYINDGVPELHLMRDNVMCCGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGEMTELQIRDEVVEFGALETVHHOSK YAKNHTTENISVLEAARAQLVEFSNVYGESIYVGENTELQIRDEVVEFGALETVHHOSK YAKNHTENISVLEAARAQLVESFVSTFFEGVQNDFTDRVFVDAIEHNGALEAVLHOSK YASNYSVENITILQSAKAQLVEFSVYTSGNGDFGMHIKALEHQISSYGAFDAVRHOSV : * * * *::**
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	6K2/VPg GIIKTLNLQGKWKGTLITRDLLVCAGLACGGVWLLYQYIRNFMNEPVEHQAKNKRQKG GISKCLKLKGTWNGSLITRDVLIAAGVACGGAWMIYQYFIDNERVDHQAQKKNKRQKG EIGKFLGLKGFWNKKLLTRDVLIGAGVACGGAWMLYQYFVDSFGDDVDHQAQGRNKRQKG DISKFLKLKGVWNGALLTRDVLVGGVAGGAWMIYQYLMDSFSDNVDHQAQNKSKRQRG GVSKALKLKSRWNKSLITRDLLVCFGVAAGGAWMIYQYLMNKCNEVVEHQGRNKKGAG GVSKALKLKSRWNKSLITRDVLVCAGVAVGGVWLLYQYLVDQFKAPVSHQARNKRSNG DILRTLDIRGKWKGSVLARDILITAGVAAGATWMLYEYFTTKL-ESVTHQGKNKRQNG GVASALELKGQWNTTLITNDILIGLATVTGEARMLYEYVFEGLIQPVQHQGFNRRQRG : * ::. *: ::::::: *::: * **. :::

HaMV\* KLKFRDARDRKVGRIVDAENGSEAVEFLFGDAYTKKGKKGGKTRGMGTKTRRFVNMYGFD KLKFRDAHDQKVGRII-VDDDSGAVEHFFGSAYTKKGKSKGKTHGMGKKNRRFVNMYGFD KLKFRDARDAKLGRVV-IDDDSGAIEHFFGSAYTKKGKSKGKTHGMGKKNRRFVNMYGFD ChiVMV-PVB PVMV-P WTMV-VN KLKFRDARDSKVGRVV-VDDDSGAVEHFFGSAYSKKNKSKGKMHGMGKKNRRFVNMYGFD RLKFRNARDAKIGRVV-FDDDSGAVEHLFGAAYTKKGKKTGRAVGLGKKTRRFVNMYGFD TVBMV-YND ChiRSV-HN/14 KLKFRNARDAKVGRVI-IDDDSGAVEHFFGAAYTKKGKKSGKQVGLGKKTRRFVNMYGFD YMMV-Brazil\* KI.RFREAADRKIGHVV-FDDDSGTIEHYFGTAYAKKGKSKGKTVGMGKKTRRFVNMYGFD CBPV-CB\* KLKFRSHRDSKIGRIV-DDVGDGSVEYHFGEAYAKKAKGKGKKIGMGVKTRRFMNMYGFD \*\* \*\* • \* \* DSEYKYVRFVDPVTGEILDENVMTDISLVQDHFGELRSEYINEDKISPQALYSNPGIKAY HaMV\* ChiVMV-PVB PTEYSFIRFVDPVTGEMLDESVMADVMLVQEHFNDLRFEYLGDDKIESARLYSNPGIQAY PVMV-P PTEYSFVRFVDPITGEMLDESVMADIMLVQEHFDDLRHEYISEDKIGVQALYKNPGIQAY PTEYSFIRFVDPLTGEMLDESVMADIMLVQEHFNDLRHEYLSDDKIQAQALYSAPGLTAY PTEYAFVRFVDPVTGEMIDENPVTDIKLVEEHFDDIRFQHIQNEKVPMQALYSNPGLTAY WTMV-VN TVBMV-YND ChiRSV-HN/14 PTEYAYIRFVDPITGEMLDENPMADIMLVKDHFDDLRHEFLMDDKIDMQALYSNPGLEAY YMMV-Brazil\* PAEYOLT RET DPLTGET LDES PHVDTMLVKDHEDT TRMEKT ADDET EPOKVYKNSGT OAY CBPV-CB\* PVDYSFIRFVDPITGAQLDQGVLADIGLVQEHFDEIRTKHVEEDIVSIERINYSPGIQAY \*\* \*\* \*\*\* :\*: \*: \*\*: \*\* • \* HaMV\* FVKDKTSPVLEVDLTLHEPLKLCDNSSTIAGFPEKEGILRQTGPAKQIKYEDMP---EHD ChiVMV-PVB FVKDKVSPVLKVDLTQHVPLKVCDNSSTIAGFPEREGEFRQTGQATKVNYDELP-S-REG PVMV-P FVKDKVSPVLKVDLTQHEPLKVCDNSATIAGYPEHKGMLRQTGQATLVTHAELP-S-SEK FVKDKVPPVLKVDLTAHVPLKVCDNSSTIAGYPEHENVLROTGOGKLIDPNELP-K-SES FVKDKTSPVLKVDLTHHVPLKLCDNSSTIAGFPEMENILRQTGAAKPIDFSELPIL-VEG WTMV-VN TVBMV-YND FVKDKTSPILRVDLTGHIPLKVCDRASTIAGFPEKEGILRQTGPAQKLPFEKLPTS-KES LIKDKVSPVLKIDLTEHLPLAVCNNFETIAGFPERERELRQTGQAVKVSYTDVP-Q-KST ChiRSV-HN/14 YMMV-Brazil\* CBPV-CB\* FVKDKTTPVLKVDLTQHAPLKICD-TGNIAGFPERENELRQTGQGILIRYDEIPKPVEEN **VPg/NIa** VAHEAKSLNRGLRDYTPISKSICLLQNTSDGRSTTIHGVGYGSLIVSNAHLLMRNNGTLT VEH<mark>EA</mark>RSLNRGLRDHNQVSKLICKLENDSDDCVTSIHGVGFGSIIITNRHLLKRNNGTLR HaMV\* ChiVMV-PVB PVMV-P VEHEAKSLNKGLRDHNQISKVVCKLENESDSYVTSIHGVGFGSVIITNRHLMKRNNGQLR WTMV-VN VEHEAHSLHRGLRDYNNISKIVCKIENNSDAVSTAIHGVGFGSVIISNRHLFKRNNGELK TVBMV-YND VDHEAKSLNKGLRDYNSVAKCICLLENDSDGSSISIHGIGFGPLIITNRHLFKRNNGTLI ChiRSV-HN/14 VDHEAKSLTRGLRDYNGVSKSVCLLVNDSDGCTTTIHGVGFGPLIITNRHLFKRNNGVLT VIHEGDSLVKGLFDHNNISKAVCKITNASEGFSTTLYGIGFGALIIANRHLFKRTGGELF YMMV-Brazil\* CBPV-CB\* VGHEAYANIKGLRDYNPIAKSVCQLTNKSDGVDTRMYGIGFGPYIITNRHLFVRNNGTLI ::\* :\* : . . \* . \* . \* :\*\* \*:. \* \* \* HaMV\* IKSMHGEFTIQNTTAIRIAPIPNCDLIILRLPKDFPPFSTKLKFRVPEPNEQVCMVGTNF VKTAHGDFKVANTKEMKVFPVEKHDILLIRLPKDFPPFPVKSKFREPKVNDSICLVGTNF ChiVMV-PVB PVMV-P VKTA<mark>H</mark>GDFKIANTKEMRIHPVDKH<mark>D</mark>LILVRLPKDFPFFTKIKFREPKLTDSICLIGSNF WTMV-VN VKSTHGDFKVVNTKELKIHPIDKYDIVLIRLPKDFPPFPTKAKFRKPTLTDSICLIGTNF VKSLHGEFKVVNSASIRVFPVENCDILILRMPKDFPPFPSKLKFRAPKTSDVVCLVGSNF TVBMV-YND ChiRSV-HN/14 YMMV-Brazil\* IRSMHGEFKVVNSAAIKVYPVGNCDIVLLKMPKDFPPFPMKLKFRVPQSNDLVCLIGSNF VRTTHGEFTCPDVGKLKIHPIENRDMVIIQMPKDFPPFATKLEFRAPRASDKVKIVGTNF LQTIHGEFTCKNTQLNILPVEDRDIIIVMPKDFPFPPMTLKFRSPRRDDQICLVGTNF ::: \*\*:\*. : ::: \*:: \*::::::\*\*\*\*\*\*\*. : ::: \*: \*::::: CBPV-CB\* QEKWMSSTVSSTSYIQHIPDTQFVKHWIDTKDGHCGLPLVSAKDGAILGLHSLTNTKQEY QEKFLSSLISADSTTSPVSGSKFWRHWIDTKDGHCGLPLVARDDGAIVGFHSLTSINTEQ HaMV\* ChiVMV-PVB PVMV-P QERFLSSLVSASSETSPVENSKFWRHWIDTKDGHCGLPLVSTNDGAIVGFHSLTSMNTDQ WTMV-VN OEKFLSSLVSSFSSTGPVENSNFWRHWIDTKDGHCGLPLVAOEDGAIVGFHSLTSTSSDK TVBMV-YND QEKYTSSMVSSSSNISHVANSSFWRHWIDTQSGHCGLPLVSLSDGYLIGI<mark>H</mark>SLMSVHSEH ChiRSV-HN/14 QEKFASSTVSGSSNISHVANSNFWRHWIDTKDGQCGLPLVAQNDGHLLGIHSLTSTHSDQ QEKYISSLVSGVSAIYPVANSDFWKHWIKTDFGHCGLPVVSEIDGFIVGIHSLASTQQNH YMMV-Brazil\* CBPV-CB\* QEKYMSSMVTSQSHIAAVSGTQFWRHWIETKHGHCGLPAICSSDMHIIGLHSLSSNTDAS • \* \* \* \* HaMV\* NCFASVTSVLTEILGAPEHAEWRKGWMYNPNDISWGFMRLKESTPSGLFKPVKSINDLEL ChiVMV-PVB NYFAAVPEAFMELIAQVETLEWRKSWVYNPNEIGWGSLKLKSDQPTGMFKIEKLIEDIQS PVMV-P NYFASVPSDLAQMIKDFETLEWRKCWVYNPNEIGWGSLKLQQDKPGGMFKVDKLIEDLQS WTMV-VN NYFAAVPENMHEILKSVESLEWRKGWLYNPNEIGWGSLKLTSDTPNGMFKVSKLVEDLHS TVBMV-YND NMFTGFPETFSECIAKTDNIVWARGWKYNPSEISWGNLKLKTSAPAGLFKTSKLIEDLHR ChiRSV-HN/14 NFFTAFPENFKECLDQTDSISWAKGWLYNPNEIGWGSLKLKESSPKGLFKIEKLIEDLNT NYFTGMIEHMNDLLTTAEQLEYTKLWKYNPREISWGTLDLQNSTPSEPFVLSKLLMDLEQ YMMV-Brazil CBPV-CB\* NIa/NIb HaMV\* DIVCEOAHI----ODRWFGDOLHCNLKAIGYSESOLVTKHVIKGKCPLFERYLCETPSAS AFVREQAS-----DKWLYAQFQGFLKAVPKSESQLVPKHIVKGPCPLFHLYLSTHREAR ChiVMV-PVB PVMV-P TFVQEQGE-----EKWLYAQLYGNLKAVGKSESQLETKHVGKGQCPLFQLYLSTHKEAK TFVQEQSG-----EAWLYPQLTGNLKAVGRCESQLVTKHVVKGPCQLFQLYLQTDSEAK WTMV-VN TVBMV-YND EMVEEQSH-----EKWVYDALHGNLKAVAASESQLVTKHIVKGECQLFQLYLNNHSEAA EVVSEQSK-----TNWVFEQLSGNLKAVCKSESQLVTKHTVKGECQLFQLYLNTHEEAN TPVVEQSL-----QTWMYSSLEANLKAVGRSQAQLVTKHVVKGECVLFQQYLATHPEAQ ChiRSV-HN/14 YMMV-Brazil\*

EPVECQAEVARREHDDWLYGSIKGNIQAVGKSTSHLVTKHVVKGRAELFQLYLSLNATAE ::\*:

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CBPV-CB\*

HaMV\* NYFRPLMGAYOKSRLNRTAYAKDALKYATTTECGLVEPNAFEOATANVTOTLKKVGFSEC QFFQPFMGAYGKSRLNRIAYAKDILKYSTEIEVGKVDTCALELPVDDVIADLHAVKFDTC ChiVMV-PVB PVMV-P EYFKPLMGAYAKSRLNRIAYAKDILSMQRKLKWAKLDVACLELAVEDVICDLHAVNFTTC WTMV-VN DFFKPLMGFYGKSRLNRTAYAKDILKYSTEIEVGKVDTDLFERAIRDVIADLHAVQFNEC TVBMV-YND AFFRPLMGFYQKSKLNKVAYLKDFLKYATVIEVGVVDPETFELAVSDTVQDLKRVGFPEC ChiRSV-HN/14 NYFOPLMGHYOKSKLNKVAYLKDLLKYATVIEIGKVNSDTFELAVSDTIADLINAGFEEC YMMV-Brazil\* TFFKPFMGHYGKSRLNKEAYIKDIKKYAQPITIGMVDTSVFECAVMNVKTMLSNLDFGQF CBPV-CB\* SFFKPRMGFYQKSRLNRQAYIKDIMKYSTTIPIGDVQTDIFETAVSLVVDTLKEFGMDTC HaMV\* AYVTDPEEIFSNLNMKAAVGALYAGKKKDYFLEYTOEOREEILOOSAERLYRGLKGVWNG ChiVMV-PVB NYVTDEEEIFQSLNMKAAVGALYKGKKREYFETYTQQDKERILFESCLRLYKGNLGVWNG PVMV-P EYITDEEQIFQSLNMKSAVGAMYRGKKRDYFETYTTEDKERILYESCLRLYTGKLGIWNG WTMV-VN EYVTDEEAIFQSLNMKSAVGALYKGKKREYFETYSSEDKRRILEESCLRLYTGRLGVWNG TVBMV-YND ChiRSV-HN/14 YMMV-Brazil\* EYITDSEVIFKSLNMKAAVGAMYSGKKKEYFEGKTASELDEFLKESCKRLYTGKKGVWNG CBPV-CB\* TYITDEDEIFDSLNMKAAMGALYTGKKREALADISQQAKEDYIAASCHRLYKGQMGVWNG \*\*\*\* \* \* \* \* \* \* \* \* HaMV\* AIKAELRTREKVEADKTRTFTAAPIDTLLAGKICVDDFNLQFYSLHTKAPWSVGISKFSR ChiVMV-PVB PVMV-P SIKAELRPIEKVRANKTRTFTAAPLDTLLAGKVCVDDFNNQFYSKHTLAPWSVGISKFSG SIKAELRPMEKVQANKTRTFTAAPIDTLLAGKVCVDDFNNQFYSKHTIAPWSVGISKFSG WTMV-VN SIKAELRPMEKVQANKTRTFTAAPIDTLLAGKVCVDDFNNQFYSKHTEALWSVGISKFSG TVBMV-YND SIKAELRPKEKVLQNKTRTFTAAPLDTLLAGKVCVDDFNNFFYSFNLEGPWSVGMSKFTF ChiRSV-HN/14 SIKAELRPKEKVAQNKTRTFTAAPLDTLLAGKVCVDDFNNTFYALHLKGPWSVGMSKFSF SIKAELRPIEKVHANKTRTFTAAPIDTLLGAKTCVDDFNNFFYMQHTKGPWSVGMTKFSQ SIKAELRPLEKTLANKTRTFTAAPLDTLLSGKVCVDDFNNQFYAMNTKAPWSVGISKFHL :\*\*\*\*\*\* \*\* ::\*\*\*\*\*\*\*\*\* YMMV-Brazil\* CBPV-CB\* HaMV\* GWDALLRKLPDGWTYCDADGSRFDSSLTPYIINAIPIIRLAFMEKWDLGETMM-RNLYTE GWDRLLRKLPDGWIYCSADGSRFDSSLTPYLINAVASIRLKFMEPWGIGEQMLMRNLYAE GWDKLLRKLPDGWIYCSADGSRFDSSLTPYLINAVAQIRLAFMEKWDIGEQMI-KNLYAE ChiVMV-PVB PVMV-P WTMV-VN GWDKLLRKLPDGWVYCSADGSRFDSSLTPYLINAVLHIRLHFMEKWSIGEQML-RNLYAE GWNTLLGKLPNGWLYCDADGSRFDSSLTPYLINAVLQIRLTFMESWDIGEQML-KNLYAE TVBMV-YND ChiRSV-HN/14 GWNHLLSQLPDGWVYCDADGSRFDSSLTPYLINAVLRIRLHFMENWDIGIQML-KNLYAE YMMV-Brazil\* GWDKMLRKIPDGWIICDADGSRFDSSLTPYLINAVAHIROYFNEDWDIGDOML-RNLYTE CBPV-CB3 GWNNMLKQLPKGWVHCDADGSRFDSTLTPYLLNAVLQIRLRFMEDWALGAQML-SNLYTE \*\*: :\* ::\*.\*\* SG NT IVYTPILTADGTIVKKFKGNNSGQPSTVVDNTLMVLLAMQYSLERLGVEFSTQEQTCIYF IIYTPILTADGTIVKKSKGNNSGQPSTVVDNTLMVLVAMKYSLRRLGIIIRIKNDRGVFF IIYTPILTADGTIVKKFKGNNSGQPSTVVDNTLMVLIAMRYSLRRLGMNYKDQIKRCVFF HaMV\* ChiVMV-PVB PVMV-P IIYTPILTADGTVVKKFKGNN<mark>SG</mark>QPSTVVDNTLMVLLAMRYSLQRLGLNYKEQCKECVFF IIYTPILAADGTIVKKFKGNN<mark>SG</mark>QPSTVVDNTLMVIITMHYALRRAGISYENFSEHCAFV WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil\* IIYTPILTADGTIVKKFKGNNSGQPSTVVDNTLMVIITMHYAARRAGLNYQEFCDNVKFV IVYTPILTADGTIVKKYRGNNSGQPSTVVDNTLMVLLAVQYAMLKNGIN-DVEQKECVYF IIYTPILLADGTIVKKFKGNNSG<mark>O</mark>PSTVVDNTLMVLISVRYALLRAGIDPEKHKDICKYF CBPV-CB\* 
$$\label{eq:linear} \begin{split} & \texttt{ANGDD} \texttt{LIVAVAPGHEHILDALQGYFSELGLNYDFSSRHTDRTKLWFMSHKGIIRDDLYIP\\ & \texttt{ANGDD} \texttt{LIVSVPPSDEWILDSLQDRSSELGLSYDFNERTTDRSELWFMSHQGILIENQYIP\\ \end{split}$$
HaMV\* ChiVMV-PVB PVMV-P WTMV-VN ANGDDLIVAVRHEDEWVLDSLQAPFQELGLSYNFDDRTTNRSELWFMSHQGKLIEDMYIP ANGDDLIVAVKPHNTWILDNLSDIFSELGLSYDFSERTKDRSELWFMSHQGKLIDDMYIP TVBMV-YND ANGDDLIIAVAPGSEHILDTLQGSFHELGLNYDFSSRTHNKEELCFMSHYGVLREGCLIF ChiRSV-HN/14 ANGDDLIIAVKPCRESLLDTLODTFSELGLTYDFTNRTRDKKDLCFMSHNGVMRDGIYIF ANGDDLVIAIPPEREHVLNTMAEFFAELGLSYDFGNRHKRKEDIWFMSHKAITREGIFIF YMMV-Brazil\* CBPV-CB\* ANGDDLLISLHPDFEWILDTMSESFAELGLSYDFTSRHRDVCDLWFMSHKGILLDGAYIF \*\*\*\*\* HaMV\* KLEPERIVSILEWTRANEPAHRLEAICAAMVEAWGYDNLLHEIRLFYSWILKOOPYATLA ChiVMV-PVB KLEPERIVSILEWDRAEQPEHRLEAICASMIEAWGHKELLYEIRLFYKWVIEQAPYSQI KLEEERIVSILEWDRAEQPEHRLEAICAAMIEAWGHSELLHNIRLFYKWIIEQAPYSMLV KLEEQRIVSILEWDRAEQPEHRLEAICAAMIEAWGHPELLHQIRRFYKWILEQAPYSTLA PVMV-P WTMV-VN KLEQĒRIVSILEWDRATĒPQHRLEAICAAMVEAWGYDELLYNIRLFYAWVLEQAPYNELA KLEKERIVSILEWDRASEPQNRLEAICASMIEAWGYDELLYQIRLFYAWVLEQAPYRELA TVBMV-YND ChiRSV-HN/14 YMMV-Brazil\* KLEEERIVAILEWSRTENYEHRLEAICAAMIEAWGYDELLKQIRLFYSWVLEQEPYKTLA CBPV-CB\* NTh/CP HaMV\* QEGKAPYISECALRRLYM-DKLIEPHEHATYLEKLVASVQIF--DDSANCVLHQAS-EQR SEGKAPYISETALRCLNM-SEHGE-NDINPYLRALIEGAKREELDDDGGEVAHQAG-E-S ANGKAPYISEVALRRLYT-NGEND-DDVSEYLKALSRSQKEIERLEGDDFVLHQAG-E-T ChiVMV-PVB PVMV-P WTMV-VN EVGKAPYISETALRNLYM-NQTNG-ASIDAYIRSLIEAGRLNEHSSDDLDVRHQSG-E-1 RQGMAPYISENALRRLYL-DEEGD---ISLYLQSLVQNQW----KDEQEEVVHQND-EQT KQGKAPYISEGALKKLYT-GEDSD---FQIYLRSLIQSQW----KDEDTIVYHQAD-TQA TVBMV-YND ChiRSV-HN/14 SEGRAPYISEYALRKLYLCNDDNDAELYNRYLRALIDNYT----HDDSDVVIHQASKEQI TEGKAPYISECALRKLYT-DQDISEEKNLTYLESILASYI----DDSHVSVYHQSG--SS YMMV-Brazil\* CBPV-CB\*

vHaMV* ChiVMV-PVB PVMV-P MTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	VDATNSFGKQAQAKGSETDGSSSRDGQQKNDSVRREGSTPIAPIPDRDINAGTTGTF VDAGSVKGEDSSSKSADKQATEKKNKVSGQAQPQSRQSEMEVPQVRDRDVNVGTSGTF IDAGKSSGKEVTASKQPTTSQPTEAKTVL-DRDVNAGTQGTF VDAGKNTGLVKDPTPNKDKQVMQSQPTKDKDVNVGTGTFF VDAGKNAQSNQKQRNAQAGNTSSGVVKDKDKDVNVGTSGTF VDAGKSTQSSEKKPANPASVSKVVAETFRDRDVNVGTAGTF LDAGVLGQSKGTAGQSGSGSQAQMR
HAMV* ChiVMV-PVB PVMV-P MTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	TVPKLKGMSTKLTIPKVKGKVVVNLQHLLQYTPDQEKLSNTFATDEQFAIWYNGVKSDYE TIPRLKGIFSKLTIPKVKTKAVVNLEHLLDYAPDQIHLSNTRALQSQFASWYGGVKNDYD TIPRLKGNSSKLTLPKVSSQSVVNLEHLLNYKPDQVHLSNTRALQSQFASWYNGVKNDYD SIPRLKGISSKLTLPKTSAGMVVNLEHLLEYKPDQIHLSNARALNSQFQSWYDGVKNDYD SIPRLKGISSKLNLPRIKGKEVVNLQHLLEYYPDQVSLSNTRALNSQFASWYTGVKSDYD SVPRLKGISSKLNLPMINKKAVINLDHLLKYTPDQVTLSNTRALNSQFASWYTGVKSDYD SIPRIKTPMSKLTPKLKGKVVNLEHLLEYEPDQTDSNTRALNSQFASWYTGVKSDYD AVPRLRHLTSKLSVPKLKGESVVNLEHLLHYQPNQDRISNTRATDSQFQUWYDGVKSDYD ::*:::::**:*
HAMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	VSDDEMQIILNGLMVWCIENGTSPNLSGVWVMMDGDEQITYPIKPLLDHAQPTFRQIMHH VTDEQMQIILNGLMVWCIENGTSPNINGYWVMMDGDEQVEYPIKPLIDHAKPSFRQIMAH VDDEQMKIILNGLMVWCIENGTSPNINGMWVMDGEEQIEYPIKPLIDHAKPSFRQIMAH LDDAQMEIVLNGLMVWCIENGTSPNINGMWVMDGDEQVEYPIKPLIDHAKPSFRQIMAH LDDSQMEIVLNGLMVWCIVYGTSPNLNGMWVMMDGDEQVEYPIKPLLDHAKPTFRQIMAH VDDEQKIILNGLMVWCIVYGTSPNINGMWVMMDGDEQVEYPIKPLLDHAKPTFRQIMAH VDDEQKIILNGLMVWCIENGTSPNINGFWYMLEDGEQIKFPLKPILDHARPTRQIMAH VDDEQKKIILNGLMVWCIENGTSPNINGFWVMLENDEQIEFFIKPLIDHARPTRQIMAH
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	FSNLAEAYIEKRNYTSPYMPRYGRNRNLTDMSLARYAFDFYAITSRTPERAKEAHMQMKA FSNLAEAYIEKRNSEKPYMPRYGLQRNLTDMSLARYAFDLYEMTSKTPVRAREAHIQMKA FSNLAEAYIEKRNSEKSYMPRYGLQRNLTDMSLARYAFDFYEMTSKTPSRAREAHIQMKA FSNLAEAYIEKRNSEKPYMPRYGLQRNLTDMSLARYAFDFYENTSKTPSRAREAHIQMKA FSNLAEAYIEKRNAEKPYMPRYGLQRNLTDMTLARYAFDFYEINSKTPVRAREAHIQMKA FSNLAEAYIEKRNAEKPYMPRYGLQRNLTDMTLARYAFDFYEINSKTPVRAREAHIQMKA FSDLAEAYIEKRNAKKAYVPGYGLKNNLNDYSLARYAFDFYEITSKTPVRAREAHIQMKA FSDLAEAYIEKRNFERAYMPRYGLQRNLTDMSLARYAFDFYEITSKTPVRAREAHIQMKA
HaMV* ChiVMV-PVB PVMV-P WTMV-VN TVBMV-YND ChiRSV-HN/14 YMMV-Brazil* CBPV-CB*	AALRNTSSRMFGLDGKVGTQVEDTERHTAEDVNRNMHNLLGVRGV AALRGVSNRMFGLDGRVGTQEEDTERHTAEDVNRNMHNLLGVRGL AALRNANNRMFGLDGKVGTQEEDTERHTAEDVNRNMHNLLGVRGV AALRNANNRMFGLDGNVSTKEENTERHTAEDVNRNMHNLLGVRGV AAVANSKNNLFGLDGNVSTKEENTERHTATDVNRNMHHLLGVSGV AAVMHAKNNMFGLDGNVSTKEENTERHTATDVNRNMHHLLGVSGV AALRNTRTRLFGLDGSVGNNDENTERHTSDDVNRDMHSLLGVRRI AALRNTRNRMFGLDGKVGTQEEDTERHTSDDVRGIHSLHGVRGL **::***** *: *:***** **:

**Supplementary Fig. S2.** Phylogenetic relation of HaMV and other potyviruses. A maximum-likelihood (ML) tree was constructed using PhyML 3.0, based on the multiple amino acid sequence alignment of the full-length viral polyproteins, as described previously with minor modification [5, 14]. Subgrouping of the clades (eleven groups) is based on the report of Gibbs and Ohshima [9]. Distantly related species that formed well-supported monophyletic clades were collapsed into a triangle (subgroup 8–11). Virus names and GenBank accession numbers of their genome sequences (presented as acronyms) are listed in Supplementary Table S1. Viruses with asterisks indicate unassigned species. RyMV, genus *Rymovirus*, is used as an outgroup. The branch support values were estimated using the approximate likelihood ratio test (aLRT) with a Shimodaira–Hasegawa-like (SH-like) algorithm (only values greater than 0.9 are shown as filled circles).

