Polyvalent detection of members of the Potyvirus genus by molecular hybridization using a 'Genus-probe'

Jesús A. Sánchez-Navarro[1*], Christopher N. Cooper[2] and Vicente Pallás[1]

*Author for correspondence: jesanche@ibmcp.upv.es

[1]Department of Molecular and Evolutionary Plant Virology. Instituto de Biología Molecular y Celular de Plantas (IBMCP) (UPV-CSIC). Universitat Politécnica de Valencia, Ingeniero Fausto Elio s/n, 46022 Valencia, Spain.

[2]Georgia Institute of Technology. School of Chemistry & Biochemistry, Atlanta, GA 30332, United States.

Running title: Detection of Potyvirus genus

Keywords: molecular hybridization, Polyprobe, dig-RNA probe, genus-probe, Potyvirus

ABSTRACT

The use of a unique riboprobe named `polyprobe´, carrying partial sequences of different plant viruses or viroids fused in tandem, has permitted the polyvalent detection of up to ten different pathogens by using a non-radioactive molecular hybridization procedure. In the present analysis, we have developed a unique polyprobe with the capacity to detect all members of the *Potyvirus* genus, which we have named 'genus-probe' (GP). To do this, we have exploited the capacity of the molecular hybridization assay to cross-hybridize with related sequences by reducing the hybridization temperature. We observed that sequences showing a percentage similarity of 68% or higher, could be detected with the same probe by hybridizing at 50-55ºC, with a detection limit of picograms of viral RNA comparable to the specific individual probes. According to this, we developed several polyvalent polyprobes, containing 3, 5 or 7 different 500-nucleotide fragments of a conserved region of the NIb gene. The polyprobe carrying 7 different conserved regions was able to detect all the 32 potyviruses assayed in the present work with no signal in the healthy tissue, indicating the potential capacity of the polyprobe to detect all described, and probably uncharacterized, potyviruses being then considered as a genus-probe. The use of this technology in routine diagnosis not only for *Potyvirus* but also to other viral genera is discussed.

INTRODUCTION

Plants are affected by a large number of viruses, which in many cases cause significant economic losses, compromising the viability of agricultural industries. Effective management of viral diseases requires an integrated approach addressed to prevent or delay the progress of the infection. The use of healthy plants represents one of the main measures to manage viral diseases by reducing the initial source of inoculum. Accordingly, rapid and reliable routine virus testing procedures is a critical step in their control. Traditional detection methods include bioassays with indicator plants and serological methods such as the enzyme-linked immunosorbent assay (ELISA), although the molecular detection techniques (RT-PCR, microarrays, molecular hibridyzation, etc) have been incorporated in the routine diagnosis of plant viruses (Jeong et al., 2014).

During recent years, plant virus detection procedures have been addressed to get the simultaneous detection of the main pathogens affecting a crop, in order to save time, labor and overall cost. Several strategies have been used for simultaneous detection of plant viruses. For PCR-derived assays, two main approaches have been used according to the use of a cocktail of primers targeting different pathogens (multiplex RT-PCR) or a polyvalent primer pair (polyvalent PCR) that is able to drive the amplification of a conserved region (James et al., 2006). However, the detection limit of the multiplex RT-PCR technique appears to be affected when more than six different pathogens are detected (Sanchez-Navarro et al., 2005) and the polyvalent primers are often compromised by the lack of conserved regions. In the case of the genus *Potyvirus*, the presence of a very conserved region in the NIb gene, has permitted the detection of virus isolates from all major groups of the genus, including uncharacterized species (Zhen et al, 2010). The incorporation of the DNA-microarray technology has incremented significantly the simultaneous detection and identification of multiple plant viruses and (or) virus subgroups (Bystricka et al., 2005; Barba and Hadidi, 2011). However, the difficulty of adapting the array technology for routine screening of large numbers of samples and the high costs associated with equipment required have compromised its incorporation in routine plant virus analysis. The serological assay has been also adjusted to polyvalent detection of 33 (Jordan and Hammond, 1991) or 14 (Liu et al., 2015) potyvirus species by using broad-spectrum monoclonal antibody (MAb) that recognize a conserved core region of the potyvirus coat proteins. In the

latter case, the authors indicate that the MAb could detect many potyviruses in infected plants, but also that different binding affinities were observed in some infected samples.

Multiple detection by using the non-isotopic molecular hybridization technique was addressed first by a cocktail of the specific single probes in the hybridization solution, allowing the polyvalent detection of the different plant viruses affecting ornamental (Sánchez-Navarro et al., 1999), horticultural (Saldarelli et al., 1996; Minutillo et al., 2012) and stone fruits crops (Saade et al., 2000); and second, by using a unique riboprobe, called 'polyprobe', that contains partial nucleic acid sequences of different viruses (Herranz et al., 2005; Aparicio et al., 2009; Peiro et al., 2012;) or viroids (Cohen et al., 2006, Lin et al., 2011, Zhang et al., 2012) cloned in tandem. The polyprobe has proved the simultaneous detection of six different viruses (Herranz *et al.*, 2005) or up to eight viroids (Cohen et al., 2006; Torchetti et al., 2012), eight viruses plus two viroids (Peiro et al., 2012) or three different pathogens comprising of virus, viroid and bacteria (Zamora-Macorra et al., 2015), with the same detection limit as the single assay. Recently, an octamer of 32-nucleotide sequence derived from the central conserved region of viroids in the genus Coleoviroid was used to develop a universal probe allowing the detection at least of four coleus viroids (Jiang et al., 2013).

In the present work, we have explored the potential capacity of the polyprobe technology to develop an universal probe with the property to detect all members of a specific viral genus, in this case the genus *Potyvirus*. The cross hybridization observed at 50-55ºC between sequences sharing an identity of 68% or higher was used to design several polyprobes, carrying in tandem different 500-nucleotide fragments of the conserved NIb gene, with the capacity to cross hybridize with all potyvirus species available in the data base. A polyprobe carrying 7 different conserved regions was able to detect all the 32 potyviruses assayed in the present work, revealing the potential capacity of this technology to be applied at the genus-probe level.

MATERIAL AND METHODS

Computing analysis

The phylogenetic analysis was performed with all potyviruses for which the complete nucleotide sequence is available in the database. The phylogenetic analyses were inferred in a multi-step process: in the first step, the sequences were aligned using the CLUSTAL W program (Higgins et al., 1994) to generate, in a second step, the neighbour-joining phylogenetic trees, using the JTT model, implemented in the MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets (Kumar et al., 2016). Third, the statistical reliability of the constructed trees was assessed by the bootstrap method based on 10,000 pseudoreplicates.

The more conserved region observed in the potyvirus alignment, covering 500 nucleotides of the NIb gene (Supplementary Figure 1) was used to estimate the identity value between all the analysed potyvirus sequences. To do this, we used the MatGAT (Matrix Global Alignment Tool) application that generates similarity/identity matrices for DNA sequences (Campanella et al., 2003).

To identify the equivalent conserved region in the rest of viruses assigned to the family *Potyviridae*, the seven selected conserved regions from *Lettuce mosaic virus* (LMV), *Watermelon mosaic virus* (WMV), *Potato virus Y* (PVY), *Pepper veinal mottle virus* (PVMV), *Plum pox virus* (PPV), *Sweet potato feathery mottle virus* (SPFMV) and *Tobacco etch virus* (TEV) were aligned with all species of the corresponding Potyviridae family, for which the complete nucleotide sequence is available in the database, using the CLUSTAL W program. The selected regions (Supplementary Figure 1) were also used to estimate the identity value with the MatGAT application.

Plant materials

The plant tissue was obtained from the Leibniz Institute DSMZ-German Collection of Microorganism and Cell Cultures (https://www.dsmz.de/home.html) or from the Mediterranean Agroforestal Institute at the Polytechnic University of Valencia (http://www.upv.es/iam/ingles/bienvenida.htm). Total nucleic acid extraction was performed using 0.1 g of lyophilized or fresh leaf tissue using the Silica capture extraction protocol (MacKenzie et al., 1997) that renders total nucleic acids. The extracted nucleic acids were stored at -80 ºC until use. Alternatively, healthy and

infected tissue were homogenized with 5 volumes of cold extraction buffer (50mM sodium citrate, 5mM EDTA, pH 8.5) and directly applied (1µl) onto nylon membranes (Sanchez-Navarro et al., 1998).

Synthesis of cDNA clones

Reverse transcription and PCR reactions were carried out using specific primers (Table 1), containing the 5' and 3' *Xho*I and *Sal*I restriction sites, respectively. PCR products were digested with both restriction enzymes and extracted from the agarose gel. The purified PCR fragments were inserted in the pBluescript SK(+) plasmid, previously digested with the *Xho*I enzyme and dephosphorylated. The incorporation of the purified PCR fragment into the pSK+ plasmid in the right orientation allowed the inactivation of the original *Xho*I site, present in the pSK+ plasmid, by the compatible *Sal*I site. This permits the use of the new 5' proximal *Xho*I for the synthesis of the riboprobe or the incorporation of a new PCR fragment (Peiró et al. 2012). Using this strategy, we introduced seven cDNA fragments in the pSK+ corresponding to the partial sequences of the following viruses: *Lettuce mosaic virus* (LMV), *Watermelon mosaic virus* (WMV), *Potato virus Y* (PVY), *Pepper veinal mottle virus* (PVMV), *Plum pox virus* (PPV), *Sweet potato feathery mottle virus* (SPFMV) and *Tobacco etch virus* (TEV). We generated three polyprobes that differed in the number of viral sequences incorporated. Thus, GP3, GP5 and GP7 contained three (PPV-SPFMV-TEV), five (PVY-PVMV-PPV-SPFMV-TEV) and seven (LMV-WMV-PVY-PVMV-PPV-SPFMV-TEV) viral sequences, respectively (Fig. 2).

Synthesis of the digoxigenin-labeled riboprobes and hybridization procedure

For the synthesis of the riboprobes, 1 µg of the corresponding plasmid was linearized with *Xho*I restriction enzyme, purified by phenol–chloroform extraction and precipitated with ethanol. The linearized plasmid was used to synthesize the riboprobe as described previously (Mas et al. 1993; Pallás et al. 1998). 1 µl of the total nucleic acids preparations (undiluted or serially diluted in extraction buffer), were directly applied onto positively charged nylon membranes (Roche Diagnostics GmbH,

Manheim, Germany), air dried and cross-linked by UV crosslinker (700×100 μJ/cm^2). Prehybridizations and hybridizations with the riboprobes were conducted as described previously, with the only difference of the temperature selected for the hybridization (Pallás et al. 1998; Sánchez-Navarro et al. 1999). All riboprobes were used at the same concentration in the hybridization solution (20 ng/ml). Chemiluminiscent detection using CDP-start reagent as substrate was performed as recommended by the manufacturer (Roche Diagnostics GmbH, Manheim, Germany). Films were exposed for 30 minutes.

Estimation of the detection limit of the hybridization assays

For the estimation of the detection limit of the single or the three polyprobes, the seven DNA fragments cloned in the pSK+ were PCR amplified using the corresponding antisense primer and the reverse primer. The resultant PCR fragment contains the corresponding potyvirus clone plus the T3 promoter. The amplicons were purified from agarose gel and then used directly for the synthesis of unlabelled transcripts complementary to the corresponding dig-RNA probes. Known amounts of the free transcripts were serially diluted (five-fold) in sterile water since previous results showed similar detection limit (pg/μl of viral RNA) for the no-radioactive molecular hybridization procedure when the dilutions were performed in sterile water (Peiró et al., 2012) or heathy tissue (Sanchez-Navarro et al., 1996; 1998). The dilutions were applied directly onto nylon membranes and the dot-blot hybridization was conducted as described previously.

RESULTS

Design of the polyprobes and analysis of the cross-hybridization

In order to get representative common sequences that would allow us to design a potential polyprobe at the genus level we performed a phylogenetic analysis using all potyvirus sequences from 94 species. The resultant phylogenetic tree grouped all viruses into different clusters supported with significant bootstrap values (Figure 1). We selected the following seven potyviruses that cover the full spectrum of disparate sequences (viral names in gray boxes, Figure 1): *Lettuce mosaic virus* (LMV),

Watermelon mosaic virus (WMV), *Potato virus Y* (PVY), *Pepper veinal mottle virus* (PVMV), *Plum pox virus* (PPV), *Sweet potato feathery mottle virus* (SPFMV) and *Tobacco etch virus* (TEV). Sequence alignment of all the 94 potyvirus species revealed a highly conserved region of 500 nt in the NIb gene (Supplementary Figure 1). The corresponding regions of the seven selected potyvirus were cloned separately in a bacterial plasmid to generate the individual probes but also in tandem to obtain three different polyprobes carrying 3 (PPV, SPFMV, TEV), 5 (PVY, PVMV, PPV, SPFMV, TEV) or 7 (LMV, WMV, PVY, PVMV, PPV, SPFMV, TEV) viral sequences (Figure 2A). MatGAT analysis of the 7 selected sequences revealed a percentage identity that ranged between 64.8% and 72.5% (Figure 2B).

In the next step, we analyzed the capacity of each individual riboprobe to cross-hybridize to the rest of the selected sequences. To do this, we synthesized complementary transcripts of the 7 selected sequences that were serially diluted (1:5) and applied on nylon membranes, together with total RNA extracted from several healthy tissues (Figure 3). Replicas of the same membrane were hybridized first with the PPV riboprobe at different hybridization temperatures, to evaluate the effect of such parameter in the cross-hybridization (Figure 3A). We observed no cross-reaction when the hybridization was performed at 68ºC. However, the reduction of 8 degrees during the hybridization assay (60ºC) was sufficient to start to see cross-hybridization with the TEV sequence at high concentration (200 pg/µl), meanwhile the reduction of another 5 (55ºC) or 10 (50ºC) degrees was sufficient to detect two (TEV, SPFMV) or all sequences at different concentrations. In the case of the hybridization performed at 50ºC we also observed at weak signal in the negative controls (100ng of total RNA extracted from healthy tissue). Accordingly, we evaluated the cross-hybridization of the remaining riboprobes at 55ºC (Figure 3C). In general, we observed that sequences with an identity percentage below 65 % with the corresponding probe were not detected at 55ºC but also that sequences with such percentage higher than 67% were all detected, except the PPV probe that rendered negative results with LMV, which shared 69.7% identity. Between the 65% and 67% identity we observed different behaviors suggesting that other factors influence the cross-hybridization (e.g. the size of the identical regions, the percentage of cytosine or guanine nucleotides, etc.).

Next, we evaluated the cross-reactivity of the three polyprobes (GP3, GFP5 and GP7) (Figure 4). For this purpose, we used replicas of the same membrane described in Figure 3 that were hybridized at 50ºC, since no cross-hybridization was observed with the negative controls at this temperature. First, we observed that the shorter polyprobe carrying only three sequences (GP3: PPV, SPFMV, TEV) was able to detect the 7 potyvirus sequences in which the lower detection limit corresponded to the PVMV transcripts at 8 pg/µl (Figure 4). The inclusion of another two viral sequences in the GP5 polyprobe (PVY, PVMV, PPV, SPFMV, TEV) allowed the detection of all 7 viral sequences with lower detection limits, at least for the sequences present in the polyprobe. Thus, we observed positive hybridization signal for all sequences included in the GP5 until a concentration of 0.06 pg/µl, meanwhile the other two sequences not present in the polyprobe were detected until a concentration 1.6 pg/µl, five times less sensitive than the GP3. Apparently, the enlargement of the polyprobe has a slight negative effect in the detection limit of the heterologous sequences. Finally, we hybridized the membrane with the GP7 polyprobe and we obtained the same detection limit for all analyzed viruses, corresponding to 0.32 pg/µl. As observed for the GP5, the increment of the size of the polyprobe affected the detection limit, reducing five times the best signals obtained with GP3 or GP5.

In silico analysis of the capacity of GP to detect all potyviruses available at the database and other members of the family _Potyviridae_

According to the results obtained, sequences showing an identity percentage of 68% or higher with the selected probes, could be detected by cross-hybridization. To identify how many potyvirus sequences could be potentially hybridized with the cloned potyvirus sequences, we performed a MatGAT analysis (Campanella et al., 2003) using the equivalent region of the 94 potyvirus species used for the phylogenetic analysis (Supplementary figure 2). The results showed that all potyvirus species presented an identity percentage of 68% or higher with two or more of the 7 selected sequences. Only *Onion yellow dwarf virus*, with a percentage of 69.3%, showed such identity with only PPV. In addition, we observed that the majority of the sequences presented identity percentages of 70% or higher with any of the selected sequences. Only *Daphne mosaic virus, Habenaria mosaic virus, Hordeum mosaic virus, Onion yellow dwarf virus,*

Ornithogalum mosaic virus and *Vallota speciosa virus* presented identity percentages below 70%. Also, we observed that the 94 potyvirus species could be theoretically detected with the smaller genus-probe of GP3, since all sequences presented an identity percentage higher than 68% with any of the PPV, TEV and SPFMV cloned fragments.

To identify if other members of the family *Potyviridae* could be potentially detected with the seven selected potyvirus sequences, the equivalent regions from 27 species representatives of the seven genera of the family *Potyviridae*, except Potyvirus (Supplementary Figure 1), were subjected to a MatGAT analysis (Campanella et al., 2003) to determine the identity percentage (Supplementary Figure 2). The results obtained revealed that all viruses, except Rymovirus, presented an identity percentage below 65%, suggesting that they should be not detected with any of the different probes assayed herein. In the case of rymovirus, the three species analyzed showed identity percentage of 68% or higher with one or more of the 7 selected sequences and, thus, susceptible of being detected by the GPs.

Analysis of field samples by non-radioactive nucleic acids spot hybridization (NASH)

Finally, we evaluated the capacity of the three GP to detect heterologous potyviruses or other viral species of the family *Potyviridae* by analyzing 49 different field samples, including different hosts, for the presence of 32 potyvirus species or 7 viral species assigned to the genus *Bymovirus, Ipomovirus, Rymovirus and Tritimovirus* (Table 2). First, it should be mentioned that the infected starting material was lyophilized or fresh tissue proportionated by the German Collection of Microorganisms and Cell Cultures (DSMZ) or the Mediterranean Agroforestal Institute of the Polytechnic University of Valencia. The samples were extracted using the Silica protocol (MacKenzie et al., 1997) but also with a fast protocol in which the tissue is homogenized with citrate buffer and directly applied onto the membrane (Sanchez-Navarro et al., 1998, Sanchez-Navarro et al., 1999). First, we observed no hybridization signal with any of the 8 healthy hosts analyzed, in spite of that the hybridization was performed at 50ºC. The 32 potyviruses and the 2 rymoviruses were detected by NASH

with the three GPs except for PVMV that rendered negative signal with GP3. Interestingly, GP3 presents the most unfavorable situation for PVMV detection since its identity percentage with the three cloned sequences present in GP3 is around 66-68% (Figure 3 and 5). On the other hand, we observed that *Onion yellow dwarf virus*, which theoretically could be detected only with the PPV clone (identity percentage of 69.3%), was detected with all three GPs. In addition, *Ryegrass mosaic virus* was clearly detected with GP3 and GP5, in spite that the higher identity percentage in both probes corresponded to the PPV cloned sequence with a 67.2%. When the plants were analyzed using the fast citrate buffer protocol, we observed that the 90.2% of Silica positives (83 out 92) were correctly detected. We also observed two samples that were positive by citrate buffer extraction and negative by Silica extraction, using the GP3 and GP5 probes (samples 30 and 34, Table 2). These results could indicate differences in the viral titer associated to the extraction protocol used but we cannot discard other effects derived of the starting material (lyophilized) or the host (*Nicotiana benthamiana* or *Cucurbita pepo*) that could interfere with the detection procedure.

DISCUSSION

In the last few years, a significant effort has been made to develop strategies for simultaneous detection of multiple plant viruses. Although PCR-based approaches have received special attention, molecular hybridization assay represents an attractive methodology for the detection of plant viruses since it is accurate, sensitive (pg/µl of viral RNA), robust and very powerful for large screening with a reduced cost (see James et al., 2006; Pallás et al., 2011; 2017 for review). Previous works showed that this technology allows the multiple detection of plant viruses by a cocktail of specific probes or by a unique probe carrying the different viral fragments fused in tandem called a polyprobe. The polyprobes permit the detection of several pathogens with comparable detection limit to the individual probes (e.g. Herranz et al., 2005) although with long polyprobes (e.g. 10 probes in tandem or more) a reduction of the hybridization temperature is required (e.g. Peiró et al., 2012). A challenge of this strategy has been its adaptation by generating a polyvalent polyprobe able to detect all the species within a genus, named genus-probe. To answer this question we have selected the genus *Potyvirus* for three reasons: i) it is one of the largest groups of plant viruses including

146 species (Revers and Garcia, 2015), ii) potyviruses affect many species which are economically important (Scholthof et al., 2011) and iii) some other diagnosis assays have been adjusted for the detection of a broad spectrum of potyviruses with varied success (Liu et al., 2015, Wei et al., 2009, Hsu et al., 2005, Chen et al., 2001; Jordan and Hammond, 1991). To obtain the genus-probe we have used the versatility of the molecular hybridization that permits the detection of closely related sequences by reducing the hybridization temperature. Thus, we selected the more conserved region, representing 500 nt of the NIb gene, of seven potyviruses distributed along the genus phylogenetic tree and we observed that cross-hybridization occurs at 55ºC (single probes) or 50ºC (polyprobes) when the target sequences share a 68% or higher identity percentage with the probe, meanwhile negative hybridization signal was obtained when the percentage was below 65%. We observed some exceptions to these rules (e.g. LMV is not detected by PPV probe sharing 69%) suggesting that factors other than the identity percentage are important in the cross-hybridization. In this sense, the presence of large identical regions, the percentage of cytosine and guanines or the probe mismatches, among others, are critical factors to take into account (Kessler, 2000). In these hybridization conditions, there were no positive signals in the different healthy controls used, opening the applicability of this assay for routine diagnosis. According with the identity percentage required for cross-hybridization, the three GP described herein have the capacity to detect the 94 potyvirus species analyzed. However, we observed some negative results (samples 29, 30, or 33) using the GP3 that were positive by GP5 o GP7. Apparently, the presence of more conserved fragments with the capacity to hybridize with a target sequence increments the detection limit of the genus-probe. In our hands, we were able to detect 100% of potyviruses analyzed (32 species in 34 samples), representing a comparable (33 species in 55 samples; Jordan and Hammond, 1991) or a significant increment from previous approaches using broad-spectrum monoclonal antibody (14 species; Liu et al., 2015) or polyvalent primer pairs that ranged between the 100% (23 species in 40 samples; Zheng et al., 2010), 80% (32 out 40 samples corresponding to 21 species out 23; Pappu et al., 1993) or 50% (20 out 40 samples corresponding to 15 species out 23; Gibbs and Mackenzie, 1997). We also observed a positive hybridization signal with the two rymovirus analyzed, meanwhile no hybridization was observed with the rest of viral species assigned to the genus bymovirus, ipomovirus or tritimovirus. Interesting, the two rymovirus AgMV and RGMV (samples 39, 40) plus BrSMV (tritimovirus, sample 41) and BaYMV

(bymovirus, sample 25) were also detected by RT-PCR using the universal potyviruses NIb primers (Zhen et al., 2010) (data not shown), indicating high conserved sequences in this region in the family *Potyviridae*. Positive hybridization signal was also observed in some species that share only an identity percentage close to the estimated limit of 68% for cross-hybridization, with one of the conserved fragments of the GP (e.g. *Onion yellow dwarf virus* or *Ryegrass mosaic virus*). In addition, the possibility to use a fast protocol, which detected the 90% of positive samples analyzed by NASH, together with the robustness of the methodology that permits the detection of species with significant nucleotide sequences variability or even uncharacterized potyviruses and the reduced time and cost make the non-radioactive hybridization using a GP a very suitable approach for the routine diagnosis of potyvirus in large surveys. Currently, the use of a broad-spectrum MAb PTY1 (Jordan and Hammond, 1991), combined with a direct tissue extract procedure, represents a valuable tool for diagnostic and screening applications for the detection of aphid-transmissible potyviruses, although it is not known how large is the spectrum of viruses that could be detected by the MAb PTY1. The genus-probed developed in this work anticipates that all potyviruses can be broadly detected (identity percentage of 68/69% or higher). Furthermore, this technology presents the advantage to be easily updated by introducing new sequences of interest (e.g. new potyviruses, etc.). In addition, the use of this new GP, in conjunction to other molecular techniques that permit the identification of the corresponding potyvirus species (e.g. degenerate primer-based RT-PCR or HTS methods, etc.), could be a very good approach to detect any potyvirus isolate, previously described or uncharacterized. Finally, the observation that the GP could detect also members of the genus *Rymovirus*, opens the possibility to design GP against the family *Potyviridae*. An open question related to the GP technology is the size of the conserved regions to be introduced in the polyprobe. In the present work we have selected fragments of around 500 nt but further analysis will be addressed to delimitate the minimal size of the conserved regions that still are able to cross-hybridize.

ACKNOWLEDGEMENTS

We thank L. Corachán for her excellent technical assistance. We also thank Isabel Font and Ana O. Alfaro, from the Mediterranean Agroforestal Institute at the Polytechnic University of Valencia, for provide part of the potyvirus infected field samples. This work was supported by grant BIO2017-88321-R from the Spanish Direccion General de Investigacion Cientifica y Tecnica (DGICYT-MINECO).

Figure 1. Phylogenetic trees of the 94 potyviruses for which the complete sequence is known. Trees were developed using nucleotide sequences of the complete genome and inferred by the minimum-evolution method. Values at the nodes are bootstrap values based on 10,000 pseudoreplicates. Nodes with bootstrap support <50% are not indicated. Sequences in gray boxes were used for the synthesis of the genus-probes. Sequences underlined correspond to the potyvirus used for the hybridization detection using the genus-probes.

Figure 2. Schematic representation of the different genus-probes (GP) 3, 5 and 7 clones introduced in the pSK+ plasmid. A) The corresponding virus fragments are indicated by a box in which the numbers represent the corresponding nucleotide of the data base sequences: X97704 (*Lettuce mosaic virus*, LMV), EU660589 (*Watermelon mosaic virus*, WMV), AJ890346 (*Potato virus Y*, PVY), DQ645484 (*Pepper veinal mottle virus*, PVMV), KU508427 (*Plum pox virus*, PPV), KU511268 (*Sweet potato feathery mottle virus*, SPFMV) and DQ986288 (*Tobacco etch virus*, TEV). The *Xho*I restriction site used either to synthesize the riboprobe with the T7 RNA polymerase or to insert additional cDNA probes is indicated. B) Schematic representation of the identity

percentage estimated by MatGAT between the sequences used for the genus-probes LMV, PPV, PVMV, PVY, SPFMV, TEV and WMV.

Figure 3. Evaluation of the cross hybridization between the seven potyvirus sequences indicated in Figure 2. A) Influence of the temperature in the cross hybridization between the PPV probe and the rest of the indicated potyvirus sequences. Known amounts of the positive transcripts corresponding to the sequences indicated in Figure 2, were applied on nylon membranes. For the healthy control 100 ng of total RNA extracted from melon (A), cucumber (B), N. benthamiana (C), tomato (D), chrysanthemum (E) and gynura (F), were apllied. Replicas of the same membrane were hybridized with the PPV riboprobe, complementary to the sequence indicated in Figure 2, at 68ºC, 60ºC, 55ºC and 50ºC, respectively. Numbers on the top of the left panel indicate the picograms of transcripts applied on the membrane meanwhile numbers on the right side indicate the identity percentage estimated by the MatGAT program (Campanella et al., 2003) between the PPV sequence and the rest of the potyvirus sequences indicated in Figure 1. B). Summary of the results obtained in A. Numbers represent the identity percentage between the PPV sequence and the rest of the potyvirus sequences meanwhile the colors indicate the lowest amount for which transcripts showed hybridization with the PPV probe. The colors used are blue (200 pg), dark blue (40 pg), green (8 pg), yellow (1.6 pg), orange (0.32 pg) and red (0.06 pg). White color indicates no hybridization signal. C) Schematic representation of the hybridization observed with the seven individual potyvirus probes. Replicas of the membrane described in A were hybridized at 55 ºC with the indicated probes. Numbers represent the corresponding identity percentage estimated by MatGAT program meanwhile the colors represent the lowest amount of transcripts showing hybridization with the corresponding probe, as indicated in B. Films were exposed for 15 min.

Figure 4. Evaluation of the cross hybridization between the seven potyvirus sequences and the genus-probes (GP) 3, 5 and 7. A) Replicas of the membrane described in Figure 3A were hybridized with the indicated genus-probe at 50ºC. For the healthy control 100 ng of total RNA extracted from melon (A), cucumber (B), N. benthamiana (C), tomato (D), chrysanthemum (E) and gynura (F) were applied. Numbers on the top of the left panel indicate the picograms of transcripts applied on the membrane. Films were

exposed for 15 min. B) Summary of the results obtained in A. The colors indicate the lowest amount of transcripts showing hybridization with the corresponding genus-probe. The colors used are blue (200 pg), dark blue (40 pg), green (8 pg), yellow (1.6 pg), orange (0.32 pg) and red (0.06 pg). White color indicates no hybridization signal.

Supplementary Figure 2. Schematic representation of the identity percentage estimated by MatGAT between the sequences used for the genus-probes of LMV, PPV, PVMV, PVY, SPFMV, TEV, WMV and the equivalent sequence of the indicated potyvirus, brambyvirus, bymovirus, ipomovirus, macluravirus, poacevirus, rymovirus and tritimovirus. Identity percentage values of 68% and 69% are labelled in green meanwhile values of 70% and higher are marked in orange. Sequences in gray boxes correspond to the virus used for the hybridization detection using the genus-probes.

LITERATURE CITED

Aparicio, F., Soler, S., Aramburu, J., Galipienso, L., Nuez, F., Pallás, V. and López, C. 2009. Simultaneous detection of six RNA plant viruses affecting tomato crops using a single digoxigenin-labelled polyprobe. Eur. J. Plant Pathol. 123:117-123.

Barba, M. and Hadidi, A. 2011. DNA microarrays and other future trends in detection and typing of viruses, viroids and phytoplasmas. Pages 363-372 in: Virus and Virus-Like Diseases of Pome and Stone Fruits. A. Hadidi, M. Barba, T. Candresse, and W. Jelkmann, eds. The American Phytopathological Society Press, St. Paul, MN, USA.

Bystricka, D., Lenz, O., Mraz, I., Piherova, L., Kmoch, S. and Sip, M. 2005. Oligonucleotide-based microarray: A new improvement in microarray detection of plant viruses. J. Virol. Methods 128:176-182.

Campanella, J. J., Bitincka, L. and Smalley, J. 2003. MatGAT: An application that generates similarity/identity matrices using protein or DNA sequences. BMC Bioinformatics 4:29.

Chen, J., Chen, J. and Adams, M. J. 2001. A universal PCR primer to detect members of the Potyviridae and its use to examine the taxonomic status of several members of the family. Arch. Virol. 146:757-766.

Cohen, O., Batuman, O., Stanbekova, G., Sano, T., Mawassi, M. and Bar-Joseph, M. 2006. Construction of a multiprobe for the simultaneous detection of viroids infecting citrus trees. Virus Genes 33:287-292.

Gibbs, A. and Mackenzie, A. 1997. A primer pair for amplifying part of the genome of all potyvirids by RT-PCR. Journal of Virological Methods, 63:9-16.

Herranz, M. C., Sanchez-Navarro, J. A., Aparicio, F. and Pallas, V. 2005. Simultaneous detection of six stone fruit viruses by non-isotopic molecular hybridization using a unique riboprobe or 'polyprobe'. J. Virol. Methods 124:49-55.

Higgins D., Thompson J., Gibson T. Thompson J.D., Higgins D.G., Gibson T.J., 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res. 22:4673-4680.

Hsu, Y. C., Yeh, T. J. and Chang, Y. C. 2005. A new combination of RT-PCR and reverse dot blot hybridization for rapid detection and identification of potyviruses. J. Virol. Methods, 128:54-60.

James, D., Varga, A., Pallas, V. and Candresse, T. 2006. Strategies for simultaneous detection of multiple plant viruses. Can. J. Plant Pathol. 28:16-29.

Jeong, J., Ju, H. and Noh J. 2014. A Review of Detection Methods for the Plant Viruses. Res. Plant Dis. 20:173-181.

Jiang, D., Hou, W., Sano, T., Kang, N., Qin, L., Wu, Z., Li, S. and Xie, L. 2013. Rapid detection and identification of viroids in the genus Coleviroid using a universal probe. J. Virol. Methods 187:321-326.

Jones, R. A. 2006. Control of plant virus diseases. Adv. Virus Res. 67:205-244.

Jordan, R. and Hammond, J. 1991. Comparison and differentiation of potyvirus isolates and identification of strain-, virus-, subgroup-specific and potyvirus group-common epitopes using monoclonal antibodies. J. Gen . Virol. 72:25-36.

Kessler, C. 2000. Overview on Factors Influencing Nucleic Acid Hybridization. In: Kessler, C. ed), Nonradioactive Analysis of Biomolecules. Berlin, Heidelberg, Springer Berlin Heidelberg, pp. 437-442.

Kumar S., Stecher G., Tamura K., 2016. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol. Biol. Evol. 33:1870-1874.

Lin, L., Li, R., Mock, R. and Kinard, G. 2011. Development of a polyprobe to detect six viroids of pome and stone fruit trees. J. Virol. Methods 171:91-97.

Liu, H.-L., Lin, W.-F., Hu, W.-C., Lee, Y.-A. and Chang, Y.-C. 2015. A Strategy for Generating a Broad-Spectrum Monoclonal Antibody and Soluble Single-Chain Variable Fragments against Plant Potyviruses. Appl. Environ. Microbiol. 81:6839-6849.

MacKenzie, D. J., McLean, M. A., Mukerji, S. and Green, M. 1997. Improved RNA extraction from woody plants for the detection of viral pathogens by reverse transcription-polymerase chain reaction. Plant Dis. 81:222-226.

Mas P., Sánchez-Navarro J.A., Sánchez-Pina M.A., Pallás V., 1993. Chemiluminescent and colorigenic detection of Cherry Leaf Roll Virus with digoxigenin-labeled RNA probes. J. Virol. Methods 45:93-102.

Minutillo, S. A., Mascia, T. and Gallitelli, D. 2012. A DNA probe mix for the multiplex detection of ten artichoke viruses. Eur. J. Plant Pathol. 134:459-465.

Pallás, V., Más, P. and Sánchez-Navarro, J. 1998. Detection of Plant RNA Viruses by Nonisotopic Dot-Blot Hybridization. Pages 461-468. In: Plant Virology Protocols. G. Foster and S. Taylor, eds. Humana Press.

Pallas, V., Faggioli, F., Aparico, F. and Sanchez-Navarro, J. A. 2011. Molecular hybridization techniques for detecting and studying fruit tree viruses and viroids. Pages 333-339 in: Virus and Virus-Like Diseases of Pome and Stone Fruits. A.

Hadidi, M. Barba, T. Candresse, and W. Jelkmann, eds. APS Press/American Phytopathological Society. St. Paul, Minnesota.

Pallás, V., Sánchez-Navarro, J., R. Kinard, G. and Di Serio, F. 2017. Molecular Hybridization Techniques for Detecting and Studying Viroids. Pages 369-379 in: Viroids and Satellites. A. Hadidi, R. Flores, J. W. Randles, and P. Palukaitis, eds. Academic Press Inc., London.

Pappu, S. S., Brand, R., Pappu, H. R., Rybicki, E. P., Gough, K. H., Frenkel, M. J. and Niblett, C. L. 1993. A polymerase chain-reaction method adapted for selective amplification and cloning of 3' sequences of potyviral genomes application to Dasheen mosaic virus. J. Virol. Methods 41:9-20.

Peiró, A., Pallás, V. and Sánchez-Navarro, J. 2012. Simultaneous detection of eight viruses and two viroids affecting stone fruit trees by using a unique polyprobe. Eur. J. Plant Pathol. 132:469-475.

Revers, F. and Garcia, J. A. 2015. Molecular biology of potyviruses. Adv. Virus Res. 92:101-199.

Saade, M., Aparicio, F., Sanchez-Navarro, J. A., Herranz, M. C., Myrta, A., Di Terlizzi, B. and Pallas, V. 2000. Simultaneous detection of the three ilarviruses affecting stone fruit trees by nonisotopic molecular hybridization and multiplex reverse-transcription polymerase chain reaction. Phytopathology 90:1330-1336.

Saldarelli, P., Barbarossa, L., Grieco, F. and Gallitelli, D. 1996. Digoxigenin-labeled riboprobes applied to phytosanitary certification of tomato in Italy. Plant Dis. 80:1343-1346

Sanchez-Navarro, J. A., Aparicio, F., Herranz, M. C., Minafra, A., Myrta, A. and Pallas, V. 2005. Simultaneous detection and identification of eight stone fruit viruses by one-step RT-PCR. Eur. J. Plant Pathol. 111:77-84.

Sanchez-Navarro, J. A., Aparicio, F., Rowhani, A. and Pallas, V. 1998. Comparative analysis of ELISA, nonradioactive molecular hybridization and PCR for the detection of prunus necrotic ringspot virus in herbaceous and Prunus hosts. Plant Pathol. 47:780-786.

Sanchez-Navarro, J. A., Canizares, M. C., Cano, E. A. and Pallas, V. 1999. Simultaneous detection of five carnation viruses by non-isotopic molecular hybridization. J. Virol. Methods 82:167-175.

Sanchez-Navarro, J. A., Cano, E. A. and Pallas, V. 1996. Non-radioactive molecular hybridization detection of carnation mottle virus in infected carnations and its comparison to serological and biological techniques. Plant Pathol. 45:375-382.

Scholthof, K.-B. G., Adkins, S., Czosnek, H., Palukaitis, P., Jacquot, E., Hohn, T., Hohn, B., Saunders, K., Candresse, T., Ahlquist, P., Hemenway, C. and Foster, G. D. 2011. Top 10 plant viruses in molecular plant pathology. Mol. Plant Pathol. 12:938-954.

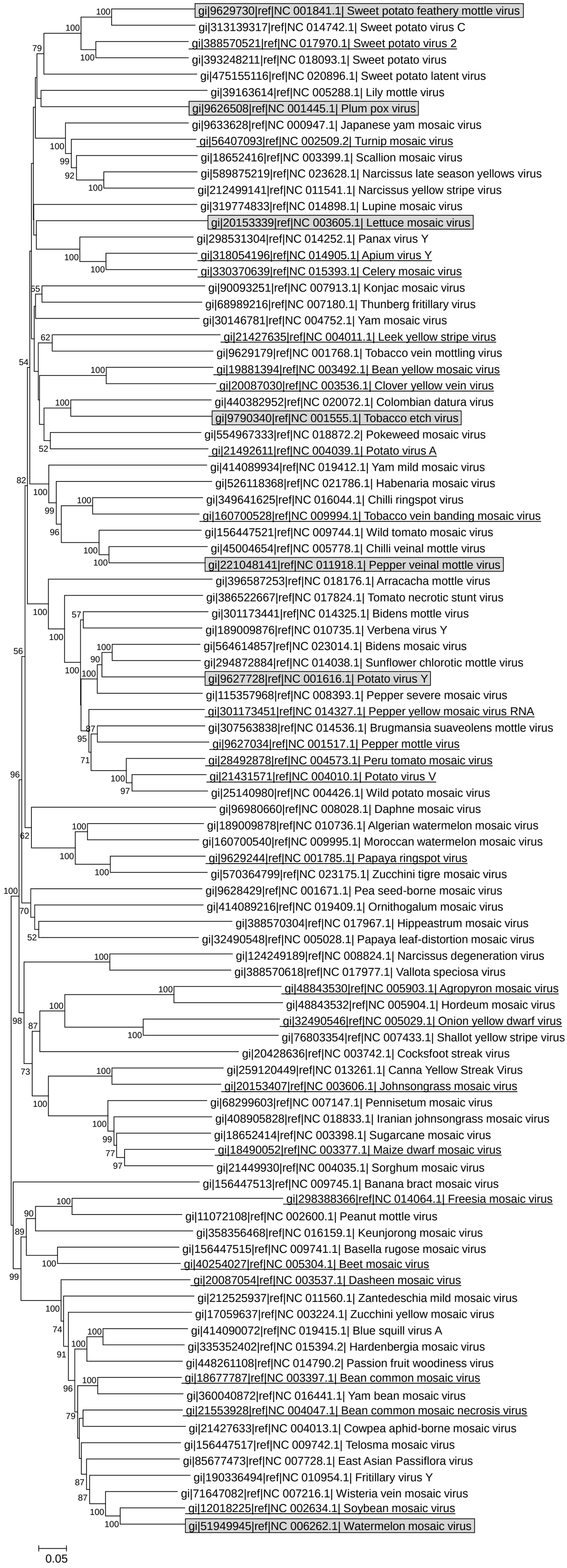
Torchetti, E. M., Navarro, B. and Di Serio, F. 2012. A single polyprobe for detecting simultaneously eight pospiviroids infecting ornamentals and vegetables. J. Virol. Methods 186:141-146.

Wei, T., Pearson, M. N., Blohm, D., Nolte, M. and Armstrong, K. 2009. Development of a short oligonucleotide microarray for the detection and identification of multiple potyviruses. J Virol. Methods 162:109-118.

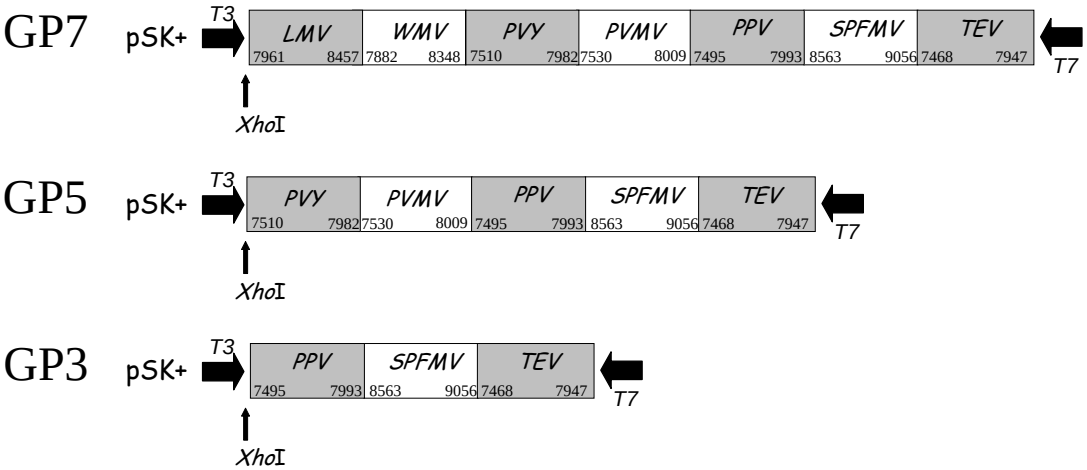
Zamora-Macorra, E., Leobardo Ochoa-Martinez, D., Valdovinos-Ponce, G., Rojas-Martinez, R., Ramirez-Rojas, S., Sanchez-Navarro, J.A., Pallas, V. and Aparicio, F. 2015. Simultaneous detection of Clavibacter michiganensis subsp michiganensis, Pepino mosaic virus and Mexican papita viroid by non-radioactive molecular hybridization using a unique polyprobe. Eur. J. Plant Pathol. 143:779-787.

Zhang, Z., Peng, S., Jiang, D., Pan, S., Wang, H. and Li, S. 2012. Development of a polyprobe for the simultaneous detection of four grapevine viroids in grapevine plants. Eur. J. Plant Pathol. 132:9-16.

Zheng, L., Rodoni, B. C., Gibbs, M. J. and Gibbs, A. J. 2010. A novel pair of universal primers for the detection of potyviruses. Plant Pathol. 59:211-220.



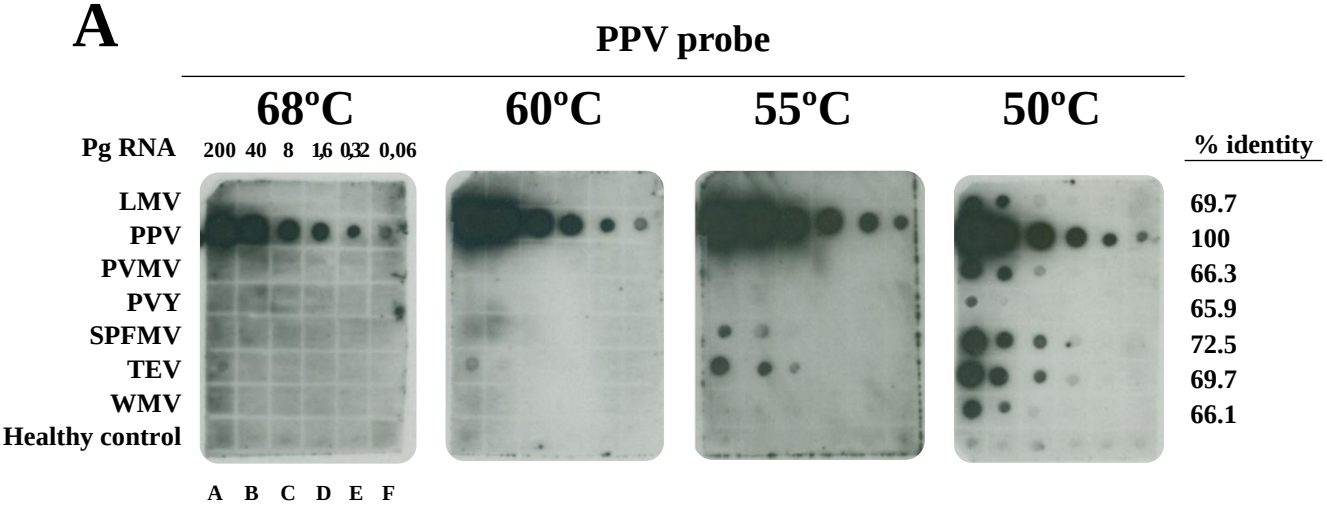
A



B

	LMV	PPV	PVMV	PVY	SPFMV	TEV	WMV
LMV	100						
PPV	69.7	100					
PVMV	67.6	66.3	100				
PVY	64.8	65.9	66.5	100			
SPFMV	69.6	72.5	66.0	67.0	100		
TEV	67.8	69.7	66.7	69.2	67.8	100	
WMV	65.8	66.1	66.1	67.3	67.6	70.3	100

A

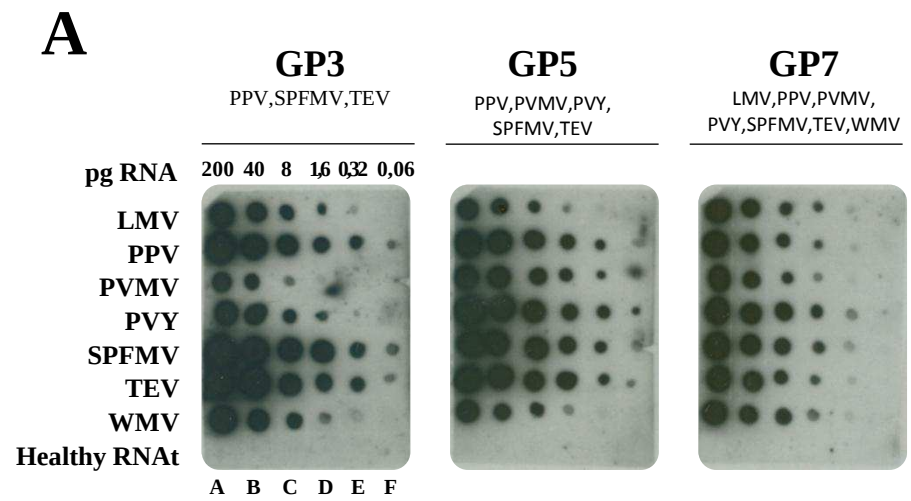


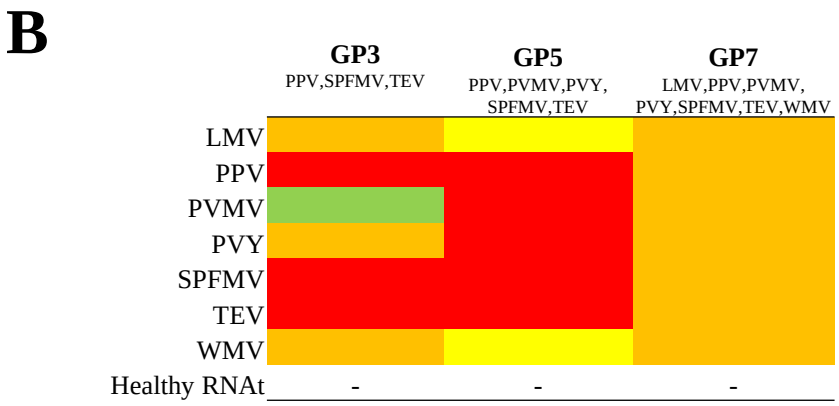
B

PPV probe	(68ºC)	(60ºC)	(55ºC)	(50ºC)
LMV	69.7	69.7	69.7	69.7
PPV	100	100	100	100
PVMV	66.3	66.3	66.3	66.3
PVY	65.9	65.9	65.9	65.9
SPFMV	72.5	72.5	72.5	72.5
TEV	69.7	69.7	69.7	69.7
WMV	66.1	66.1	66.1	66.1
Healthy control	-	-	-	+

C

Probe (55ºC)	LMV	PPV	PVMV	PVY	SPFMV	TEV	WMV
LMV	100	69.7	67.6	64.8	69.6	67.8	65.8
PPV	69.7	100	66.3	65.9	72.5	69.7	66.1
PVMV	67.6	66.3	100	66.5	66.0	66.7	66.1
PVY	64.8	65.9	66.5	100	67.0	69.2	67.3
SPFMV	69.6	72.5	66.0	67.0	100	67.8	67.6
TEV	67.8	69.7	66.7	69.2	67.8	100	70.3
WMV	65.8	66.1	66.1	67.3	67.6	70.3	100
Healthy control	-	-	-	-	+/-	-	-





Primer name	Nucleotide sequence (5´-3´) [a]	Target viral species	Expected Fragment (bp)	Acc. No. and location in the genome[b]
2847-s	CACACTCGCGGTAAGTTTGGAGTGTGGAA	*Lettuce mosaic virus*, LMV	496	X97704
2848-As	CACAGTCGACGTCATAGCTAGCACAACCAT			7961-8457
2869-s	CACACTCGAGAAGGGAATTTGGAAYGGTTC	*Watermelon mosaic virus*, WMV	466	EU660589
2870-As	CACAGTCGACTTGTCAACGACTGTAGATGG			7882-8348
2845-s	CACACTCGAGATTTGGAACGGATCATTGAA	*Potato virus Y*, PVY	472	AJ890346
2846-As	CACAGTCGACACCATGAGAGAATTATCCAC			7510-7982
2865-s	CACACTCGAGGTAAACTTGGGATTTGG	*Pepper veinal mottle virus*, PVMV	479	DQ645484
2866-As	CACAGTCGACCATGAGAGTGTTATC			7530-8009
2871-s	CACACTCGAGGAAAGAAAGGAGTGTGGAATGG	*Plum pox virus*, PPV	498	KU508427
2872-As	CACAGTCGCGTCATTGCCAAAATAACCAT			7495-7993
2873-s	CACACTCGAGATGGGATACAAAGGTCTYTGGAA	*Sweet potato feathery mottle virus, SPFMV*	493	KU511268
2874-As	CACAGTCGACGCTAACACAACCATAAGTGT			8563-9056
2861-s	CACACTCGAGGAAAGCTGGGAATTTGG	*Tobacco etch virus*, TEV	479	DQ986288
2862-As	CACAGTCGACCATGAGTGTGTTGTC			7468-7947

Table 1. Primer pairs used in the amplification of the genus-probes.

[a] Restriction sites of the *Xho*I and *Sal*I are underlined.
[b] Numbers are referred to the corresponding nucleotide of the sequence available in the indicated accession number of the GenBank database.

Table 2. Analysis of the capacity of the genus-probes (GP) 3, 5 and 7 to detect different potyvirus, bymovirus, ipomovirus, rymovirus and tritimovirus in field samples by nucleic acids spot hybridization (NASH). All samples were extracted with the Silica and the citrate buffer protocols. The hybridization was performed at 50ºC.

	Virus	Acronym	Genus	Source [a]	Host	NASH (Silica/Citrate buffer)		
						GP3	GP5	GP7
1	Carrot virus Y	CarVY	*Potyvirus*	UPV	*Daucus carota*	+ / +	+ / +	+ / +
2	Onion yellow dwarf virus	OYDV	*Potyvirus*	UPV	*Allium cepa*	+ / -	+ / -	+ / +
3	Turnip mosaic virus	TuMV	*Potyvirus*	UPV	*Lactuca sativa*	+ / +	+ / +	+ / -
4	Bean common mosaic necrosis virus	BCMNV	*Potyvirus*	DSMZ	*Phaseolus vulgaris*	+ / +	+ / +	+ / +
5	Bean common mosaic virus	BCMV	*Potyvirus*	DSMZ	*Phaseolus vulgaris*	+ / +	+ / +	+ / +
6	Beet mosaic virus	BtMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
7	Johnsongrass mosaic virus	JGMV	*Potyvirus*	DSMZ	*Zea mays*	+ / +	+ / +	+ / +
8	Leek yellow stripe virus	LYSV	*Potyvirus*	DSMZ	*Chenopodium quinoa*	+ / +	+ / +	+ / +
9	Pepper mottle virus	PepMoV	*Potyvirus*	DSMZ	*Nicotiana tabacum*	+ / *	+ / +	+ / +
10	Peru tomato mosaic virus	PTV	*Potyvirus*	DSMZ	*Nicotiana tabacum*	+ / *	+ / +	+ / +
11	Potato virus A	PVA	*Potyvirus*	DSMZ	*Nicotiana occidentalis*	+ / +	+ / +	+ / +
12	Potato virus V	PVV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
13	Potato virus Y	PVY	*Potyvirus*	DSMZ	*Nicotiana tabacum*	+ / *	+ / +	+ / -
14	Soybean mosaic virus	SMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / *
15	Tobacco vein banding mosaic virus	TVBMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
16	Maize dwarf mosaic virus	MDMV	*Potyvirus*	DSMZ	*Zea mays*	+ / +	+ / +	+ / +
17	Dasheen mosaic virus	DsMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
18	Apium virus Y	ApVY	*Potyvirus*	DSMZ	*Ami majus*	+ / +	+ / +	+ / +
19	Pepper yellow mosaic virus	PepYMV	*Potyvirus*	DSMZ	*Nicotiana tabacum*	+ / *	+ / +	+ / +
20	Sweet potato virus 2	SPV-2	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
21	Bean yellow mosaic virus	BYMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
22	Carrot thin leaf virus	CTLV	*Potyvirus*	UPV	*Daucus carota*	+ / +	+ / +	+ / +
23	Celery mosaic virus	CeMV	*Potyvirus*	UPV	*Apium graveolens*	+ /nt	+ /nt	+ /nt
24	Clover yellow vein virus	ClYVV	*Potyvirus*	UPV	*Phaseolus vulgaris*	+ /nt	+ /nt	+ /nt
25	Freesia mosaic virus	FreMV	*Potyvirus*	UPV	*Freesia*	+ / +	+ / +	+ / -
26	Papaya ringspot virus	PRSV	*Potyvirus*	UPV	*Citrullus lanatus*	+ /nt	+ /nt	+ /nt

27	Tobacco etch virus	TEV	*Potyvirus*	UPV	*Nicotiana tabacum*	+ / +	+ / +	+ / +
28	Tobacco etch virus	TEV	*Potyvirus*	UPV	*Physalis floridana*	+ / +	+ / +	+ / +
29	Lettuce mosaic virus	LMV	*Potyvirus*	DSMZ	*Chenopodium quinoa*	- / +	- / +	+ / +
30	Pepper veinal mottle virus	PVMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	- / -	+ / +	+ / +
31	Sweet potato feathery mottle virus	SPFMV	*Potyvirus*	DSMZ	*Nicotiana benthamiana*	+ / +	+ / +	+ / +
32	Tobacco etch virus	TEV	*Potyvirus*	UPV	*Nicotiana tabacum*	+ / +	+ / +	+ / +
33	Watermelon mosaic virus	WMV	*Potyvirus*	DSMZ	*Cucurbita pepo*	- / +	- / +	+ / +
34	Plum pox virus	PPV	*Potyvirus*	Lab	*Prunus domestica*	+ /nt	+ /nt	+ /nt
35	Barley yellow mosaic virus	BaYMV	*Bymovirus*	DSMZ	*Hordeum vulgare*	- / -	- / -	- / -
36	Ugandan cassava brown streak virus	UCBSV	*Ipomovirus*	DSMZ	*Manihot esculenta*	- / -	- / -	- / -
37	Cucumber vein yellowing virus	CVYV	*Ipomovirus*	UPV	*Cucumis sativus*	- / -	- / -	- / -
38	Sweet potato mild mottle virus	SPMMV	*Ipomovirus*	DSMZ	*Nicotiana tabacum*	- / -	- / -	- / -
39	Agropyron mosaic virus	AgMV	*Rymovirus*	DSMZ	*Triticum aestivum*	+ / +	+ / +	+ / +
40	Ryegrass mosaic virus	RGMV	*Rymovirus*	DSMZ	*Lolium multiflorum*	+ / +	+ / +	+ / +
41	Brome streak mosaic virus	BrSMV	*Tritimovirus*	DSMZ	*Hordeum vulgare*	* / -	* / -	* / -
42	Healthy control			Lab	*Cucumis melo*	- /nt	- /nt	- /nt
43	Healthy control			Lab	*Cucumis sativus*	- /nt	- /nt	- /nt
44	Healthy control			Lab	*Nicotiana benthamiana*	- / -	- / -	- / -
45	Healthy control			Lab	*Solanum lycopersicum*	- /nt	- /nt	- /nt
46	Healthy control			Lab	*Chrysanthemum*	- /nt	- /nt	- /nt
47	Healthy control			Lab	*Gynura aurantiaca*	- /nt	- /nt	- /nt
48	Healthy control			Lab	*Nicotiana tabacum*	- / -	- / -	- / -
49	Healthy control			UPV	*Arabidopsis thaliana*	- / -	- / -	- / -

+, - and * correspond to positive, negative and uncertain results, respectively.
nt, no tissue available.
[a], samples obtained from the Isabel Font's group at the Universidad Politécnica de Valencia (UPV), the German Collection of Microorganisms and Cell Cultures (DSMZ) or our laboratory (Lab).

Conserved regions between viral species belonging to the family *Potyviridae*

>gi|48843530|ref|NC_005903.1|_Agropyron_mosaic_virus_complete_genome

AAAGTTTGGTGTATGGAACGGATCGTTGAAAGCTGAGCTTAGACCAAATGCAAAGGTTGAAGCGAACA
AAACCCGAGTCTTCACAGCAGCACCTCTGGACACACTTCTTGCAGCGAAGGGTTGTGTTGACGACTTCA
ACAACCAATTCTATAGCAAGCACCTCGAAGGCCCGTGGACGGTGGGAATCACAAAATTCAAAGGCCGA
TGGAACGATTTTCTTCGTCTCTTACCGGATGGGTGGATCTATTGCGATGCGGATGGTTCTCAATTTGATA
GCTCATTAACTCCTTATCTCATAAACGCCATTCTCAATGTTCGATTGCAGTTCATGCAGGAATGGAACAT
TGGAAAGAGATGTTTGGAGAACCTCTACACTGAAATTGTCTACACAGCCATAGCAACTCCAGATGGGTC
AGTCATTAAGAAGTTCAGAGGGAACAATAGCGGACAGCCATCAACAGTCGTTGACAATACATTAATGG
TTGTCTTAGCTATGCA

>gi|189009878|ref|NC_010736.1|_Algerian_watermelon_mosaic_virus_complete_genome

GAAAATGGGAATATGGAATGGTTCTTTAAAGGCTGAAATTAGGCCAGCTGAAAAGGTGCTAGCTAATA
AAACACGCTCATTTACAGCGGCTCCTATAGATACCTTGTTAGGTGCCAAAGTTTGCGTAGACGATTTCA
ATAATTGGTTCTACAGTAAGAACATGGAGTGCCCTTGGACAGTTGGCATGACAAAGTTTTACAAGGGA
TGGGATGAGTTTTTGCGAAAGTTTCCAGATAATTGGGTTTACTGTGATGCTGATGGGTCTCAGTTTGAT
AGTTCTCTATCTCCTTACTTGATCAATGCTGTGTTGCAAATCCGCCTATGGGCCATGGAAGAATGGGATA
TTGGAGAGCAAATGCTTCGCAATTTGTATGGGGAAATCACATACACACCTATTGCCACTCCAGATGGCA
CAATCGTCAAGAAATTCAAAGGCAATAACAGTGGTCAACCGTCAACAGTTGTAGATAATACGCTCATGG
TTCTGTTAACCATGCA

>gi|318054196|ref|NC_014905.1|_Apium_virus_Y_complete_genome

GAAAATGGGCGTCTGGAATGGTTCACTCAAGGCAGAATTGAGACCGATCGAAAAGGTGCAAGAAAAC
AAGACTAGATCATTCACAGCAGCGCCCATTGACACATTACTGGCAGGAAAAGTCTGTGTGGATGATTTT
AACAACCAGTTTTATGCCATGCATTTTAAATGTCCATGGAGTGTTGGGATGACGAAATTCTATGGTGGA
TGGGACAAACTTCTTTCAATCTTACCGGATGGTTGGACATACTATGATGCTGATGGCAGCCAGTTTGAT
AGCTCTCTGTCTCCATATCTGATAAATGCAGTACTTCAAATAAGATTACACTTTATGGAAGCATTTGATA
TTGGAGAACAGATGTTATCCAATCTGTACACAGAAATTGTTTACACCCCGATCCTAACACCAGATGGAA
CAATAGTGAAAAAGTTTAAAGGGAACAATAGTGGCCAACCATCTACTGTAGTTGACAACACACTAATG
GTTGTGTTGGCTATGAC

>gi|396587253|ref|NC_018176.1|_Arracacha_mottle_virus_complete_genome

GAAGATGGGTGTTTGGAATGGATCTCTAAAGGCAGAGCTGAGATCAAAGGAGAAAATCGAAGCGAAC
AAAACGAGAACGTTCACAGCAGCCCCAATTGACACATTATTAGCTGGCAAAGTTTGTGTTGATGATTTC
AATAATCAATTCTACTCAATGAACCTCAATTGTTGTTGGACTGTAGGGATGACAAAATTCTATGGAGGA
TGGAACACTTTGCTAAGCCAATTACCAGAAGGTTGGGTTTATTGTGATGCTGATGGATCCCGATTTGAT
AGTTCATTAACGCCATATCTTATAAATGCAGTACTTGCCATAAGAGAGGCATTTATGGAGGAATGGGAT
ATTGGGTGGCACATGCTAAGGAACTTATACACTGAGATCATTTATACACCAATATCTGCTGCAGATGGT
ACAGTGCTAAAGAAATTTAGAGGGAACAATAGTGGACAGCCCTCAACGGTTGTTGATAATTCTTTGATG
GTAGTGCTAGCAATGCA

>gi|156447513|ref|NC_009745.1|_Banana_bract_mosaic_virus_complete_genome

ATATCTAGGCATATGGAATGGATCTTTGAAAGCTGAATTACGGCCAAATGAAAAGAATGAGTTAAACA
AAACACGCGTGTTCACAGCAGCTCCGTTAGACACATTACTTGGAGGTAAAGTATGTGTGGATGATTTCA
ACAACTTGTTTTATGATAAACACATTGAATGTCCTTGGACTGTCGGTATGACTAAATTTTATACTGGTTG
GGATCAATTGTTGCGGAAGTTACCAGATGGCTGGGTTTATTGTGATGCTGATGGCTCGCAGTTTGATAG
TTCACTGTCTCCATACTTAATTAACTCAATTCTTCGATTGAGACTTGAGTTCGCAGAAGATTGGGACGAA
GGGAAGCAAATGTTGCGCAATTTGTACACTGAGATTGTGTATACACCAATACTAGTTCCAGATGGTACA
GTGGTCAAGAAATTTAAGGGAAATAATAGCGGACAACCATCTACCGTTGTAGATAATACATTAATGGTT
GTTCTTGCTATGCA

>gi|156447515|ref|NC_009741.1|_Basella_rugose_mosaic_virus_complete_genome

TGAAATGGGCGTTTGGAACGGCTCTTTAAAAGCAGAACTTAGAGCCAAAGAGAAGTTGGAACAGAAC
AAGACACGCACTTTCACTGCAGCTCCAATTGATACATTACTTGGCGGGAAGGTATGTGTTGATGACTTT
AATAACAGATTCTATTCACTAAATCTTGAGGCACCGTGGTCGGTTGGCATGACAAAGGTCTATGGTGGA
TGGAATAAGCTGTTAAGTAAACTGCCAGAGGGGTGGATTTATTGTGATGCTGATGGTTCACAGTTTGAT
AGTTCGTTAACCCCATACTTGATCAATTCAGTTGTACAAATCAGAGAGCACTTCATGGAACCATGGGAT
GTTGGTGTTAGGATGTTACGGAATTTTTACACAGAAATCATTTACACACCAATTCTAGCACCAGATGGT
ACAATAGTAAAGAAATTCAAAGGGAACAATAGTGGTCAGCCATCAACTGTTGTAGATAACACTATAAT
GGTTGTTCTGGCAATGCA

>gi|21553928|ref|NC_004047.1|_Bean_common_mosaic_necrosis_virus_complete_genome

CCAAAAAGGAATTTGGAATGGATCACTCAAAGCTGAATTGAGACCGTTAGAAAAAGTACAAGCTAACA
AGACTCGAACGTTCACAGCTGCTCCAATTGACACATTGCTCGGGGCGAAGGTGTGCGTTGATGACTTTA
ACAACCAATTCTATTCCTTCAACTTAATTTGTCCTTGGACAGTAGGAATGACAAAATTTTATGGGGGCTG
GGACAAGTTGATGCGAGCACTTCCTGATGGGTGGGTTTACTGTCATGCGGATGGATCACAATTTGACA
GTTCGCTCACACCTTTGTTGCTCAACTCTGTTCTTAGCATAAGAAGTTTCTTCATGGAGGACTGGTGGGT
TGGAAAAGAAATGCTGGAGAACTTGTATGCTGAAATTGTCTACACACCAATACTCACACCAGATGGGA
CGATTTTCAAGAAGTTCAGGGGCAACAACAGTGGACAACCTTCAACAGTTGTGGACAACACACTGATG
GTTGTCATTTCCATGTA

>gi|18677787|ref|NC_003397.1|_Bean_common_mosaic_virus_complete_genome

TAAGAAAGGGCTTTGGAATGGCTCCCTTAAAGCAGAATTGAGACCATTAGAAAAGGTTGAGGCCAATA
AAACACGCACTTTCACAGCCGCTCCCATGGATACATTACTTGGAGCGAAGGTTTGTGTGGATGATTTCA
ACAACCAATTTTATAGTCTCAACCTGGAGTGTCCATGGACTGTTGGAATGACAAAATTCTATGGCGGAT
GGGACACTCTAATGAGAAAGTTGCCTGATGGATGGATTCACTGTCACGCAGATGGTTCTCAATTTGATA
GTTCACTAACACCACTTCTACTCAATTCAGTACTTGGAATCAGAAGATTCTTCATGGAGGATTGGTGGGT
TGGTGAAGAGATGCTTGAGAATTTGTATGCTGAAATAGTGTACACACCCATATTGGCACCTGATGGAAC
AGTGTTTAAAAAGTTCAGAGGAAATAACAGTGGACAACCCTCCACAGTCGTGGACAACACACTCATGG
TTGTAATGTCAGTTTA

>gi|19881394|ref|NC_003492.1|_Bean_yellow_mosaic_virus_complete_genome

TCGAATGGGTGTTTGGAATGGATCATTGAAAGCAGAGCTGAGACCACAAGAAAAAGTGCTCGCAAATA
AAACTCGATCATTTACAGCAGCACCAATTGACACACTTTTGGCTGGAAAGGTTTGTGTGGATGATTTCA
ACAATAAGTTCTACAGTTTGCACCTGAAGATCCCGTCGACAGTGGGAATAACAAAGTTCTATGGTGGTT
GGGATCGGCTGCTCAATTCTTTACCAGATGGATGGGTGTACTGCGATGCTGATGGTTCCCAATTTGACA
GCTCACTCACTCCATACCTTTTGAATGCTGTCCTTGAGATGCGGTTGAGACTTATGGAAGAATGGGATT
TGGGTGAACAGATGTTGAAAAATCTTTATACAGAAATTGTGTACACACCCATATTGACACCAGATGGAA

CGGTTGTCAAGAAGTTTAAAGGGAATAACAGTGGACAGCCATCCACAGTGGTTGACAACACGCTCATG
GTTATTATGGCAGTTTA

>gi|40254027|ref|NC_005304.1|_Beet_mosaic_virus_complete_genome

CAAGATGGGCGTGTGGAACGGATCTCTCAAAGCTGAACTGCGCCCCAAGGAAAAGCTAGAACAGAAT
AAGACTCGCACATTTACTGCAGCACCTATTGATACTTTGCTTGGCGGGAAAGTTTGTGTTGATGACTTCA
ACAACAGGTTTTACTCGTTGAACCTCAAGGGTCCATGGTCTGTCGGGATGACGAAGTTTTATGGGGGAT
GGAATGAACTACTACAGAAACTTCCAGATGGTTGGATTTATTGTGACGCTGACGGATCACAATTTGATA
GCTCTCTTACACCTTACCTGATCAACGCAGTCGTGCAAATAAGAGAGCATTTCATGGAGGATTGGGAAA
TTGGTAGAACCATGCTTCGGAATTTCTACACTGAGATAGTGTACACACCAATTCTCACACCGGATGGAA
CAATAGTGAAGAAGTTCAAGGGGAACAACAGCGGCCAACCATCAACAGTTGTTGATAACACTCTCATG
GTCATCCTTGCAATGCA

>gi|564614857|ref|NC_023014.1|_Bidens_mosaic_virus_isolate_SP01_complete_genome

ACAAATCGGAGTTTGGAATGGGTCTCTAAAAGCAGAACTGCGGTGCAAAGAGAAAATTCTTGCGAACA
AGACACGCACGTTTACTGCAGCACCATTAGATACACTTCTGGGTGGAAAGGTTTGTGTTGACGATTTCA
ACAACCAGTTTTACTCAAAGAACATTGAGTGTTGTTGGACTGTTGGAATGACCAAGTTTTATGGCGGAT
GGAATAGATTGCTCAGAAGCCTACCTGATGGTTGGATTTATTGTGATGCAGACGGATCACGATTTGACA
GTTCTTTAACTCCATATTTAATAAATGCAGTGTTGTCGATTCGTAGTACATACATGGAAGATTGGGACAT
TGGTTTACAAATGTTAAAGAACTTGTACACAGAGATAATTTACACGCCAATCGCCACACCAGACGGAAC
AATTGTGAAAAAGTTTAGAGGGAACAACAGCGGTCAGCCTTCTACAGTTGTTGACAACTCTCTAATGGT
TGTTCTGGCCATGCA

>gi|301173441|ref|NC_014325.1|_Bidens_mottle_virus_complete_genome

ATCTTTGGGGGTGTGGAATGGTTCTTTAAAAGCTGAGTTACGGTGCAAAGAAAAGATTGATGCCAACA
AGACGAGAACTTTCACGGCAGCACCAATAGACACACTTTTGGCTGGAAAGGTATGCGTGGATGATTTT
AATAACAATTTCTACGCCAAAAACATTGAATGCTGCTGGACAGTCGGAATGACGAAGTTCTATGGAGG
CTGGAACAAATTACTCACAGCACTACCGAACGACTGGCTTTATTGTGATGCAGATGGTTCACGATTTGA
CAGCTCTCTGACACCATATTTGATCAATGCTATCATTACCATCAGAAGTGCATACATGGAAGAATGGGA
CATCGGTGAACAAATGTTAAGGAATTTATACACTGAAATTGTGTATACTCCAATCTCAACACCAGATGG
CACAATCGTGAAGAAGTTCAGAGGGAACAACAGTGGGCAACCATCAACGGTGGTAGACAACTCGCTA
ATGGTCGTCCTAGCTATGCA

>gi|414090072|ref|NC_019415.1|_Blue_squill_virus_A_complete_genome

CGAAAAAGGTATTTGGAATGGATCTCTCAAAGCTGAGTTGAGGCCTATCGAAAAGGTGCAACAAAACA
AGACAAGAACTTTTACAGCGGCACCGATAGATACCTTACTTGGAGCAAAGGTTTGTGTTGATGATTTCA
ACAATCAATTCTATAGCTTTCACTTGGAATGCCCATGGACGGTTGGTATGACGAAATTTTATGGTGGTT
GGGATAAGCTGATGCGCAAATTACCAGATGGGTGGGTATACTGTCATGCGGATGGATCGCAATTTGAT
AGCTCTCTTACGCCCTTACTCATTAACGCAGTTTTGGATATCCGGTGCTTCTTTATGGAAGATTGGTGGG
TTGGGCAAGAGATGTTAGAGAATTTATACGCAGAGATAGTCTATACACCAATTCTGGCACCTGATGGA
ACCATTTTCAAGAAGTTCAGAGGCAATAACAGTGGGCAGCCTTCAACAGTTGTGGACAATACGCTCATG
GTCGTCATAGCAGTTTA

>gi|307563838|ref|NC_014536.1|_Brugmansia_suaveolens_mottle_virus_complete_genome

ACAACTAGGTGTATGGAACGGATCACTGAAGGCAGAATTAAGGCCAATGGAAAAGATTAAAGAGAAC
AAAACAAGGTCTTTTACAGCAGCACCACTCGACACCCTACTTGGTGGGAAGGTTTGTGTTGATGATTTC
AACAATCAATTTTACTCGAAAAACATCGAGTGCTGTTGGTCAGTTGGAATGACAAAGTTCTATGGTGGG

TGGAATAAATTGCTAACTGCTCTACCGGAAGGATGGGTTTATTGTGATGCCGATGGATCTCAGTTTGAT
AGTTCTTTGACCCCTTATCTGATCAATGCAGTTCTTGCTATTAGATGTACATTTATGGAAGATTGGGACA
TAGGACACAAGATGTTGGAGCACCTATACACAGAAATAATCTACACTCCAATATCTACTCCGGATGGAA
CAATCATTAAAAAGTTTAAAGGAAACAACACAGGTCAACCATCCACGGTTGTGGATAATTCACTGATGG
TGGTACTTGCAATGAA

>gi|259120449|ref|NC_013261.1|_Canna_Yellow_Streak_Virus_complete_genome

TAAGATTGGCGTTTGGAATGGTTCATTGAAGGCGGAATTAAGACCGACTGAAAAGTTAATCGCAAATA
AAACGAGAACATTCACTGCAGCTCCTTTAGAAACATTGTTGGGTGGAAAGGTATGTGTCGATGATTTCA
ATAATCAATTCTATTCAAACCACCTTAAGGGACCATGGACAGTTGGCATTTCAAAGTTTTATAGAGGAT
GGGACAAACTCTTACGCGCGTTACCAGACGGTTGGATTTATTGTGATGCAGATGGATCGCAGTTTGATA
GTTCATTAACACCATTTTTGTTGAATGCAGTACTACGAATTAGACTCGCATGTATGGAAGAGTGGGAGA
TTGGAGAGCAAATGTTGAGAAATTTGTATACTGAAATTGTTTATACGCCAATCGCAACACCGGATGGGA
GCATTATAAAGAAACACAAAGGCAACAATAGTGGACAGCCATCAACAGTCGTGGACAATACACTCATG
TTGATACTTGCATTCAC

>gi|330370639|ref|NC_015393.1|_Celery_mosaic_virus_complete_genome

TAAAATGGGCATTTGGAATGGTTCATTGAAAGCAGAACTCAGGCCTATAGAGAAAATTCAAGAGAACA
AGACGAGATCATTTACAGCAGCGCCAATAGACACTTTATTGGCCGGAAAAGTTTGTGTGGATGATTTTA
ACAACCAGTTCTATGCTTCACATTTTAAGTGCCCGTGGAGTGTTGGAATGACAAAATTTTATGGGGGTT
GGAACAAGCTCTTATCGCTCTTGCCTGATGGATGGGTTTACTATGATGCTGATGGTAGTCAATTCGACA
GTTCTTTGTCACCATACCTCATCAATGCCGTTTTGCAAATTCGGTTGCATTTCATGGAGGATTTTGACATT
GGTGAGAAGATGCTATCAAATTTGTACACAGAAATAGTCTACACACCCATTCTCACGCCAGATGGAACG
ATTGTGAAGAAGTTTAAGGGAAACAACAGTGGGCAACCATCAACAGTAGTGGACAATACTTTGATGGT
GGTTTTGGCAATGAC

>gi|349641625|ref|NC_016044.1|_Chilli_ringspot_virus_complete_genome

AAAACTCGGTGTATGGAATGGTTCAATAAAAGCAGAATTGAGGCCGAAGGAAAAGGTTGCACAAAAT
AAAACTAGAACATTCACAGCCGCACCCCTCGACACTCTGCTAGCTGGCAAGGTGTGTGTTGATGACTTC
AATAACACTTTCTATGCTTTGCATCTTAAAGGTCCTTGGAGCGTTGGCATGTCAAAATTCTCAAGAGGCT
GGAATCATTTACTGAGTCAATTGCCAGATGGATGGGTCTATTGTGATGCTGATGGTAGCAGATTTGATA
GTTCGCTAACTCCATACTTGATCAATGCAGTGCTCAGAATAAGATTGCACTTCATGGAAAACTGGGATA
TTGGTATTCAGATGCTTAAAAATTTATATGCTGAGATTATCTACACACCAATACTCACGGCTGATGGCAC
AATCGTTAAGAAGTTCAAAGGAAACAACAGTGGCCAACCCTCCACAGTTGTCGACAACACACTCATGGT
GATAATAACAATGCA

>gi|45004654|ref|NC_005778.1|_Chilli_veinal_mottle_virus_complete_genome

AAACCTTGGAGTGTGGAATGGTTCAATCAAGGCTGAGCTTAGACCTATTGAGAAAGTGCGTGCTAACA
AGACGCGAACTTTTACAGCAGCACCATTGGATACGCTACTAGCTGGCAAAGTTTGCGTTGATGATTTCA
ACAACCAGTTCTACTCAAAGCACACACTTGCACCATGGAGTGTCGGAATTTCAAAATTCTCGGGTGGTT
GGGATAGATTGTTGAGGAAACTACCTGACGGATGGATATACTGTAGCGCAGATGGCAGTAGATTTGAT
AGTTCTTTAACACCATATCTCATAAATGCTGTGGCGTCCATCCGTCTGAAATTCATGGAACCGTGGGGA
ATCGGGGAGCAAATGCTAATGAGGAACTTGTATGCCGAAATCATATATACTCCCATTCTCACTGCTGAT
GGAACGATAGTTAAGAAGTCCAAAGGCAATAACTCGGGACAACCATCGACAGTCGTGGATAACACACT
CATGGTGTTAGTGGCAATGAA

>gi|20087030|ref|NC_003536.1|_Clover_yellow_vein_virus_complete_genome

GAAAATGGGAGTTTGGAATGGCTCGTTAAAGGCTGAACTTAGACCACAAGAAAAGGTTTTGGCAAACA
AGACAAGGTCCTTCACAGCAGCACCAGTGGACACATTACTGGCTGGAAAGGTTTGTGTGGATGATTTC
AATAACAAGTTCTACAGTCTCCATCTTGAGATACCCTCCACAGTTGGTATCACCAAATTTTATGGTGGTT
GGGATTCATTGTTGAATAAGCTACCAGATGGATGGGTGTATTGTGATGCTGATGGCTCGCAGTTTGATA
GTTCTCTAACACCATACCTGATAAATTCTGTTCTGAGACTTCGACTGAACTTCATGGAAGAGTGGGACAT
TGGTGAGGAAATGCTTAAGAACTTGTACACGGAGATCATATATACACCAATCCTAACACCTGATGGTAC
AATAATCAAGAAGTTCAAAGGGAACAACAGTGGACAACCATCGACAGTTGTCGACAACACACTAATGG
TGATAATGGCTATGTA

>gi|20428636|ref|NC_003742.1|_Cocksfoot_streak_virus_complete_genome

GCAATTGGGTTTATGGAACGCCTCTCTGAAAGCAGAAATCCGTCCGATGGAGAAGGTTTCCTTAAACAA
AACGCGTACTTTCACTGCAGCACCACTCGAAACCCTCTTGGCCGGGAAAGTTTGTGTGGATGATTTCAA
TAACTGGTTCTACACAAAACACACAGAATGCCCTTGGACTGTTGGAATCTCAAAATTCTATGGTGGTTG
GAATGAGATGTTGACGCGGTTGCCTGATAACTGGATCTACTGCGATGCCGACGGTACACGATTCGATA
GCTCCCTATCTCCATACTTGATCAATGCAGTGCTGGAAATACGACTATCATGCATGGAGAATTGGGACA
TTGGCGAGAAAATGCTTGAAAATTTGTACACGGAAATTGTCTATACGCCTATCCTAACGCCAGACGGAT
CTGTCGTCAAGAAATTCAAAGGCAATAACAGCGGTCAACCCTCCACAGTGGTAGACAATTCCTTGATGG
TTCTAATAGCTATGAC

>gi|440382952|ref|NC_020072.1|_Colombian_datura_virus_complete_genome

CAAACTTGGGTTGTGGAATGGCTCACTTAAAGCTGAATTGCGGCCAATTGAAAAGGTTGAGCAAAACA
AGACACGAACTTTTACAGCAGCACCAGTTGATACATTACTGGCTGGAAAAGTTTGTGTGGATGATTTTA
ATAACCAATTCTATTCTCTCAACTTGCAGATACCCTCAACTGTCGGAATGACAAAATTTTTCAGAGGGTG
GGATAAATTGATGAGAGGGCTTCCTGATGGATGGACTTATTGTTATGCTGACGGATCAAGGTTTGATA
GTTCTCTATCACCATACCTTTTGAATGCTATTATTCAAGTCAGACTCTACTTCATGGAAGAATGGGATATT
GGTGAAGTGATGTTGAAGAACTTGTACACCGAAATTGTGTACACACCAATATCCACACCAGATGGCACT
GTAATAAAGAAACATAAGGGCAATAATAGTGGACAACCATCTACAGTCGTTGACAACACACTGATGGT
TAACATAGCCATGTT

>gi|21427633|ref|NC_004013.1|_Cowpea_aphid-borne_mosaic_virus_complete_genome

AAAGAAAGGTCTGTGGAATGGATCACTTAAGGCAGAACTGCGACCACTTGAAAAAGTGGAGGCAAAC
AAAACCCGGACTTTTACAGCAGCACCAATAGACACATTGCTAGGTGCAAAGGTTTGCGTTGATGATTTC
AACAATCAATTTTACAATTTCAATCTACAATGCCCTTGGACTGTTGGCATGACAAAGTTCTATGGGTTGG
GGGATAAATTGATGAGATCACTACCAGAAGGCTGGATCTATTGCCATGCAGACGGATCACAATTTGAT
AGTTCTCTCACACCATTACTTCTGAATGCTGTGCTGGATCTTAGAATGTTCTTTATGGAAGATTGGTGGG
TTGGACAAGAGATGCTTGAAAATCTATATGCAGAGATAGTGTTCACACCCATCCTTACACCAGATGGAA
CTGTTGTTAAGAAGTTCAGGGGTAACAATAGTGGGCAACCATCCACAGTGGTTGACAACACACTCATG
GTCGTCATTTCAGTCTA

>gi|96980660|ref|NC_008028.1|_Daphne_mosaic_virus_complete_genome

CCAAATGGGAGTGTGGAATGGAAATCTCAAAGCCGAGTTGCGACCAGTTGAGAAAATTCGTGAAAACA
AGACAAGGACATTCACAGCCGCTCCGATTGAAACATTGCTTGGGGCGAAAGTTTGTGTTGATGACTTTA
ACAATCAGTTTTACGATCATCACACAGAGTGTCCATGGACTGTTGGAATTTCAAAGTTCTATGGTGGAT
GGGACAAACTTATGCGCAAGCTGCCTGAAGGCTGGATTTACTGTGATGCAGATGGCTCACGGTTCGAT
AGCTCTTTGACACCATATCTCATAAACAGCGTCCTGCAAATTCGACTTATGTTTGCCGAGGATTGGGACA
TAGGGCGTGAAATGCTCAAGAATTTGTACACCGAGATTATGTACACGCCGATCGCAACACCAGATGGT

ACCATTTACAAGAAGTTCAGGGGGAATAACAGCGGGCAACCTTCAACGGTTGTAGATAACACACTGAT
GGTGTTCATTTCACTCTT

>gi|20087054|ref|NC_003537.1|_Dasheen_mosaic_virus_complete_genome

GAAGAAGGGAGTCTGGAATGGTTCACTAAAGGCAGAGTTGCGTCCAATTGAGAAAACGCAACTCAATA
AAACAAGAACATTCACCGCCGCTCCTCTTGACACATTGCTTGGGGCAAAAACATGTGTGGATGATTTTA
ATAATCAATTTTACAGTCTCAACCTAAAGTGTCCATGGACAGTTGGTATGACCAAATTCTATAGAGGTTG
GGATACACTAATGAGGAAACTTCCTGAAGGGTGGGTATATTGTCATGCAGATGGATCCCAATTTGACTC
ATCACTAACACCACTCCTCATCAACGCAGTTGTGGATATTAGAAAGTTCTTTATGGAAGAGTGGTGGGT
TGGAGAAGAGATGCTTGATAATTTATATGCTGAGATTGTTTACACTCCTATATTAACCCCAGATGGCAC
AATTTTCAAGAAATTTAGGGGAAATAATAGTGGTCAGCCATCAACAGTTGTGGATAATACATTAATGGT
TGTTATCTCAGTTTA

>gi|85677473|ref|NC_007728.1|_East_Asian_Passiflora_virus_complete_genome

GAAGAAGGGTCTTTGGAATGGGTCTCTTAAAGCTGAATTGAGGCCAAAAGAGAAAGTGCAAGCTAAT
AAGACCAGAACATTCACTGCTGCTCCCATTGACACTCTGTTAGGCGCCAAAGTTTGTGTGGATGACTTC
AACAATCAATTTTACAGTTTAAATTTGGCTTGTCCATGGACTGTTGGGATGACAAAGTTCTACGGTGGA
TGGGATAAGTTGATGCGTAGTTTACCAGATGGGTGGCTATATTGTCACGCAGATGGTTCTCAATTCGAT
AGTTCCCTAACACCACTTTTGCTTAATGCAGTCTTGGACATCAGAAGGTTTTTCATGGAAGAATGGTGG
GTTGGTCAAGAGATGCTCGAGAATTTGTATGCAGAAATTGTGTATACTCCAATCCTAGCACCAGATGGG
ACAATATTCAAAAAGTTCAGGGGCAATAACAGTGGGCAACCATCAACTGTGGTGGACAATACTTTAAT
GGTTGTTCTTGCTATGTA

>gi|298388366|ref|NC_014064.1|_Freesia_mosaic_virus_complete_genome

CAAAACTTGAGCGAGAGCGGATTGTTTCTATATTGGAATGGGATAGAAGTCATGCCATCGAACACAGA
GCAGAGGCAATTTGCGCAGCTATGATTGAAGCATGGGGGTACCCTGATCTTCTTTTGGAAATCAGAAA
ATTCTACGCATGGATTCTTGACCACGACATGTTTCACGATTTGGCAGCAATAGGCAAGTTGCCGTATATT
GCTGAGACAGCACTGAGGAAATTATACACAGATCGTGATTGTGAAGATGAAGAGCTGTTACATTACCT
TAGAGCTTTTAACTTTGAAGGAGAGCTGGTGGGAACGGACGAGGTGCGATACCAAGGGAAGTCAATG
TGCAGAGGGTTACGCAATTACAATCCAGTCGCATCCTGTATTTGCAAATTAGTCAATGATTCTGATGGC
ATAGTCACCACAATATTCGGCCTTGGATACGGACCAGTGATTATCACCAATGGACATCTATTTAATAGA
AACAATGGAACTTTG

>gi|190336494|ref|NC_010954.1|_Fritillary_virus_Y_complete_genome

TGAGAAAGGCATTTGGAATGGATCCCTGAAAGCTGAATTGAGGCCAATTGAGAAGGTGCAAGCCAAC
AAGACGAGAACATTCACAGCAGCACCAATTGACACACTCTTGGGCGCAAAAGTTTGTGTGGACGATTTT
AACAATCAGTTCTACAGTCTGAATTTGAAATGTCCGTGGACGGTTGGCATGACGAAGTTTTATGGTGGC
TGGGACAAGCTAATGAGGAGTCTCCCCGATAACTGGATATATTGTCATGCAGATGGATCACAATTTGAC
AGCTCACTTACACCTTTGTTGCTAAATGCAGTCCTAGGTATAAGGAGGGCATTCATGGAGGAATGGTG
GGTTGGACAAGAAATGCTCGATAATTTGTATGCTGAGATCGTGTACACGCCAATTCTTACACCAGATGG
AACTATTTTCAAGAAGTTCAGAGGAAACAATAGTGGTCAACCATCCACAGTGGTTGATAATACATTGAT
GGTTGTTATTGCTGTGTA

>gi|526118368|ref|NC_021786.1|_Habenaria_mosaic_virus_genomic_RNA_complete_genom
e_isolate:_Ha-1

CCTTAAAGGCGTTTGGAATGGTGCCATTAAAGCGGAGCTGCGAACGCGCGAGAAAGTAGAGGCAGAC
AAGACGAGAACTTTTACAGCAGCGCCCATTGATACGCTACTGGCAGGCAAAATATGTGTTGACGATTTC

AACCTTCAGTTCTACAGTCTGCACACAAAAGCTCCATGGAGCGTTGGCATCTCTAAGTTTTCGCGTGGAT
GGGATGCATTGTTGCGGAAGTTACCAGATGGATGGACATATTGTGACGCTGATGGGAGTCGTTTTGAT
AGTTCCTTAACTCCATACATTATTAACGCGATCCCAATCATTCGGCTTGCTTTCATGGAAAAGTGGGATC
TTGGCGAAACTATGATGCGGAATCTATACACAGAAATCGTGTACACGCCAATTCTCACTGCAGACGGCA
CAATCGTTAAGAAGTTCAAAGGCAACAATAGTGGACAACCATCCACAGTCGTCGATAATACTCTCATGG
TATTGCTAGCTATGCA

>gi|335352402|ref|NC_015394.2|_Hardenbergia_mosaic_virus_complete_genome

TGAGAAAGGAATATGGAATGGGTCTCTCAAGGCTGAGCTGAGACCTAATGAAAAAGTGCAACAAAAT
AAAACAAGAACTTTTACAGCAGCGCCTATAGACACATTGTTAGGTGCAAAGACATGCGTGGATGACTTC
AACAACCTTTTTTATAGTCTCCACCTCAAATGTCCTTGGACTGTGGGAATGACAAAATTTTATGCAGGTT
GGGATAAATTGATGAGGTCTTTGCCAGATGGATGGGTGTATTGCCATGCTGACGGCTCTCAGTTTGATA
GTTCATTAACACCATTACTCATCAATGCAGTGCTTGACATCAGGAAGTTCTTTATGGAAGACTGGTGGG
TTGGGACAGAAATGCTGGAGAATCTGTACGCAGAAATTGTGTATACGCCAATTCTCGCACCTGATGGC
ACAATTTTCAAGAAGTTCAGAGGGAACAACAGTGGACAACCTTCTACGGTTGTGGACAACACTCTGAT
GGTAGTGATAGCTGTTTA

>gi|388570304|ref|NC_017967.1|_Hippeastrum_mosaic_virus_complete_genome

AAAGATGGGAGTGTGGAATGGCTCTTTAAAAGCTGAGTTGCGACCAACAGAGAAAATTTCTTTAAACA
AAACTCGAACTTTCACAGCAGCTCCGCTTGATTCGTTACTTGGAGGAAAAGTTTGTGTTGACGATTTCAA
CAACCAGTTTTATGAGGGGCATATGAAAGGACCATGGACTGTTGGCATGACTAAGTTTTATAAACAATG
GGATGTATTATTCAGAATGCTCCCAGATGGTTGGGTTTATTGTGATGCGGATGGTTCGCGCTTTGATAG
TTCATTAACACCAGTTCTTTTGAATTGCGTGTTGAACATCCGGTCGGAATTTTTGGAGGATTGGGACATT
GGAGAACAAATGCTCAGAAATTTTTACACAGAGATTGTGTACACACCCATTGCAGTACCAGATGGAAG
TATAATAAAGAAATGCAAAGGCAACAATAGTGGACAGCCATCGACTGTTGTGGATAACACTCTAATGG
TTATGTTGGCTATGCA

>gi|48843532|ref|NC_005904.1|_Hordeum_mosaic_virus_complete_genome

CAAGCTAGGAGTTTGGAACGGATCGCTCAAAGCAGAGTTGAGGCCCAACGAAAAGGTGGAAGCGAAT
AAAACAAGAGTATTTACAGCTGCTCCACTTGATACGCTACTAGCAGCTAAAGGGTGCGTGGACGATTTC
AATAACCAATTTTATGACGCACATCTTAAGGGCCCATGGACTGTTGGTATAACCAAATTTAAAGGCAGG
TGGAACGACTTTCTACGATTACTGCCAGATGGATGGGTGTATTGCGATGCTGACGGTTCACAATTCGAT
AGTTCACTCACGCCTTATCTGATAAACGCAGTGTTAAATTTGCGATTACAATTCATGGAGGATTGGGCC
ATTGGGAAGGAGTGTCTCGCTAACTTGTACACTGAAATTGTATACACTCCTATAGCAACACCTGATGGA
TCAGTGGTTAAGAAGTACCGGGGAAACAACAGCGGTCAACCGTCAACAGTGGTTGACAACACATTAAT
GGTGGTGTTGGCGATGCA

>gi|408905828|ref|NC_018833.1|_Iranian_johnsongrass_mosaic_virus_complete_genome

TCAGCTCGGAGTGTGGAATGGATCTCTAAAGGCTGAAATTAGATCTATTGAGAAAACTTTGGAAAATA
AGACGAGGACATTCACAGCGGCACCACTCGAGACACTTCTCGGAGGAAAAGTTTGTGTTGATGATTTC
AACAATCAATTTTACGAACACCATCTCGTAGGTCCCTGGACTGTAGGAATCACTAAGTTTTATGGAGGT
TGGAATCGTTTGCTTGAAGCGTTACCAGATAACTGGATATATTGTGATGCAGATGGTTCACAATTCGAT
AGTTCATTGACCCCATACCTCATAAATGCTGTTTTACAAATCCGGTTGAATTTTATGGAGGCATGGCCGA
TTGGTGAACAAATGCTGAAAAACCTTTACACAGAAATTGTCTTCACACCAATAGCAACACCTGATGGAT
CAATCATCAAGAAGTTTAAAGGGAACAACAGTGGACAGCCATCAACAGTTGTGGACAACACTATTATG
GTCATATTAGCATTTAA

>gi|9633628|ref|NC_000947.1|_Japanese_yam_mosaic_virus_complete_genome

AAAAATGGGTTTATGGAATGGCTCTCTGAAAGCAGAACTACGCCCTTTAGAAAAGGTTCAAGCCAACA
AAACCCGCACTTTCACAGCGGCACCACTTGATACATTGCTGGGTGGAAAAGCATGCGTCGATGATTTCA
ACAACCAATTTTATGAGCTAAACATAAAAGGGCCATGGAGTGTTGGCATGACAAAGTTTTACGGAGGA
TGGAATGAACTTTTAACGAAGCTACCAGATGGGTGGATTCACTGTGATGCCGATGGTTCCCAGTTTGAT
AGTTCTTTATCGCCCTATCTCATAAACGCAGTCTTAAACATAAGATTACATTTCATGGAAACATGGGACA
TAGGGGAGCAAATGCTGCGGAATTTATACACAGAAATTGTGTACACCCCAATTGCAACACCAGATGGA
ACAATTGTAAAGAAATTTAAAGGGAATAACAGTGGGCAACCGTCAACTGTCGTGGACAACACACTTAT
GGTGTTATTAGCTCTCAA

>gi|20153407|ref|NC_003606.1|_Johnsongrass_mosaic_virus_complete_genome

CAAACTCGGTGTTTGGAATGGTTCGCTTAAAGCAGAGATTCGTCCAATGGAGAAAATACTTGCAAACA
AGACACGAACATTCACAGCAGCACCCCTCGAGACACTGCTAGGTGGGAAAGTTTGCGTTGATGACTTC
AACAATCAGTTCTACCAGAATCATCTCAAAGGACCCTGGACAGTAGGAATCTCAAAATTCTACAAGGGT
TGGGATTCCTTAATGAGGAGATTACCGGAGAACTGGGTGTATTGCGATGCAGATGGATCTCAGTTCGA
TAGTTCACTGACACCATATCTAATAAATGCAGTTCTGCAAATCCGATTGGCTTGCATGGAAAAGTGGGA
CATTGGTGAAAAGATGCTGTCAAATCTGTACACAGAAATAGTCTATACACCAATAGCAACACCAGATGG
AAAGGTCGTCAAGAAATTCAAAGGAAACAATAGTGGACAGCCATCAACAGTCGTGGACAACACACTCA
TGCTCATCCTGGCATTTAC

>gi|358356468|ref|NC_016159.1|_Keunjorong_mosaic_virus_isolate_Cheongwon_complete_
genome

GAACATGGGCGTTTGGAATGGGTCCTTAAAGGCTGAGTTGCGGCCAATTGAAAAACTGAAAGAGAAT
AAAACCAGGACTTTCACAGCAGCACCAATTGACACATTGCTTGGTGCAAAAGTGTGTGTTGATGATTTT
AATAACAGGTTTTATGAGCTAAATCTGAGAGGCCCCTGGACTGTTGGAATGACTAAGTTCTATGGAGGT
TGGAACAAATTACTGCAATCCTTACCAGTGGGTTGGGTGTATTGTCACGCTGATGGTTCTCGCTTTGAC
AGCTCATTAACACCTTATCTTATCAATGCAATAATACACATTCGACAGTTTTTCATGGAAGATTGGTGGA
TCGGACACCACATGCTCGAAAATCTGTATACGGAGGTTGTGTACACACCCATCTTAACACCGGACGGAA
CGGTCGTCAAGAAATTCAAAGGAAACAACAGCGGGCAACCCTCAACTGTTGTTGACAACACCTTGATG
GTCATTCTGGCTGTGTA

>gi|90093251|ref|NC_007913.1|_Konjac_mosaic_virus_complete_genome

AGATATGGGCATTTGGAATGGATCTTTAAAAGCAGAACTGAGGCCAATCGAGAAGGTTGAGCAGAAT
AAAACACGAACATTTACAGCAGCTCCTCTGGATACACTTTTAGCTGGCAAAGTTTGTGTTGATGACTTCA
ACAACTATTTTTACTCAAAGCACACAGTTTGTCCTTGGAGTGTGGGGATGACAAAATTTTATGGGGGCT
GGAATGTCTTGCTAGAATCCTTACCAGAGAATTGGATTTATTGTGACGCGGATGGCAGTCAATTCGACA
GCTCTCTATCGCCATACCTAATTAATTCGATACTCAATGTAAGGTTAAAAATGATGGAACCATGGGATAT
TGGTGAGCAAATGCTACGCAATCTGTATACAGAGATAACGTACACGCCAATTGCAACCCCAGATGGGA
CCATCGTCAAGAAATTCAAAGGAAACAACAGTGGACAACCTTCAACTGTGGTTGACAATACACTGATG
GTGTTGACGGCAATGTA

>gi|21427635|ref|NC_004011.1|_Leek_yellow_stripe_virus_complete_genome

AAAGATGGGTGTGTGGAATGGTTCCCTAAAAGCTGAATTACGACCAATTGAGAAGGTCATGGCTAACA
AAACACGTTCATTCACTGCAGCACCTTTGGATACACTCCTTGGCGGAAAAGTTTGTGTGGATGACTTCA
ACAATCAATTCTACAGTCGACACTTCGACTTGCCTTGGACAGTTGGTATGAGTAAATTTCGTAAAGGGT
GGGACACTCTACTAAGGAAGCTTCCTGAAAATTGGGTGTATTGTGATGCGGATGGCTCTCAGTTCGATA
GCTCATTGTCACCTTATTTGATAAACGCTGTCCTTAGACTTCGACTACACTTCATGGAAGATTGGGATGT
TGGGGAGACTATGCTGAAAAACTTATACACAGAGATTGTGTACACACCAATAGCAACACCAGATGGTA

CGATAGTCAAGAAGTTCAAGGGGAACAATAGTGGACAACCATCTACTGTAGTTGATAATTCACTGATG
GTTGTCTTCTCAATGTA

>gi|20153339|ref|NC_003605.1|_Lettuce_mosaic_virus_complete_genome

TAAGTTTGGAGTGTGGAATGGGTCACTCAAGTCGGAACTGAGACCTATGGAGAAAGTTATGGCAAATA
AGACACGTGTCTTTACAGCAGCGCCGCTCGACACTCTGCTTGCTGGAAAAGTCTGTGTTGATGACTTCA
ACAATTACTTCTACAGCAAAAACATCGAGGCACCTTGGACAGTTGGCATGACGAAGTTTTATGGTGGGT
GGAACGAACTCCTTACGAAGTTACCAGACGGCTGGGTTTATTGCGATGCAGATGGATCACAATTCGAT
AGTTCTTTGTCACCATTTCTCATCAACTCAGTTCTCAGAATACGTTTAAAGTTCATGGAAGATTGGGATC
TTGGTGAACAAATGCTCAAAAATTTGTACACAGAAATTGTATATACAGCGATCCTCACTCCAGATTCAAC
CATAGTGAAGAAATTCAAGGGGAATAACAGCGGACAGCCATCCACGGTAGTAGATAACACATTGATGG
TCGTGCTAGCAATGAC

>gi|39163614|ref|NC_005288.1|_Lily_mottle_virus_complete_genome

CAAGATGGGAGTGTGGAACGGCTCTTTGAAAGCGGAGTTGCGAGCAAAGGAGAAGGTGGACCTAAAC
AAAACGCGAACCTTTACAGCGGCGCCCGTGGATACACTACTTGGTGGGAAAACGTGCGTGGACGACTT
TAACAACAGGTTTTATTCTTTGAACATTGCGTGTCCCTGGAGCGTTGGCATGACAAAGTTTTACAAAGG
TTGGGATGAAATGCTGCGCAAATTACCTGAAGGATGGGTTTACTGCGATGCTGATGGATCACAATTCG
ACAGCTCGTTGTCACCCTACCTCATAAACGCAGTTTTGAATCTACGACTACACTTTATGGAGGAGTGGG
ACGTGGGAGCGCAAATGCTACAGAACCTGTATACTGAAATAATATACACACCAATAGCCACACCTGATG
GCACAATTATAAAGAAATTTAAAGGTAATAATAGTGGGCAGCCATCAACAGTTGTCGACAATACCATTA
TGGTCATATTGGCCATACA

>gi|319774833|ref|NC_014898.1|_Lupine_mosaic_virus_complete_genome

CAAACTTGGTATATGGAACGGTGCTTTGAAGGCGGAATTACGACCAATTGAAAAGGTCTTAGCAAATA
AAACACGAACATTTACTGCAGCACCAATTGATACACTATTGAGTGGTAAAGTCTGTGTAGATGATTTCA
ACAATCAATTCTATGATTTACACACAAAAGGACCATGGAGCGTTGGAATAACAAAATTTTACGGAGGTT
GGAACGAACTTTTATCACAACTGCCAAATGGATGGGTTTATTGTGACGCAGATGGGTCACAGTTTGATA
GTTCGCTAACACCATATTTAATCAATGCAGTGCTGGATATACGCCTGAGTTTAATGGAGGAATTCCCTTT
GGGGCATCATATGTTGCGTAACCTATATACTGAGATCATATATACGCCCATATTAGCAGCAGACGGGAC
AGTTGTGAAAAAGTTCCGTGGGAACAACAGTGGGCAACCATCTACAGTTGTTGATAACTCTCTAATGGT
AATTCTGGCAATGCA

>gi|18490052|ref|NC_003377.1|_Maize_dwarf_mosaic_virus_complete_genome

CAAGCTTGGAATTTGGAATGGGTCTCTCAAGGCTGAAATAAGACCTATAGAGAAAACGGAAGCAAATA
AGACAAGGACATTCACAGCCGCACCATTGGAAACATTGCTAGCGGGTAAGGTGTGTGTCGATGATTTC
AATAATCAATTTTATGCACACCACTTAAATGGACCGTGGACAGTTGGAATAACTAAATTCTACGGTGGT
TGGAATAGATTACTTGAGAAGCTACCAGATGGCTGGATCTACTGTGATGCAGATGGTTCGCAACTCGA
CAGTTCGCTCACTCCTTATCTGATAAATGCAGTGCTCAACATTCGATTACAATTTATGGAGCCGTGGAAC
ATTGGTGAACAAATGCTTAAAAATTTATACACGGAAATTGTTTTTACACCAATTGCAACACCTGATGGGT
CAGTCATCAAAAAGTTTAAAGGCAACAATAGTGGACAGCCATCAACAGTTGTTGGCAACACACTAATG
GTGATCATAGCCTTTAA

>gi|160700540|ref|NC_009995.1|_Moroccan_watermelon_mosaic_virus_complete_genome

GAAGTTAGGTATTTGGAACGGGTCTTTGAAAGCCGAAATTCGCCCTGCTGAGAAAGTACTAGCGAACA
AAACCCGAACCTTTACGGCAGCTCCACTCGACACATTGTTAGGAGCCAAAGTTTGTGTTGATGATTTCA
ATAACTGGTTTTACAGCAAGAACATTGAGTGTCCCTGGACAGTTGGAATGACAAAATTTTACAAGGGAT

GGGATGAGTTTCTACGAAAGTTCCCTGATGGATGGGTTTATTGTGATGCTGATGGATCGCAATTCGATA
GCTCGCTTTCCCCGTACTTAATCAATGCTGTTCTCCAAATTCGATTGTGGGCCATGGAGGAGTGGGACA
TTGGGACCGAGATGCTTAAGAATCTTTACACAGAGATCACATACACCCCAATTGCAACACCCGACGGTA
CCATCATCAAGAAATTTAAGGGAAATAACAGCGGACAGCCATCGACAGTTGTTGATAATACTCTTATGG
TGTTATTGGCTATGCA

>gi|124249189|ref|NC_008824.1|_Narcissus_degeneration_virus_complete_genome

GAAGATGGGAGTTTGGAATGGTTCTCTGAAAGCAGAGATCAGACCTGTGGAGAAAGTTATACAAAAC
AAGACGCGATCCTTCACAGCGGCGCCCATAGAAACATTACTTGGTGGGAAAGTGTGTGTTGACGACTT
CAATAACGCTTTTTATAAAGCTCATCTTAAAATACCATCAACCGTTGGCATCACTAAGTTCTATAAAGGA
TGGGATACATTACTTCGGAAATTGCCAGAGGGCTGGATTTACTGTGATGCAGATGGGAGCCAATTCGA
CAGCTCGTTAACTCCGTATTTATTAAATGCGGTGATAACAATTCGAGAGGAGTTCATGGAAGAGTGGG
ATGTTGGGAAACAGATGCTTAGAAATTTGTACACAGAAATAGTGTACACCCCCATTGCAGCTCCTGATG
GTTCATTGATAAAGAAGTTTAAAGGCAACAACGGTGGTCAGCCTTCGACGGTAGTTGATAATACGCTTA
TGGTGATGTTGGCGATGCA

>gi|589875219|ref|NC_023628.1|_Narcissus_late_season_yellows_virus_isolate_Marijiniup8
_complete_genome

AGAAATGGGTGTCTGGAATGGCTCACTGAAGTCTGAACTGCGGCCAATTGAGAAAGTTGAAGCAAACA
AAACACGCACATTTACAGCTGCACCAATTGACACATTACTAGCTGGAAAAGTTTGCGTGGATGATTTCA
ATAATCAATTCTATGACTACCACCTACAAGGTCCGTGGAGCGTGGGGATGACAAAATTTTATGGCGGTT
GGGATGAACTCCTATCGAAGTTGCCAGACGGATGGGTGTATTGTGATGCAGATGGTTCTCAATTTGATA
GTTCATTATCACCGTATCTAATAAACGCAGTTCTGCACATACGACAAGAGTTTATGGAAGTGTGGGATA
TTGGAGAGCGAATGCTAAGCAACTTGTATACGGAGATTGTCTACACCCCGATTTCCACTCCAGATGGCA
CACTAGTGAAGAAGTTTAAGGGTAACAACAGTGGTCAACCTTCAACTGTCGTCGATAACACACTAATGG
TCATTTTGGCGATGCG

>gi|212499141|ref|NC_011541.1|_Narcissus_yellow_stripe_virus_complete_genome

AGAAATGGGAGTGTGGAACGGATCTCTGAAAGCTGAGTTGAGGCCACTGGAAAAAGTTGAGGCGAAT
AAGACACGAACTTTTACAGCGGCGCCAATAGACACACTACTAGCAGGAAAAGTTTGTGTTGATGACTTC
AACAATCAGTTTTATGATCACCATTTAAATGGACCGTGGAGTGTTGGAATGACGAAATTCTATGGAGGT
TGGGATACACTTCTTAATAAATTGCCGGATGGTTGGGTACACTGTGACGCAGATGGTTCACAGTTTGAC
AGCTCTTTGTCTCCATATTTGATCAACGCCGTATTGCGAATCAGGCAGAAATTCATGGAACCATGGCAG
GTTGGGGAACAGATGCTTTTGAATCTGTACACGGAAATTGTGTACACACCAATTTCAACACCAGATGGT
ACTCTGGTCAAGAAGTTCAAAGGGAACAACAGTGGACAACCTTCAACTGTTGTTGATAACACACTCATG
GTTGTCTTGGCAATGAG

>gi|32490546|ref|NC_005029.1|_Onion_yellow_dwarf_virus_complete_genome

AAAGATGGGCGTTTGGAACGGATCACTGAAGGCTGAAATACGTTCTATTGAGAAGATTGCATTAAATA
AAACTCGATCATTTACAGCAGCTCCCATTGAAACTTTACTTGGCGGTAAGGTGTGTGTTGACGATTTCAA
TAATAAATTTTATAGTTGTAATCTATCAATACCATCAACTGTTGGTATCACGAAGTTTTATAGAGGTTGG
AACAACATGTTAACAGCCTTGCCCGATAATTGGATTTATTGTGATGCTGATGGTTCTCGGTTTGATAGTT
CGCTAACACCCTATTTGCTTAATGCTGTTCTGTCTGTTCGACTCGAGTTTATGGAACCATGGGATATAGG
TGAGAAGATGATGAGTAATCTGTATACTGAAATAATCTACACAGCAATTGCAACACCTGACGGGTCTGT
GATTAAGAAATTTAAAGGTAACAATAGTGGGCAGCCATCTACCGTTGTTGATAACACAGTTATGGTGAT
GTTAAGTGTACA

>gi|414089216|ref|NC_019409.1|_Ornithogalum_mosaic_virus_complete_genome

GAAGTTTGGGTTGTGGAACGGATCGCTTAAGGCTGAGTTGCGACCAATTGAAAAAGTTCGAGCTGGCA
AGACAAGAACTTTCACAGCAGCACCCTTGGACACGTTGTTAGGTGCAAAAGTTTGTGTTGATGACTTCA
ATGCACAATTTTATGCAAAGCACTTACAAGCGCCTTGGACTGTTGGAATATGCAAGTATTACAGAGGAT
GGGATGAGTTTATGGCCAAGCTTCCGACTGGTTGGTTGTATTGTGACGCAGATGGTTCGCAATTTGATA
GCTCACTAACACCTTTTCTTATCAACAGTGTTTTGAGGTTACGCCTAGAATTCATGGAGGAGTGGGATAT
TGGTGAACAAATGTTGTCGAATCTTTACACTGAGATTATATATACTCCGATTGCCACACCTGACGGAAC
AGTTGTTAAGAAGTTTCGTGGCAATAATAGTGGGCAACCGTCGACAGTTGTTGACAACACACTGATGG
TGGTTTTGGCAATGAA

>gi|298531304|ref|NC_014252.1|_Panax_virus_Y_complete_genome

TAAGCTTGGTATTTGGAATGGCTCACTAAAAGCTGAGTTAAGGCCAATTGAAAAAGTGCAAGAGAATA
AGACACGATCGTTCACAGCAGCCCCTCTTGATACATTGTTGGCTGGAAAGGTGTGTGTAGACGATTTCA
ATAATCAATTTTACTCAATGCATTTCAAGTGCCCATGGAGTGTTGGAATGACAAAATTCTACACTGGATG
GAACACACTCCTTAGGAAGCTTCCAAATGATTGGGTATATTGTGATGCAGATGGTAGTCAATTCGACAG
TTCATTATCACCTTATTTGATAAATGCAATTTTACAATTACGCTTGCATTTTATGGAACCATTTGATATTG
GTGAAGTGATGTTGTCGAATTTGTACACTGAGATTATATATACACCCATACTCACACCCGATGGAACAA
TAGTCAAGAAGTTTAAAGGCAATAACAGCGGGCAACCCTCAACAGTCGTCGATAACACACTGATGGTT
GTCATCGCTATGAC

>gi|32490548|ref|NC_005028.1|_Papaya_leaf-
distortion_mosaic_potyvirus_complete_genome

TGATTTGGGAATTTGGAATGGAAGTCTTAAAGCTGAATTAAGACCAATTGAAAAGGTTGAAGCAAACA
AAACGCGAACATTCACAGCAGCTCCAATTGAAACTTTACTTGGCGGAAAGGTTTGCGTCGATGATTTCA
ACAACCAATTTTATGATCTTAATATGAAATGCCCATGGACAGTCGGGATGACTAAGTTTTATTGCGGAT
GGAATGATCTTCTAGGTAAACTTCCTGATGGTTGGATATACCGCGATGCTGACGGATCACGATTTGACA
GTTCTCTTACACCATACTTGCTGAATGCAGTGCTCGGGATTAGGGAGTTTTTCATGGAAGATTGGGACA
TAGGCGTGCAGATGCTTCGAAATTTGCACACTGAAATAATTTACACCCCCATTGCAACACCTGATGGAA
CAGTCGTCAAAAAGTTTCGAGGAAATAATAGTGGTCAACCGTCAACAGTCGTAGATAACACATTGATG
GTCTGTATTTGTGTGCA

>gi|9629244|ref|NC_001785.1|_Papaya_ringspot_virus_complete_genome

GAGAATGGGCGTCTGGAACGGTTCGCTGAAGGCAGAACTGAGACCAGCTGAGAAAGTGCTCGCGAAA
AAGACAAGGTCATTTACAGCAGCCCCTCTTGACACACTATTAGGAGCCAAAGTCTGCGTTGATGATTTC
AACAACTGGTTTTACAGTAAGAATATGGAGTGCCCATGGACCGTCGGGATGACAAAATTTTACAAAGG
CTGGGATGAGTTCCTGAAGAAATTTCCTGACGGCTGGGTGTACTGTGATGCAGATGGTTCCCAGTTCG
ATAGCTCATTAACACCATACTTGTTGAATGCTGTGCTATCAATTCGGTTATGGGCGATGGAGGATTGGG
ATATTGGAGAGCAAATGCTTAAGAACTTGTACGGGGAAATCACTTACACGCCAATACTGACGCCAGAT
GGAACAATTGTCAAGAAATTCAAGGGCAATAATAGTGGCCAACCTTCGACAGTTGTTGATAATACATTG
ATGGTTTTAATCACAATGTA

>gi|448261108|ref|NC_014790.2|_Passion_fruit_woodiness_virus_complete_genome

TGAAAAGGGTGTCTGGAATGGTTCTTTGAAAGCAGAACTTAGGCCCAAAGAGAAGGTTGAGATGAAC
AAGACCCGCACTTTCACAGCAGCGCCAATTGATACATTACTCGGTGCTAAGGTATGTGTGGATGATTTT
AACAACCAATTCTACAGTCTGAATTTAACCTGTCCATGGACAGTTGGCATGACAAAGTTTTATGGTGGA
TGGGATAAGTTGATGAAAAGTCTGCCAGACCATTGGATATATTGCCATGCTGATGGGTCGCAATTTGAC
AGTTCTTTGACACCACTTCTACTTAACTCAGTGCTCGATATTCGCAAGTTTTTCATGCAGGAATGGTGGG
TTGGTGAAGAGATGTTGGAGAATCTTTATGCTGAAATTGTGTATACTCCAATCTTGACACCCGATGGCA

CAATTTTCAAGAAGTTTCGGGGAAACAACAGTGGACAGCCCTCAACAGTTGTTGATAACACACTCATGG
TTGTGGTATCAGTTTA

>gi|9628429|ref|NC_001671.1|_Pea_seed-borne_mosaic_virus_complete_genome

CAAGAAAGGGGTGTGGAATGGTTCTTTGAAAGCAGAGCTGAGACCTATAGAAAAAGTGCATGAGAAT
AAAACAAGAACTTTCACAGCAGCTCCGCTTGACACACTACTTGGTGGTAAGGTCTGCGTGGATGACTTC
AATAATTTCTTTTATTCATGTCATCTTAGGGGGCCATGGACCGTAGGAATCACGAAGTTTTACGCTGGG
TGGAACGAATTCCTAAGCAAGCTACCTGACGGTTGGCTGTATTGTGACGCGGATGGCTCGAGATTTGA
TAGCTCTCTGACACCGTACCTTATCAATGCTGTGCTAGAGTTAAGATTAAGGTTTATGGAAGAGTGGGA
TGCTGGCGAGCAAATGTTGAAGAATCTTTACACAGAAATCATTTACACTCCAATAGCAACACCAGATGG
CTCAGTCATAAAGAAGACGAAAGGAAATAATAGTGGACAACCATCAACAGTTGTTGATAACACATTGA
TGGTGATTCTTGCTATGCA

>gi|11072108|ref|NC_002600.1|_Peanut_mottle_virus_complete_genome

AGAGATGGGAGTGTGGAATGGATCCCTCAAGGCTGAATTGAGACCAAAAGAGAAAGTTGCACTTAAC
AAGACAAGGACATTCACAGCCGCTCCTATTGATACACTGCTGGGAGGGAAGTGCTGTGTGGATGATTT
CAATAATAGGTTTTATAGTTTAAATATAGAAGGCCCTTGGACTGTGGGTATGACTAAGTTTTATGGTGG
ATGGGATAAGTTAATGCGCAAACTACCTGACGGATGGCGCTACTGTCACGCTGATGGTTCACAGTTTGA
TAGTTCCTTAACACCATTTCTGTTAAATGCAGTTTTAGCGGTGCGACTAATGTTTATGGAAGACTGGTGG
GTAGGTGAGCAAATGCTGCGCAATTTTTACACTGAAATCATCTACACCCCGATTCTCACACCAGATGGC
ACTATAGTCAAAAAGTTCAAGGGAAATAATAGCGGTCAGCCATCCACTGTGGTTGATAACACGCTAAT
GGTTATGATAGCTATGTT

>gi|68299603|ref|NC_007147.1|_Pennisetum_mosaic_virus_complete_genome

AGAACTCGGAGTATGGAATGGATCACTCAAAGCAGAAGTGCGACCAATTGAGAAAACAATGGCCAAC
AAGACACGTACCTTCACAGCGGCACCACTTGAAACACTACTTGGTGGAAAAGTTTGTGTCGATGATTTC
AACAATCAGTTTTACGCACATCATTTAATTGGCCCATGGACAGTCGGAATAACGAAATTCTATGGTGGT
TGGAACCAATTATTAGGGAAGCTGCCAGACGGCTGGATATACTGTGGCGCAGATGGTTCGCAATTTGA
TAGCTCACTTACACCGTACCTGATAAATGCCGTTTTAGACATTAGATTGAGTTTCATGGAAGAATGGGA
CATCGGTGAAAGAATGCTCGAAAATTTGTACACGGAAATTGTTTTTACACCAATAGCGACACCAGATGG
ATCCGTCATCAAGAAGTTTAAAGGAAACAATAGTGGGCAACCATCAACAGTTGTAGATAACACGCTCAT
GGTAATATTAGCATTTAA

>gi|9627034|ref|NC_001517.1|_Pepper_mottle_virus_complete_genome

TAAACTGGGTGTGTGGGAATGGGCTCTAAAAGCTGAACTGAGAAGTAAGGAAAAGATAGAAGCCAAT
AAGACACGGACTTTCACAGCAGCCCCAATTGATACACTATTAGGTGGTAAGGTGTGTGTAGATGATCTC
AACAACCAGTTTTATTCGAAAAATATTGAATGTTGTTGGACGGTTGGAATGACCAAATTCTATGGTGGA
TGGGATAAGCTTTTGACAGCTCTGCCTGCTGGATGGATATATTGCGATGCAGATGGTTCGCAATTCGAT
AGTTCATTGACACCTTATCTCATAAATGCTGTATTGACTATACGGTATGCTTTTATGGAAGATTGGGACA
TTGGGTATAAGATGTTGCAAAACTTGTACACAGAAATAATCTACACACCAATATCCACGCCTGATGGAA
CAATTGTGAAGAAGTTCAGAGGCAATAACAGTGGGCAACCTTCCACCGTTGTAGACAACTCACTTATGG
TTGTGCTTGCTATGCA

>gi|115357968|ref|NC_008393.1|_Pepper_severe_mosaic_virus_complete_genome

TCAGCTCGGTGTTTGGAATGGTTCTTTAAAAGCTGAATTACGTTGTAAGGAGAAAATTCTAGCAAACAA
AACTAGAACGTTCACAGCTGCACCACTCGATACTTTGTTAGGGGGAAAAGTGTGTGTTGACGATTTTAA
TAATCAGTTCTATTCCAAAAACATTGAATGTTGTTGGACAGTGGGGATGACAAAATTCTATGGAGGGTG

GGACAAGCTGCTTCGGAAGTTGCCTGATGGTTGGACTTATTGTGATGCAGATGGCTCGCAGTTTGATA
GTTCTTTAACTCCATACCTCATCAATGCAGTACTTACCATTCGAACATTCTATATGGAAGATTGGGACAT
AGGATTACAGATGCTCAAAAATCTTTACACAGAGATTGTGTACACACCAATTTCAACCCCTGATGGCAC
AATTGTAAAGAAATTCAGAGGGAACAATAGTGGGCAACCATCAACTGTTGTCGATAACTCATTAATGGT
AGTTCTAGCCATGCA

>gi|221048141|ref|NC_011918.1|_Pepper_veinal_mottle_virus_complete_genome

TAAACTTGGGATTTGGAACGGTTCAATCAAGGCCGAACTTCGCCCAATGGAGAAAGTTCAAGCAAACA
AGACGAGAACATTCACAGCTGCTCCAATTGATACGCTTTTGGCTGGAAAGGTGTGTGTTGATGACTTCA
ACAATCAATTTTACTCAAAGCACACAATAGCACCCTGGAGTGTGGGTATTTCCAAGTTCTCTGGTGGCT
GGGATAAGCTTCTCAGAAAATTACCTGATGGTTGGATCTATTGCAGTGCCGATGGGAGCCGTTTTGATA
GCTCGTTGACTCCTTATTTGATTAACGCTGTTGCACAGATCAGGTTAGCATTCATGGAGAAGTGGGACA
TAGGTGAACAAATGATCAAGAACCTCTATGCCGAAATCATTTACACACCTATACTTACAGCTGATGGCA
CAATTGTGAAGAAGTTCAAAGGTAATAACTCTGGGCAGCCGTCAACTGTTGTTGATAACACTCTCATGG
TCTTAATTGCTATGAG

>gi|301173451|ref|NC_014327.1|_Pepper_yellow_mosaic_virus_RNA_complete_genome_str
ain:_DF

TGATTTGGGGGTTTGGAACGGTTCACTAAAGGCTGAGCTCAGATCGAAGGAGAAAATTGCAGCCAACA
AAACGCGAACTTTCACAGCTGCACCAATTGATACACTGCTTGGTGGCAAAGTTTGCGTTGATGATTTCA
ACAACCAATTTTATTCAAAGAACATTGATTGTTGTTGGACAGTCGGCATGACAAAGTTCTATGGAGGAT
GGAATAGATTGCTCACAGCGCTGCCAGACGGATGGGTTTACTGTGACGCAGATGGATCGCAGTTCGAC
AGCTCTCTAACTCCTTATTTAATCAATGCTGTTCTCTCAATTCGATTAGCATTCATGGAGGACTGGGATAT
TGGGTTCCAAATGCTGCAAAATTTGTACACAGAGATAATTTACACTCCAATCTCGACCCCAGATGGTAC
AATTGTGAAGAAATATCGAGGAAACAATAGTGGACAACCTTCCACTGTTGTGGATAATTCACTAATGGT
TGTGCTAGCAATGCA

>gi|28492878|ref|NC_004573.1|_Peru_tomato_mosaic_virus_complete_genome

AGAACTTGGAGTATGGAATGGGTCACTAAAAGCAGAGCTTCGATGCAAGGAGAAGATTGAAGCAAAC
AAAACACGAACCTTTACAGCAGCTCCAATCGACACATTACTGGCTGGTAAAGTTTGTGTTGACGACTTC
AATAACCAATTCTACAGTAGAAATATTGATTGTTGTTGGACCGTTGGGATGACTAAGTTTTATGGTGGT
TGGGATAAATTGTTGAGAGCATTGCCAGATGGATGGACATACTGTGATGCTGATGGATCTCAATTTGAT
AGTTCTTTAACTCCATACCTGATTAATGCTGTTTTGGCAATTCGATATGCTTTCATGGAGGAATGGGACA
TCGGTTTCAAGATGTTGCAAAATCTTTACACAGAGATTATCTACACTCCCATTTCCACACCAGATGGAAC
CATAGTCAAGAAGTTTAGAGTTAACAATAGTGGTCAACCTTCGACGGTTGTGGACAACTCACTCATGGT
TGTTCTAGCTATGCA

>gi|9626508|ref|NC_001445.1|_Plum_pox_virus_complete_genome

AAAGAAAGGAGTGTGGAATGGCTCTTTGAAGGCAGAATTGCGCCCTAAAGAGAAGGTAGAGGCTAAT
AAAACTCGATCATTCACAGCAGCACCGATTGATACCCTTCTGGGGGGAAAAGTGTGCGTTGATGACTTC
AATAATCAGTTTTACAGCCTGAATTTACATTGTCCATGGAGCGTTGGGATGACAAAATTCAGAGGTGGT
TGGGACAAACTGCTTAAAGCACTGCCAGAAGGATGGATTTACTGTGATGCCGATGGCTCTCAATTTGAC
AGTTCCCTCTCACCGTACTTAATCAATGCAGTTCTCAATATTCGTCTGGCATTTATGGAAGAATGGGACA
TTGGTGAACAAATGCTTTCAAACCTGTATACGGAGATTGTATATACACCAATTGCTACACCAGATGGCA
CTATTGTTAAGAAGTTCAAGGGAAACAATAGTGGTCAACCCTCGACAGTTGTTGACAATACACTCATGG
TTATTTTGGCAATGAC

>gi|554967333|ref|NC_018872.2|_Pokeweed_mosaic_virus_isolate_PkMV-PA_complete_genome

CAAGTTGGGCATATGGAATGGTTCCCTGAAAGCGGAACTGAGACCAGAAGAGAAAGTGTCGCAGAAC
AAAACTCGTACGTTTACAGCGGCACCATTAGACACATTACTTGGTGGCAAAGTTTGTGTTGATGACTTC
AACAATCAGTTCTACTCACTAAACCTTAAATGTCCGTGGAGTGTTGGAATGACCAAGTTCTACGGTGGT
TGGAATTCACTGATGACTCAACTACCAGATGGGTGGTTGTATTGCGATGCTGATGGTTCTCAGTTTGAT
AGTTCTCTATCACCGTATCTCATCAACGCAGTGCTAAACCTACGCTTGTCATTTATGGAAGATTGGGAAC
TTGGCGAACAAATGCTCAAGAATCTCTACACAGAGATCGTCTACACTCCAATTGCCACTCCCGATGGAA
CAATTGTCAAAAAGTTCAAGGGGAACAACAGCGGACAACCCTCCACTGTTGTTGATAACACACTGATG
GTTATTTTGGCTATGTA

>gi|21492611|ref|NC_004039.1|_Potato_virus_A_complete_genome

GCAATTAGGTGTGTGGAATGGGTCTCTCAAAGCAGAGCTGCGACCAAAGGAAAAAGTTGATCTGAACA
AGACTCGAACATTCACAGCTGCACCAATTGAAACGTTGCTTGGTGGAAAAGTCTGTGTAGACGACTTCA
ACAACATGTTCTATTCACTTCACCTAAAAGCCCCATGGAGCGTAGGGATGACAAAATTCTATGGCACAT
GGAACCAACTGATGTGTAAGCTACCAGATGATTGGGTGTATTGTGATGCCGATGGATCGCAGTTTGAC
AGCTCAATATCACCATACATGATAAATGCTGTGCTTAGAATCCGATTGCATTTTATGGAGGATTGGGAC
ATTGGATCTCAGATGCTACAGAACTTGTACACAGAAATTGGTACACACCAATCTCAACACCAGATGGCA
CAGTTGTTAAAAAAGTTCAAAGGAAATAATAGTGGGCAGCCATCAACTGTGGTGGATAACACACTTCT
AGTTGTGCTAGCTTTGCA

>gi|21431571|ref|NC_004010.1|_Potato_virus_V_complete_genome

TGAACTTGGAGTGTGGAATGGCTCACTCAAAGCTGAGTTGCGCTGCAAAGAGAAAATTGAAGCAAACA
AGACACGCACTTTCACAGCTGCTCCAATTGACACCTTACTAGCAGGAAAGGTGTGTGTTGATGATTTTA
ACAATCAGTTCTACAGCAAGAACATCGACTGTTGCTGGACAGTTGGCATGACAAAATTCTATGGCGGTT
GGAACAAGCTGCTCACGGCATTACCAGATGATTGGACATATTGTGATGCTGACGGATCTCAGTTCGACA
GCTCTTTGACACCTTATCTGATCAATGCAGTTCTAGCTGTGAGGTATGCATTTATGGAGGAATGGGATA
TTGGTTTTCAAATGTTACAAAACTTGTACACTGAGATCGTTTACACACCAATCTCCACACCAGATGGTAC
CATAGTTAAGAAGTTTAGGGGAAACAATAGTGGCCAACCCTCTACAGTTGTTGACAACTCGCTCATGGT
TGTTTTAGCCATGCA

>gi|9627728|ref|NC_001616.1|_Potato_virus_Y_complete_genome

TTTGCTTGGCATTTGGAACGGATCATTGAAGGCAGAGCTCCGGTGTAAGGAGAAGATACTTGCAAATA
AGACGAGGACGTTCACTGCTGCACCTCTAGACACTTTGCTGGGTGGTAAAGTGTGTGTTGATGACTTCA
ATAATCAATTTTATTCAAAGAATATTGAATGCTGTTGGACAGTTGGGATGACTAAGTTTTATGGTGGTT
GGGATAAACTGCTTCGGCGTTTACCTGAGAATTGGGTATACTGTGATGCTGATGGCTCACAGTTTGATA
GTTCACTAACTCCATACCTAATCAATGCTGTTCTCACCATCAGAAGCACATACATGGAAGACTGGGATG
TGGGGTTGCAGATGCTGCGCAATTTATACACTGAGATTGTTTACACACCAATTTCAACTCCAGATGGAA
CAATTGTCAAGAAGTTTAGAGGTAATAATAGTGGTCAACCTTCTACCGTTGTGGATAATTCTCTCATGGT
TGTCCTTGCTATGCA

>gi|18652416|ref|NC_003399.1|_Scallion_mosaic_virus_complete_genome

AAAAATGGGTGTTTGGAATGGATCACTGAAGGCTGAGTTACGGCCATTAGAGAAAACTGAGGCGAAC
AAAACACGGACATTCACAGCAGCGCCACTAGACACGCTGCTGGCGGGAAAAGTGTGTGTGGATGATTT
CAATAATCAATTCTACGACTTTAATTTAATCGCACCTTGGAGTGTCGGAATGACTAAATTTTATGGCGGC
TGGGATCAGCTACTAACAGCACTACCTGATGGGTGGGTGTATTGTGACGCAGATGGATCACAGTTTGA
TAGCTCCTTATCACCCTATTTGATAAACGCCGTATTAGACGTTCGATTGGAATTGATGGAGGAATGGGA

CATAGGGGAACAAATGTTGAGAAATCTATACACAGAGATCGTCTACACACCAATATCAACACCTGATGG
GACAATCATAAAGAAGTTCAAAGGTAATAACAGTGGACAGCCCTCAACAGTTGTTGACAACACACTCAT
GGTCATCTTAGCAGTAAA

>gi|76803354|ref|NC_007433.1|_Shallot_yellow_stripe_virus_complete_genome

AAAGATGGGTATCTGGAATGGCTCACTCAAAGCAGAAATACGACCAATTGAGAAAGTCCAGGCAAATA
AAACACGATCATTCACAGCAGCTCCAATTGAAACACTATTGGGTGGAAAAGTTTGTGTCGATGATTTCA
ACAACAACTTTTACAGAAGGAACTTAGCAATCCCTTCAACAGTTGGGATTACGAAGTTTTACAAAGGAT
GGGATGATCTTATGTGCTCATTGCCGGATGGATGGATTTACTGCGACGCAGATGGTTCACGCTTTGATA
GCTCACTAACGCCGTATCTAATGAACGCAGTATTAAACATTAGATTACGATTTATGGAAGAATGGGACA
TTGGACAAGAGATGCTCAAGAATTTGTACACTGAGATCATTTACACACCAATCGCAACACCCGATGGCT
CAATCATTAAGAAATTTAAAGGGAATAACAGTGGGCAGCCTTCTACGGTGGTGGACAATACATTGATG
GTGATGCTTAGTGTTCA

>gi|21449930|ref|NC_004035.1|_Sorghum_mosaic_virus_complete_genome

GCAACTTGGAGTTTGGAATGGTTCTCTTAAAGCAGAAATTCGACCAATTGAGAAAACAGAAGCAAATA
AGACAAGATCCTTCACAGCAGCTCCATTGGAAACATTACTTGGCGGGAAAGTGTGCGTAGATGACTTTA
ACAATCAATTCTATTCGCATCATTTGGAAGGACCTTGGACTGTAGGAATTACAAAATTCTATGGAGGTT
GGGATAGACTCTTAAACAAGCTCCCTGAGGGTTGGGTTTACTGTGATGCAGACGGTTCACAATTCGATA
GTTCTTTAACGCCTTATCTTATCAACGCGGTTTTAGACATCAGATTGCATTTCATGGAGGATTGGAACAT
TGGGGAAAGAATGCTCAAAAATCTCTATACAGAAATCGTCTACACTCCTATAGCAACACCAGATGGATC
CGTAATTAAGAAATTCAAAGGAAATAATAGTGGACAACCATCTACTGTTGTTGACAACACATTAATGGT
GATCATAGCTTTTAA

>gi|12018225|ref|NC_002634.1|_Soybean_mosaic_virus_complete_genome

GGAAAAAGGAGTGTGGAATGGATCCCTGAAAGCAGAGCTAAGGCCAATTGAAAAAGTGCAAGCAAAC
AAAACTAGAACATTCACAGCAGCACCAATTGACACATTACTTGGAGCAAAAGTTTGTGTTGATGACTTC
AACAACCAATTTTACAGCCTCAATCTTACATGTCCATGGACAGTTGGGATGACCAAATTTTATAGAGGTT
GGGATAAATTGATGAGAAGTTTACCCGATGGATGGGTGTACTGTCATGCAGATGGCTCACAGTTTGAT
AGCTCCCTGACGCCCTTACTACTGAATGCAGTTCTTGATGTTAGGAGCTTTTTCATGGAAGACTGGTGG
GTTGGAAGAGAAATGCTAGAGAACCTCTATGCTGAGATAGTCTACACACCAATTCTAGCACCTGATGGC
ACAATTTTTAAGAAGTTCAGAGGAAACAACAGTGGGCAACCATCTACAGTTGTGGACAATACCTTGATG
GTAGTCATTGCCATGTA

>gi|18652414|ref|NC_003398.1|_Sugarcane_mosaic_virus_complete_genome

ACACCTTGGCGTGTGGAATGGTTCACTCAAAGCTGAAATAAGGCCTATAGAGAAAACAATGTTAAATA
AGACTCGGACTTTTACAGCAGCACCATTAGAAACTTTACTTGGTGGCAAGGTCTGTGTTGATGATTTCA
ACAACCAATTCTACTCGCACCACTTAGAAGGTCCTTGGACAGTTGGAATAACAAAGTTTTATGGTGGGT
GGAACCGTTTGTTGGAAAAATTGCCAGATGGTTGGATATACTGCGACGCCGATGGATCACAGTTCGAC
AGCTCTTTGACACCATATCTCATCAACGCCGTATTACACATTCGATTACAATTCATGGAAGAATGGAACT
TAGGAGAACAAATGTTGCGAAACTTGTACACTGAAATCGTGTACACACCAATTGCAACACCAGATGGAT
CTGTAATCAAGAAATTTAAAGGTAATAATAGTGGGCAACCGTCAACAGTTGTAGACAACACACTCATGG
TGATATTAGCATTTAA

>gi|294872884|ref|NC_014038.1|_Sunflower_chlorotic_mottle_virus_complete_genome

GGAATTGGGAATTTGGAATGGTTCACTGAAAGCGGAGCTACGTTGTAAAGAGAAAATTATGGCAAATA
AAACACGCACCTTCACAGCAGCTCCTCTTGACACGCTTCTTGGTGGAAAGGTTTGTGTTGACGATTTCAA

CAACCAATTTTATTCGAAGAACATTGAATGTTGTTGGACAGTCGGAATGACCAAGTTTTATGGAGGATG
GAATAAATTGCTCAGAAGTCTGCCTGACAACTGGATATACTGTGACGCGGATGGATCCCGATTTGACA
GCTCATTAACTCCATACCTCATAAATGCAGTCTTGGCAATTCGAGCAACTTACATGGAGGATTGGGATA
TTGGATATCAAATGTTGCAGAACTTGTACACAGAAATTGTGTATACCCCAATCTCAACACCAGATGGAA
CAGTTGTCAAGAAATTCAGAGGCAACAACAGCGGACAACCATCCACAGTTGTTGACAATTCCTTGATGG
TTGTGCTTGCAATGCA

>gi|9629730|ref|NC_001841.1|_Sweet_potato_feathery_mottle_virus_complete_genome

ATACAAAGGTCTTTGGAACGGGTCCTTGAAAGCTGAGCTGAGGCCTATGGAAAAAGTGGAACTCAACA
AAACAAGAACTTTCACAGCGGCCCCTCTTGACACGCTACTTGGTGGCAAGGTGTGTGTGGATGATTTTA
ATAACATGTTCTACAACCACCATTTAAAGTGTCCATGGACGGTGGGAATAACTAAATTCTATCAAGGAT
GGGATAGACTACTCACATCTCTACCTGAGGGATGGATCTATTGTGACGCCGACGGCTCGCAATTTGACA
GCTCTCTTTCTCCATACTTGATTAATTCAGTTCTTAATATAAGAAGAGAATTTATGGAAGATTGGGATGT
CGGTGATCAAATGCTCCGGAATTTATACACAGAGATAGTATACACACCAATACTGACACCAGACGGAAC
TATAGTGAAGAAATTCAAAGGTAACAACAGTGGACAACCATCCACTGTGGTTGATAACACACTTATGGT
TGTGTTAGCAGTACA

>gi|475155116|ref|NC_020896.1|_Sweet_potato_latent_virus_complete_genome

CAAACTTGGTGTATGGAATGGATCGCTGAAAGCAGAATTGCGACCTTTGGAGAAGGTACAGGCCAATA
AAACACGAACATTCACAGCAGCTCCACTAGATACCTTACTCGCCGGAAAGGTATGTGTAGACGCGTTCA
ATAACAGATTTTATGATCTGCACATCCAATGTCCGTGGAGTGTTGGAATGACGAAATTCTATGGAGGTT
GGAATGAATTGTTAACAGCATTACCTGATGGGTGGAGGTATTGTGACGCTGATGGATCTCAATTCGAC
AGTTCTCTTTCTCCTTACTTAATAAATGCAGTGTTACAATTACGCTTGCATTTTATGGAGGAATGGGACA
TAGGAGAGCAAATGCTGAGAAATCTGTACACTGAGATCGTCTACACACCAATACTAACACCAGACGGC
ACAATCATAAAGAAGCATAAAGGAAATAATAGCGGACAACCGTCAACAGTTGTTGATAATACATTGAT
GGTTATACTAGCAATGTA

>gi|388570521|ref|NC_017970.1|_Sweet_potato_virus_2_complete_genome

GCGGAAAGGCTTATGGAATGGATCTCTCAAAGCTGAATTAAGACCGATGGAGAAGATAAATGCAAACA
AAACGCGAACCTTTACAGCCGCTCCACTTGATACCTTACTTGGGGGAAAAGTTTGTGTGGATGATTTTA
ACAATATGTTTTATAATCACCATCTTAAATGTCCATGGACAGTTGGTATTACAAAGTTTTACAAGGGATG
GGACACATTGCTTAACAAGCTACCGGAGGGTTGGTTGTATTGTGATGCTGATGGTTCTCAATTTGATAG
TTCATTGTCTCCATACTTGATTAACGCAGTGCTCAATATCAGGTTAGCATTTATGGAAGACTGGGAGATT
GGTGCACAAATGCTGAAGAACCTATACACTGAGATTGTATACACACCAATCTTGACACCAGATGGTACA
ATTGTCAAAAAGGTGAAGGGAAATAATAGTGGTCAACCTTCTACAGTGGTGGACAACACACTTATGGT
TGTTTTGGCTATGAC

>gi|313139317|ref|NC_014742.1|_Sweet_potato_virus_C_complete_genome

GCAAAAAGGACTTTGGAATGGTTCCTTAAAGGCTGAGCTCAGGCCCATGGCAAAAGTTGAATTGAACA
AAACAAGGACTTTTACAGCGGCCCCACTTGACACACTTTTGGGCGGTAAAACATGTGTTGATGATTTCA
ACAACATGTTTTACAACAACCATCTTAAGTGCCCATGGACAGTAGGTATCACAAAATTCTATCAAGGGT
GGGATAGACTGTTAACATCGTTGCCTGAAGATTGGATTTATTGTGATGCGGATGGTTCACAATTTGACA
GTTCTCTGTCACCATATCTTATTAATGCTGTCCTTAATATACGGAGAGAATTCATGGAAGAATGGGACAT
AGGTGACCAAATGCTCCGAAATTTGTACACAGAGATTGTATATACGCCGATTTTAACACCAGATGGAAC
CATAGTGAAGAAGTTCAAAGGAAATAACAGTGGACAACCATCAACCGTCGTGGACAACACACTAATGG
TTGTGTTAGCCGTCTA

>gi|393248211|ref|NC_018093.1|_Sweet_potato_virus_G_isolate_Jesus_Maria_complete_genome

AAAACTTGGTCTATGGAATGGATCATTGAAAGCAGAGTTGCGCACACGTGAGAAAATTGATGCCAATA
AGACAAGAACGTTCACAGCAGCACCTCTTGACACCTTGTTAGGAGGAAAAGTTTGTGTTGATGATTTCA
ACAATATGTTTTATAATCTTCATCTGCAATGCCCATGGACAGTTGGAATCACAAAGTTTTATAAAGGGTG
GGACACACTTCTCAGAAAACTACCGGAAGGATGGGTTTATTGTGATGCCGATGGTTCACAATTCGATAG
TTCGCTATCGCCATATCTTATCAATTCAGTTTTGAACATCAGGCTACATTTTATGGAGAAGTGGGAAATT
GGTCAAACAATGTTGAAAAATCTCTACACTGAGATTGTTTACACACCCATACTCACACCAGATGGCACA
ATTGTGAAGAAATTTAAAGGCAACAACAGTGGTCAACCTTCAACAGTTGTTGACAACACACTCATGGTT
GTACTAGCTATGAC

>gi|156447517|ref|NC_009742.1|_Telosma_mosaic_virus_complete_genome

AAGGAAAGGGCTGTGGAATGGTTCACTTAAAGCTGAGTTAAGGCCACTTGAGAAAGTTCAAGCTAACA
AAACAAGGACATTCACAGCAGCACCCATTGACACACTTCTTGGTGCAAAGGTTTGTGTGGATGACTTTA
ACAATCAATTCTATAGTCTGCACTTTAAGTGTCCCTGGACGGTTGGAATGACAAAGTTTTATGGTGGAT
GGGACTCGCTCATGAGAAGATTACCAGATGGTTGGTTATATTGCCATGCTGATGGATCCCAATTTGATA
GTTCATTGACCCCTTTGTTGCTAAATGCAGTGCTTGACATTAGATTGTTTTTCATGGAAGATTGGTGGGT
TGGGCAAGAAATGCTCACTAACCTGTATGCTGAAATTGTGTACACACCAATCCTCGCACCCGATGGCAC
CATTTTCAAGAAATTCAGGGGAAACAATAGTGGACAACCTTCTACAGTTGTAGACAATACTTTGATGGT
TGTGATCTCTGTTTA

>gi|68989216|ref|NC_007180.1|_Thunberg_fritillary_virus_complete_genome

GAAGATGGGAGTCTGGAATGGGTCATTAAAGGCTGAATTAAGACCGATTGAGAAGTGTATTGCAAATA
AAACAAGATCATTCACAGCAGCACCGATTGACACGCTACTTGGGGGAAAAACATGTGTGGATGATTTC
AACAACCAATTTTACTCGCTGCATTTTGCTCTACCATCTAGTGTTGGTATGACTAAATTTTATGGTGGTTG
GAATGACTTGCTTTGCAGACTACCTGATAACTACGTATACTGTGATGCAGATGGGTCGCAATTTGATAG
TTCTCTATCACCATACTTAATTAATGCGGTGCTTAATCTTCGACTACACTTTATGGAGGACTGGGGTGTT
GGACACACCATGCTTGAAAACTTGTACACAGAGATTGTATATACTCCAATCGCTACACCCGACGGAACA
ATTATAAAGAAATTTAAAGGCAATAATAGTGGACAGCCTTCAACAGTAGTTGACAACACGATAATGGT
GATGTTAGCAGTGAA

>gi|9790340|ref|NC_001555.1|_Tobacco_etch_virus_complete_genome

AAAGTTGGGAATTTGGAATGGCTCATTGAAAGCAGAGTTGCGTCCAATTGAGAAGGTTGAAAACAACA
AAACGCGAACTTTCACAGCAGCACCAATAGACACTCTTCTTGCTGGTAAAGTTTGCGTGGATGATTTCA
ACAATCAATTTTATGATCTCAACATAAAGGCACCATGGACAGTTGGTATGACTAAGTTTTATCAGGGGT
GGAATGAATTGATGGAGGCTTTACCAAGTGGGTGGGTGTATTGTGACGCTGATGGTTCGCAATTCGAC
AGTTCCTTGACTCCATTCCTCATTAATGCTGTATTGAAAGTGCGACTTGCCTTCATGGAGGAATGGGATA
TTGGTGAGCAAATGCTGCGAAATTTGTACACTGAGATAGTGTATACACCAATCCTCACACCGGATGGTA
CTATCATTAAGAAGCATAAAGGCAACAATAGCGGGCAACCTTCAACAGTGGTGGACAACACACTCATG
GTCATTATTGCAATGTT

>gi|160700528|ref|NC_009994.1|_Tobacco_vein_banding_mosaic_virus_complete_genome

GAAACTTGGAGTGTGGAATGGCTCAATTAAGGCAGAACTTAGGCCTAAAGAGAAAGTGCTCCAGAATA
AAACACGAACCTTCACAGCAGCACCTCTAGACACCTTGCTAGCCGGAAAAGTATGTGTTGATGATTTCA
ACAATTTCTTTTATTCATTCAACCTGGAGGGACCATGGAGTGTTGGAATGTCTAAGTTCACCAGAGGAT
GGAACACATTGCTTGGAAAATTGCCAAATGGCTGGTTGTACTGTGATGCAGATGGAAGTCGTTTCGAC
AGCTCATTGACACCATATCTCATTAATGCTGTTTTGCAAATTAGACTGACCTTCATGGAGTCCTGGGATA

TTGGTGAGCAGATGCTTAAGAATTTGTATGCTGAGATCATTTACACACCCATTTTGGCAGCAGATGGGA
CAATAGTTAAGAAATTCAAAGGCAACAATAGCGGGCAACCATCAACAGTTGTTGATAACACACTTATGG
TTATCATCACAATGCA

>gi|9629179|ref|NC_001768.1|_Tobacco_vein_mottling_virus_complete_genome

TAAACTAGGCGTCTGGAATGGATCACTTAAAGCGGAACTTAGACCGTTCGAGAAGCTCATCGAGAATA
AAACACGGACATTCACAGCAGCACCAATTGAGACATTGCTCGGAGGAAAAGTCTGTGTTGATGATTTTA
ACAATCATTTCTACAGCAAGCACATACAATGCCCTTGGAGCGTTGGAATGACAAAGTTCTATGGAGGCT
GGAATGAACTTCTTGGAAAGCTTCCTGATGGATGGGTATATTGCGATGCTGATGGTTCACAATTTGATA
GCTCATTATCCCCATATTTAATAAATGCAGTGCTCCGTCTACGATTGTCAAGCATGGAAGAGTGGGATG
TTGGACAGAAGATGTTGCAAAATCTCTACACGGAGATTGTTTACACACCAATATCAACACCAGATGGCA
CAATTGTTAAGAAGTTTAAGGGCAACAACAGTGGACAGCCATCTACGGTTGTGGACAACACACTCATG
GTGGTGCTTGCAATGTA

>gi|386522667|ref|NC_017824.1|_Tomato_necrotic_stunt_virus_complete_genome

AAAACTCGGTGTTTGGACTGGCTCATTAAAGTCAGAGTTGAGACCCATGGAAAAAGTTCTGGCCAACA
AAACAAGAACTTTCACTGCTGCTCCAATTGACACACTGCTGGCTGGGAAGGTTTGTGTGGATGATTTTA
ATAATCAATTCTACTCGAAGAATATTGAATGCTGCTGGACTGTGGGCATGACCAAGTTTTATGGGGGTT
GGAATAAGCTTCTTACAGCTTTACCAGATGGATGGCTCTATTGTGATGCTGATGGTTCTCAATTTGACA
GCTCCCTGACACCATACTTGATCAATGCTGTACTTGGTATTCGTCTTGCATTTATGGAGGATTGGGATAT
TGGTTTTAAAATGCTAGAGAATCTCTACACAGAGATTATTTACACACCAATTTCCACACCGGATGGGACT
GTTGTGAAGAAATTCAGAGGGAATAACAGTGGTCAACCTTCCACAGTTGTAGATAATTCATTAATGGTT
GTCTTAGCTATGAA

>gi|56407093|ref|NC_002509.2|_Turnip_mosaic_virus_complete_genome

AAAGATGGGAGTGTGGAACGGCTCGCTGAAGGCAGAGTTGCGACCACTAGAAAAAGTGGAAGCAAAC
AAAACACGGACGTTTACTGCCGCACCACTAGACACACTGTTGGGTGGAAAAGTTTGCGTGGATGATTTC
AACAACCAGTTCTATGATCACAACCTTAGAGCTCCTTGGAGCGTTGGCATGACAAAGTTTTATTGTGGTT
GGGATCGCTTGTTGGAGTCGTTGCCAGATGGTTGGGTGTATTGCGATGCTGATGGCTCACAGTTCGAC
AGCTCGCTATCGCCATACTTGATCAACGCAGTACTCAACATCCGCTTAGGATTCATGGAAGAGTGGGAC
ATAGGGGAGGTAATGCTGAGAAATTTGTACACCGAAATCGTGTATACCCCTATTTCTACACCAGATGGT
ACACTCGTCAAGAAGTTCAAAGGAAACAATAGCGGACAGCCATCGACTGTTGTGGACAACACGCTCAT
GGTCATATTGGCAGTCAA

>gi|388570618|ref|NC_017977.1|_Vallota_speciosa_virus_complete_genome

GAAATTCGGCATTTGGAACGGATCATTAAAAGCCGAGCTTCGATCAATGGAGAAGGTGTTGAGTAACA
AGACGAGATCATTTACAGCAGCGCCAATTGAAACGCTGCTAGGAGGGAAAGTGTGTGTGGATGACTTC
AACAACGCCTTTTACAAAGCCCACTTGAAAATTCCCTCTACAGTGGGAATAACAAAGTTTTATAAGGGT
TGGGATCGTTTACTGAGATCTTTACCGGAAGGATGGTTGTATTGTGATGCGGACGGAAGCAGATTTGA
TAGTTCGTTAACACCGTATCTAATTAATTCTGTCATCACAATACGAGAACGCTTCATGGAAGACTGGAA
AGTTGGGAGAAGGATGCTACGAAATCTTTACACTGAAATTGTGTACACTCCAATTGCTACACCGGATGG
GTCGTTACTCAAGAAATTCAAGGGTAATAATAGTGGTCAACCATCCACAGTTGTTGATAACACACTCAT
GGTCATGATGGCAGTTCA

>gi|189009876|ref|NC_010735.1|_Verbena_virus_Y_complete_genome

ACAACTTGGTGTTTGGAACGGGTCATTGAAGGCTGAATTACGTAGCCAAGAAAAGATTCAAGAGAACA
AAACCCGAACGTTCACAGCAGCGCCCATAGATACCTTGCTGGCTGGAAAGGTGTGTGTGGATGATTTT

AACAACCAGTTTTATTCAATGAATACACATTGCAGTTGGACTGTTGGAATGACCAAGTTCTATGGTGGA
TGGGACAGGCTTTTAAGAAGCCTTCCGGATGGTTGGATTTATTGTGACGCTGATGGCTGGAGGTTCGA
TAGCTCACTTACACCTTACCTCATCAATGCAGTTCTGGCAATTCGTAGTGCATACATGGAGGATTGGGA
CATTGGTTTTCAGATGTTGAGGAATCTCTACACAGAGATAATCTACACACCCATAGCAACTCCAGATGG
AACCATTGTCAAGAAATTCAGAGGAAATAACAGTGGGCAACCCTCCACAGTGGTTGACAATTCACTCAT
GGTAATCTTAGCTATGCA

>gi|51949945|ref|NC_006262.1|_Watermelon_mosaic_virus_complete_genome

AGAGAAAGGAATTTGGAACGGTTCCTTGAAAGCGGAGTTGAGGCCAATTGAAAAAGTGCAGGCAAAC
AAAACTAGAACATTTACAGCAGCACCGATTGATACATTGCTTGGAGCTAAAGTTTGCGTCGATGATTTT
AATAATCAATTCTACAGCTTCAACTTAAAATGTCCATGGACAGTTGGCATGACTAAGTTTTATGGGGGTT
GGGATAAGCTAATGAGGAGTTTGCCTGATGGCTGGACATATTGCCACGCAGACGGTTCACAGTTCGAC
AGTTCTTTGACTCCCTTATTGTTGAATGCTGTCCTCAGTATTAGATGTTGCTTCATGGAAGATTGGTGGG
TTGGAAAGGAAATGCTTGAAAACCTTTACGCTGAGATAGTTTACACACCAATCTTAGCACCTGATGGCA
CAATTTTCAAAAAGTTTAGAGGGAATAACAGTGGACAGCCATCTACAGTTGTTGACAATACGCTTATGG
TTGTCATTGCTATGTA

>gi|25140980|ref|NC_004426.1|_Wild_potato_mosaic_virus_complete_genome

TGACCTTGGAGTGTGGAACGTTTCACTAAAGGCTGAATTGCGCTGCAAAGAGAAAATCGCGGCAAATA
AGACACGCACTTTCACAGCTGCACCCATTGATACATTGCTGGCAGGAAAAGTGTGTGTGGATGATTTCA
ACAACCAATTCTACAGCAAAAACATTGAGTGTTGTTGGACTGTTGGTATGACAAAGTTTTATGGAGGCT
GGAACAAGTTACTTACAGCTTTGCCAGACAATTGGGTTTACTGCGATGCTGATGGGTCGCAATTTGACA
GCTCACTAACCCCATACTTGATAAATGCAGTGTCGGCTGTGAGGTATGCGTTCATGGAGGATTGGGATA
TTGGATTTCAGATGCTCCAGAATCTCTACACTGAGATAGTTTATACACCAATCTCCACGCCCGATGGAAC
GATTGTCAAGAAGTTTAGAGGCAACAACAGCGGCCAACCTTCAACCGTGGTAGACAACTCGCTCATGG
TAGTCTTAGCTATGCA

>gi|156447521|ref|NC_009744.1|_Wild_tomato_mosaic_virus_complete_genome

GCGACTTGGAGTTTGGAATGGTTCAATCAAAGCTGAACTGCGACCAATGGAGAAAGTGCAAGCCAACA
AAACGCGAACATTCACAGCTGCTCCAATTGATACACTACTGGCCGGCAAAGTGTGTGTTGACGATTTCA
ATAATCAATTTTATTCAAAGCACACGGAAGCCTTGTGGAGTGTTGGAATCTCCAAATTCTCAGGTGGGT
GGGACAAGTTACTACGAAAGTTGCCGGATGGATGGGTGTATTGTAGCGCAGATGGCAGTCGTTTTGAT
AGTTCTTTAACACCATATCTTATAAATGCAGTTTTGCATATTAGACTGCATTTCATGGAAAAATGGAGTA
TTGGTGAACAGATGTTAAGGAACTTGTATGCTGAGATTATATACACCCCCATATTAACAGCAGATGGCA
CAGTTGTCAAGAAATTCAAGGGTAACAATTCAGGACAACCTTCAACTGTGGTTGACAATACATTGATGG
TCTTGTTGGCAATGAG

>gi|71647082|ref|NC_007216.1|_Wisteria_vein_mosaic_virus_complete_genome

TGAGAAAGGTGTGTGGAATGGTTCACTCAAAGCTGAATTAAGACCAATAGAAAAAGTGAATGCAAACA
AGACAAGAACATTCACTGCAGCTCCAATTGACACGTTGCTTGGAGCTAAAGTTTGTGTGGATGATTTCA
ACAATCAGTTCTACAGTTTCAATCTTGTTTGCCCTTGGACAGTGGGAATGACTAAATTCTATGGAGGAT
GGGATAAACTGATGAGAAGTCTACCGGAAGGATGGATCTATTGTCATGCTGATGGTTCTCAATTTGATA
GTTCTTTAACTCCATTATTGCTAAATGCTGTACTTGATATCAGGAGCTTCTTCATGGAAGATTGGTGGAT
CGGAAAGGAAATGCTTGAGAATTTGTATGCTGAAATAGTTTACACACCAATCCTCACCCCAGATGGGAC
AGTTTTTAAGAAGTTTAGAGGCAATAACAGTGGGCAACCTTCAACAGTTGTGGACAACACACTTATGGT
TGTCATAGCAATGTA

>gi|360040872|ref|NC_016441.1|_Yam_bean_mosaic_virus_complete_genome

AAAGAAAGGTCTGTGGAATGGTTCACTCAAAGCTGAATTGAGACCAACAGAAAAAGTTGTTGCAAATA
AAACAAGAACTTTTACAGCTGCACCAATTGACACATTATTAGGTGCGAAGGTCTGTGTGGATGACTTCA
ATAATCAGTTTTACAACTTCAATTTAATCTGTCCATGGACGGTTGGAATGACCAAATTTTATGGAGGATG
GGACAAGTTGATGAGAAAGCTACCTGATGGCTGGGTGTATTGCCATGCTGATGGATCACAGTTTGATA
GTTCATTAACACCCCTTCTCCTGAATGCTGTTTTGGGAATCAGAAAATTTTTCATGGAAGAGTGGTGGG
TTGGTGAGGAAATGTTAGAAAATCTGTACGCAGAAATTGTGTATACACCAATTTTGGCTCCAGATGGCA
CCATCTTCAAGAAGTTTCGAGGCAACAACAGTGGTCAGCCTTCTACAGTAGTTGATAATTCACTTATGGT
TGTGATAGCGGTTTA

>gi|414089934|ref|NC_019412.1|_Yam_mild_mosaic_virus_from_Brazil_complete_genome

CAAGAAAGGGGTTTGGAACGGATCAATAAAAGCTGAGTTGAGGCCAATTGAAAAAGTTCACGCGAAT
AAGACAAGAACATTCACTGCAGCCCCGATTGACACGCTACTTGGTGCAAAAACTTGTGTTGATGATTTC
AACAATTTCTTCTATATGCAACATACAAAAGGCCCATGGAGTGTTGGAATGACGAAGTTTTCTCAAGGC
TGGGATAAAATGTTGAGGAAGATACCTGATGGGTGGATCATCTGTGATGCGGATGGGAGTAGGTTCG
ATAGCTCACTCACTCCCTATTTGATCAATGCTGTTGCACACATACGGCAGTATTTTAATGAAGATTGGGA
CATAGGGGATCAAATGCTACGTAATTTGTACACAGAAATTGTGTACACACCAATCTTAACAGCTGATGG
AACCATAGTGAAGAAGTACAGAGGAAACAACAGTGGTCAACCCTCCACAGTGGTCGACAACACTCTTA
TGGTTTTATTGGCCGTACA

>gi|30146781|ref|NC_004752.1|_Yam_mosaic_virus_complete_genome

AAAGATGGGTGTATGGAATGGATCACTTAAACCAGAGTTGCGAACCGAAGAGAAAGTGAACATGAAC
AAAACTAGAACATTCACAGCAGCACCTCTTGATACCTTATTGGGTGGTAAAGTTTGCGTTGATGATTTCA
ATAATCAATTCTACAGTCGCTGTATTGATTTTCCATGGACAGTTGGAATGACTAAATTTTATGGTGGTTG
GAATGAACTGATGCGGAAGCTACCAGAAGGATGGGTGTATGTTGACGCCGATGGTTCTCAATTTGATA
GCTCGTTGTCTCCATATTTGATTAATGCTGTGCTCAACATTCGATTACACTTTATGGAGGAATGGGACAT
AGGAGAGCAAATGCTTAGGAATCTTTACACAGAAATTGTGTACACACCTATAGCAACACCAGATGGCA
CAATTGTGAAAAAGTTTAAAGGAAATAACAGTGGACAACCGTCGACTGTAGTTGATAACACTTTGATG
GTCATGCTCGCCATGTA

>gi|212525937|ref|NC_011560.1|_Zantedeschia_mild_mosaic_virus_complete_genome

GAAGAAAGGGATTTGGAACGGATCCCTCAAAGCTGAACTGAGGCCCATGGAGAAAATTCGGGCCAAT
AAAACCAGGACCTTCACAGCAGCTCCCATTGACACACTTCTCGGGGCGAAAGTGTGCGTGGATGACTTC
AACAACCAGTTCTATAGTCTGAATATGGAATGCCCGTGGACAGTGGGCATGACCAAATTTTACGGAGG
GTGGGATAAACTTATGAGGAAGCTTCCAGAAAAATGGGTGCATTGCCATGCAGATGGCTCACAATTCG
ATAGTTCCCTCACACCACTACTGCTAAATGCAGTGCTCACTCTTCGGTTGTGCTTCATGGAAGAGTGGTT
TGTTGGCCAAGAAATGCTCCAAAACCTATATGCTGAAATTGTATACACGCCCATCTTAACACCGGATGG
GACCATTTGTAAGAAGTTTAGGGGCAATAATAGTGGACAACCGTCCACTGTGGTCGACAACACTCTTAT
GGTCGTGATATCTGTGTA

>gi|570364799|ref|NC_023175.1|_Zucchini_tigre_mosaic_virus_isolate_Re01-25_complete_genome

AAGAATGGGCATTTGGAATGGTTCATTGAAAGCTGAAGTGAGACCAGCGGAAAAGGTTCTTGCTTCAA
AAACTCGCACCTTTACGGCTGCTCCGATTGACACATTACTAGGAGTTAAGGTTTGTGTTGATGATTTCAA
TAATTGGTTTTACAGCAAGAATATGGTTTGCCCTTGGACGGTTGGAATGACAAAATTCTACAAGGGATG
GGATGAGTTTCTTCGAAAGTTCCCAGACGGCTGGGTGTACTGCGACGCTGACGGATCACAATTTGACA
GTTCATTAACTCCATATCTCCTCAATGCTGTACTAGAGGTACGTTTATGGGCAATGGAACCATGGGATAT
TGGCGAACAAATGTTGCGGAACTTGTATGGAGAAATCACGTACACACCAATCCTCACACCAGACGGAA

CAATTGTCAAGAAATTCAAAGGAAACAACAGTGGTCAACCATCAACTGTTGTTGACAATACATTAATGG
TGTTGATCACGATGTA

>gi|17059637|ref|NC_003224.1|_Zucchini_yellow_mosaic_virus_complete_genome

CTACAAAGGTCTGTGGAATGGATCTTTAAAGGCCGAGCTCAGGCCGCTTGAGAAAGTCAGGGCCAACA
AAACACGAACTTTTACAGCAGCGCCCATTGATACATTGCTCGGAGCTAAAGTTTGCGTGGATGATTTCA
ATAATGAATTTTATAGCAAAAACCTCAAGTGTCCATGGACGGTTGGCATGACGAAATTTTATGGTGGTT
GGGATAGATTGATGAGATCATTACCTGATGGTTGGTTATATTGTCATGCTGATGGATCACAGTTTGACA
GTTCATTGACCCCAGCCTTACTGAATGCAGTGCTTATAATCCGATCATTTTATATGGAGGATTGGTGGGT
CGGTCAAGAGATGCTTGAAAATCTTTATGCTGAGATTGTGTACACTCCAATTCTTGCTCCGGATGGAAC
AATTTTCAAGAAATTTAGAGGTAACAACAGTGGGCAACCCTCAACAGTGGTGGATAACACACTAATGG
TTGTGATCTCTATTTA

>AY994084.1_Blackberry_virus_Y_complete_genome

AATAATTGTGATGGAGTGTGGAAAGGCTCACTTAAAGCAGAATTACGATCTAAAGAGAAAGTGCAGGA
GAACAAGACGAGAGTCTTTACATCAGCACCATATGACGTTCTCCTTGGTGGGAAAGCATGCGTTATGCA
CTTCAACAAGAAGTTTTATGCAAATAACACAAAGGGGCCGTGGACAGTTGGCATAAACAAACTTGGAT
TGGGGTGGCATCGTTTGCTTAAGAGTTTACCTGAGGGATTTGTTTATGGAACTGGTGATGGATCTCAAT
TTGACAGCAGTTTGACACCATTACTGATCAATGAAGTTTGTAGAATACGCATGTATTTCATGCAAGATG
ATGAATTAGGGCAGGCCATGCTACGCGGATTGTACAGACAAATCATTTGGACGCTCATTTCAATGCCTG
ATGGTTCGGTTGTACGGAAAGCAAAAGGGAACCCTAGTGGACAACCAAGTACAGTTGATGACAACACC
ATCATGGTAATGTTGGCAGTGGA

>NC_002350.1_Wheat_yellow_mosaic_virus_RNA_1_complete_sequence

TGCAATTCCATCGGCATTTGGAACGGATCGCTCAAAGCAGAGCTTAGGACGATTGAGAAAGTGGAAGC
TGAGAAAACCAGAGTTTTCACGGCTTCGCCAATCACGAGTTTATTCGCCATGAAGTTCTACGTTGACGA
TTTCAACAAGAAGTTCTATGCGACAAACCTGAGAGCCCCACACACGGTAGGAATCAACAAATTCAGCA
GAGGCTGGGAAATGCTCCACGACAAGCTCAACCGCCCAGGTTGGCTTCACGGCAGTGGCGATGGGTC
ACGATTTGATAGTTCAATTGACCCTTTCTTCTTCGACATAATTAAGGAGATTCGAAAGCACTTTCTACCA
GTTGAGCACCATCGCGCAATCGACCTAATATACGACGAGATTCTCAACACCAACATTTGTTTGGCAAAT
GGCATGGTAATTCGAAAGAACGTTGGGAATAACAGCGGGCAGCCAAGCACGGTCGTAGACAACACAC
TTGTTCTCATGGTCTCTTTTCT

>NC_004016.1_Oat_mosaic_virus_RNA_1_complete_genome

GGACACTCTGTTGGCGTGTGGAATGGTTCTCTTAAAGCTGAACTTCGAACAATTGAGAAAGTTGAGGCT
CAGAAAACGCGTGTTTTCACAGCCTCACCCATCACCAGCTTAATGGCCATGAAGTTCTATGTGGATGAT
TTTAACAAAGCCTTTTACACAACGAATCTCGTTGCTCCACATACCGTTGGCATAAATAAGTTTAGCCGTG
GTTGGGAAAAATTGCACAACAAGCTGGACAGACCAGGATGGCTACACGGGAGCGGCGATGGTTCACG
TTTCGACAGTTCCATTGATCCATTCTTCTTTGATGTTGTTAAGGTGATTCGGAAACATTTCATGCCTGAA
GAACATCATGTAGCTATTGATCTCATTTATGAGGAGATCTTGAACACCACAATATGCCTTGCGAATGGC

ATGGTTATTCGAAAGAATGTTGGCAACAATAGTGGGCAGCCTAGCACCGTTGTCGACAACACTCTCGTG
CTCATGGTGGCTTTCCT

>NC_002990.1_Barley_yellow_mosaic_virus_RNA_1_complete_sequence

GGCAAGTCAACCGGAGTATGGAATGGTTCTTTGAAAGCTGAGTTGAGAACCATCGAGAAAGTTGAGCC
GGAGAAAACGCGTGTTTTCACAGCCTCTCCCATAACAAGCTTGTTTGCTATGAAATTCTACGTTGATGAT
TTTAACAAGAAGTTCTACGCTACCAATCTGAAAGCCCCCCATACTGTTGGCATCAATAAGTTCGGTAGG
GGATGGGAAAGATTGCATGATAAGCTTAATCGCCCTGGATGGTTGCACGGCAGTGGAGATGGTTCTAG
GTTCGACAGCTCTATCGATCCTTTCTTCTTCGACGTTGTGAAAACTATTCGCAAGCACTTTCTCCCTTCTG
AGCATCACAAAGCCATTGATCTCATATATGATGAGATTCTCAACACAACCATCTGCCTAGCTAATGGGA
TGGTCATCAAGAAGAATGTTGGAACACAGCGGCAGCCTAGCACTGTTGTCGATAACACACTTGTGCTTA
TGACTGCATTTCT

>NC_028144.1_Rice_necrosis_mosaic_virus_RNA_1_complete_sequence

GGAAGGTTGAACGGCATTTGGAATGGGTCCCTGAAGGCTGAGTTAAGAGCTATTGAGAAAGTGGAGG
AGAGAAAGACACGAGTTTTTACCGCAGCCCCAATTACAAGCCTCTTGGCCATGAAGTTCTACGTTGACG
ATTTTAACAAGCAATTTTATGGAACACACCTCAAAGCACCACACACTGTTGGGATAAACAAATTTTCACG
TGGCTGGGAGAAGCTGTACAATAAGTTGAACCAACCCGGCTGGATGCATGGTAGTGGTGATGGCTCTC
GTTTCGACAGTTCAATAGACCCATTCCTTTTCGATGTAGTTCTTGACATACGAAAAAGGTTCATGCATGA
GAAGCATCATGCCGCGCTCCACATTATATACGGTGAAATCATGAACACGAAAATCTGCTTAGCCAACGG
GCTTATTATACAGAAGCACTGCGGCAATAACAGTGGGCAGCCAAGCACCGTTGTTGATAACACACTGG
CACTCATGACCGCTTTCCT

>NC_003483.1_Barley_mild_mosaic_virus_RNA_1_complete_sequence

GGAACGCTGGATGGAGTCTGGAACGGATCACTCAAAGCCGAACTGCGCTCTTCGCAGAAAATCCTTGA
ACGGAAAACTCGTGTTTTCACTGCTGCCCCCATCACAAGCCTAATCGCAATGAAATATTACGTGGATGA
TTTCAACAAGCAGTTCTACAAAACCCACCTCAAAGCACCACACACAGTCGGCATCAACAAGTTTAACCG
CGGATGGCAGAATCTCTATGAGAAGCTCAACAAACCTGGGTGGACGCATGGGAGCGGGGACGGCTCC
AGGTTCGATAGCTCTATTGACGGATTCCTTTTTGACGTCATCAAAGACATCCGGAAGCACTTCATGGAC
GCAGAACACCACAAGGAGCTAGACACAATTTATGAAGAGATTGTCAACACAAAAATATGTCTAGCAAA
TGGTCTCATCATCCAAAAGAACTGTGGGAACAACAGCGGGCAGCCAAGTACTGTTGTAGACAACACAC
TTGCACTCATGACTGCTTTCCT

>NC_030840.1_Coccinia_mottle_virus_isolate_Su12-25_complete_genome

CATGGAGTTGTTGGAGTTTGGAGCGGGTCTTTGAAAGCTGAACTCAGAACGAAGGCTAAGATTGCAGA
AGGAAAGACAAGAGTTTTCACAGGAGCACCAGTAGATGTTTTACTGGCAGGAAAAATTCTGGTGGATA
AGTTTAACAAGCACTTCTACTCTCAGCACTTGAAAGGACCCTGGTCCGTTGGGATTAATAAATTCAATCG
TGGTTGGAATAAACTAGCAGAATATTTTAACCATGATTGGAAATTTATTGATTGTGATGGAAGCAGATT
TGATAGTTCATTATCTCCAATTCTATTCCAAATGATTTGCCACTTGAGAGAGAGATTCGGTCATTTCGAC
TGGGGTGAGACTAATGCGTTGAGAAATCTATACGCACAAATAGTATACACTCCAATCTTAACGATCGAT

GGTAATATTGTCAAGAAACACAGAGGTAATAATAGTGGTCAGCCCTCAACAGTAGTTGACAACACATT
GATTCTAATGTTAGTTGTTGAG

>NC_010521.1_Squash_vein_yellowing_virus_complete_genome

ATGGGAGCAGTTGGTGTATGGAGCGGGTCATTGAAAGCTGAGTTGAGGAGCAGAGAGAAAATCGCTG
AAGGAAAAACGCGTGTGTTCACTGGAGCTCCAATTGATGTGTTATTAGCTGGGAAAGTCTTAGTTGACA
ATTTCAACAATTATTTCTACTCCCAGCATCTCAAAGGCCCTTGGTCAGTTGGCATAAATAAATTCAATAG
AGGGTGGGATCGCCTTGCTAACACATTTGATCACACGTGGAAATTTATCGACTGTGATGGTAGCAGGTT
CGATAGTTCTCTATCGCCCGTCCTATTTCAATTAATATGCCATCTTAGAGAGAGATTTGGAACATTTGAC
AAGGGTGAAACACGAGCATTGAGAAACTTGTATTCTCAAATTGTATACACACCAATTTTGACGATTGAT
GGGTATATAGTTAAGAAGCACAAGGGGAATAATAGTGGACAACCTTCAACAGTTGTTGACAATACGTT
AATCTTAATGATCGTTGTTGAA

>NC_014791.1_Ugandan_cassava_brown_streak_virus_complete_genome

GGTGGGGATGTTGGTATTTGGAGTGGCTCACTCAAAGCAGAATTGAGACCTGTTGAGAAAGTACTTGA
GCAGAAAACGAGAGTGTTTACTGGAGCTCCAATTGATTTGCTGTTAGGGGGAAAGATTTTAGTTGATA
ATTTTAATCATTTCTTTTATTTTAATCATTTGAAGGGACCTTGGACTGTAGGAATCAATAAATTTAATAAA
GGTTGGGATAGATTAGCTAGGTATTTTAACCATAGTTGGAACTTCATAGATTGTGATGGTAGTAGGTTT
GATACTTCTTTAGCTCCCATTTTGTTTCAATTAGTGTGTCACATGCGAGAAAAATTTGGAAATTTTGATG
ATATTGAGAGGGCAGCTCTTCGCAATTTATACACACAGATAGTGTATACGCCAATTTTAACAATTGACG
GATACATTACTAAGAAGCACCGTGGAAATAATAGTGGACAACCTTCTACAGTTGTTGATAACACTATTA
TACTAATGATTGTTGTGGAA

>NC_006941.1_Cucumber_vein_yellowing_virus_complete_genome

CATGGCGTTGTTGGTATTTGGAGTGGATCACTGAAGGCGGAGTTGCGAACTAAAGCGAAGATTGCCGA
AGGGAAAACGAGAGTGTTTACAGGCGCACCCATTGATGTGTTACTGGCCGGAAAGGTGCTCGTCGACA
AATTCAACAAGCACTTTTATACACAGCACTTAAAAGGACCTTGGTCTGTCGGGATAAATAAGTTTAATC
GTGGTTGGGACAAGCTTGCACGCTACTTTAACCATGATTGGAAGTTTATTGATTGTGATGGAAGCAGGT
TCGATAGTTCACTTTCTCCGATTTTATTTCAAATGGTGTGCCATATGAGGGAAAGGTTTGGTCATTTTGA
TTGGGCTGAAACAAACGCGCTGAGGAATTTGTATGCTCAAATCGTTTACACCCCAATTCTCACTATAGAT
GGAAACATAGTGAAGAAACATAAGGGTAACAACAGTGGTCAGCCGTCAACTGTGGTGGACAATACCCT
CATTCTCATGCTGGTTGTTGAG

>NC_003797.1_Sweet_potato_mild_mottle_virus_complete_genome

AGCGGCCATCTGGGAGTTTGGAGTGGGTCATTGAAGGCAGAGTTGCGACACGTGGACAAACTAAAGG
AAGGGAAGACTAGAGTTTTCACAGGAGCACCAATCGATACACTTCTTGCTGGGAAAATATTAGTCGAT
AACTTCAACAATTATTTCTATAAGTGTCATTTGCAAGGACCATGGACAGTTGGGATCAATAAATTCAATC
GAGGGTGGAATAAGTTGGCGAACTATTTCAATCATGATTGGGTTTTCATTGACTGTGATGGGAGTCGG
TTTGACAGTTCCATACCCCCAATTATGTTTAATGCAGTTTGCATGTTAAGATCAGTTTTTGGTGATTTGG
ATCCAGATGAAAATCAGACGTTGAGCAATCTTTACACTGAGATTGTGAACACGCCAATACTCACCATTG

AAGGGAATATCATCCGGAAATTTAGAGGCAATAACAGTGGGCAGCCTTCAACAGTTGTTGATAACACG
TTGATTCTGATGATTGCTATGGAG

>NC_012698.2_Cassava_brown_streak_virus_complete_genome

GGAGGTGATATTGGTATTTGGAGTGGTTCGTTGAAAGCTGAATTGAGACCCTGTGAGAAGGTGAAAG
AGATGAAGACAAGGGTTTTCACAGGAGCTCCAGTTGATGTCTTACTAGGGGGAAAGATTTTGGTTGAC
AATTTCAACCATCATTTTTACGAGAACCATCTTAAAGGACCATGGACTGTTGGGATTAACAAATTTAATC
GAGGATGGGACAAGTTGGCTAGATATTTTAACCATAGTTGGAACTTTATTGATTGTGATGGGAGCCGG
TTTGACACATCTTTGGCACCAATATTGTTTCAACTTGTGTGTCACATGAGAGAGAGGTTTGGTGGATTTG
ATGCAATAGAGACAGCTGCTCTGAGGAATCTCTATACACAGATTGTGTACACTCCAATTCTTACCATCGA
TGGGTACATCACGAAGAAACATAGAGGCAACAATAGTGGGCAACCCTCAACTGTTGTTGACAACACCA
TAATTTTGATGATTGTGGTTGAG

>NC_026759.1_Artichoke_latent_virus_isolate_FR37_complete_genome

GGCAAAAATGCTGGGTTGTGGAATGGCTCACTCAAGGCAGAACTGCGTCCCAAGATCAAGGTTGAAGC
AAACAAGACGCGTGTCTTCACAGCAGCACCCATAACAACACTGATCGGATCCAAGTTTTTCGTTGATGA
TTTCAACAAACAGTTCTATGCCTCTCACTTGAAAGCCCCACACACGGTCGGAATAAACAAATTCAGCAAT
GGATGGGCAAAAGTGCACGACAAGTTGAACAGGGAAGGATGGCTCCATGGGAGTGGTGATGGTTCAC
GGTTTGATTCATCAATTGACCCTTTTCTCTTTGATATGATATACACAATACGATGCCACTTCATGTGTGAT
GATGACAGGAGGGAGGCAACGCGTGCCATGAGCAACATGTTTCGTGAATTTGTGTTTACACCAATCCA
CACAATTAGCGGCAACATACTGGTGAAGAACGTTGGAAACAATAGTGGTCAGCCGAGCACGGTTGTTG
ATAACACTCTTGTATTGATGCTATCATTCTA

>NC_018455.1_Chinese_yam_necrotic_mosaic_virus_complete_genome

GGGAAGAATTGTGGAATATGGAATGGCTCGATGAAAGCTGAGCTCAGAGTTGTCGAGAAAGTGCTAC
AGAAGAAAACGAGGGTATTCACAGCAGCACCAATCACAACACTCATCGGATCGAAGTTCTTTGTTGAT
GATTTTAACAAGCAATTTTATGGAACGCATCTCAAAGCATCCCACACTGTCGGTATTAATAAATTTCAAA
GAGGTTGGGAGAAATTGTACAACTTCTTAAATGTCGACGGTTGGTTGCATGGAAGTGGAGATGGAACG
CGATTCGACTCATCCTTGGATCCTTTTTGGTTTGACATTTTATACAGCATACGTTCCAATTTCTTTTGCGA
AGAGGATAGACAGGATGCAAAAACTGCCATGGCACACATGTATCGCGAGTTTGTTTACACACCCATCC
ACACCATAACGGGGCAGGTTCTTGTCAAGAAGCTTGGAAATAACAGTGGACAGCCAAGCACTGTTGTT
GATAACACGCTTATCCTGATGCTGTCATTTCT

>NC_014037.1_Sugarcane_streak_mosaic_virus_complete_genome

AATGGCAAATTTGGTATTTGGAAGGCTTCTCTAAAGGCTGAGCTCCGACCACTCGAAAAGGTACAACA
GCACAAGACTAGGGTTTTCACGGCAGCACCCTTTGATGTCTCATTTGGAGCTAAAGCCTTTGTTGATGG
CTTTAATAACAAATTTTATGAGAGACAAGCTGGGTCACACTGGACTGTCGGAATCAACAAATTTAACTG
TGGATGGGACGAGCTAGCGAGAAGATTTGACCACAACTGGAAGTTCATTGACGCGGACGGTTCAAGA
TACGACAGTTCCCTTACACCACTGCTTTTCAATTGTGTGCTACGTATCAGAGAACACTTTATGGACCTTG
ATGAAGATGAAAAGCGCTGTTTGCGGAACTTGTACACTCAGCTCGTTTGGACCCCAGTGTCAACCATCA

CAGGCCAGATTGTGAAGAAGTGTAAAGGTGGGCCATCAGGACAACCATCAACAGTTGTGGATAACACC
CTTATGCTCATGATTGCCGTTGA

>NC_012799.1_Triticum_mosaic_virus_complete_genome

ACTGGTAAGTTAGGATTATGGAAAGCTTCGCTTAAAGCTGAGTTGAGACCGAAAGAAAAAGTGCTTGA
GAAGAAGACACGTGTGTTTACAGCAGCACCGTTTGATGTGTCTTTTGGCGCGAAGGCATTTGTTGACGA
TTTTAATAATAAATTTTATGCTACACAGGCAGGCTCGAATTGGACTGTTGGGATAAACAAATTTAATTGT
GGCTGGGATGAACTAGCACGTCGATTTAATCCAGATTGGAAATTCATTGATGCTGATGGTTCAAGATAT
GATAGCAGTTTAACCCCTCTGTTGTTTAATGCTGTGTTGCGAATCAGGCAACACTTTTTAAGGGCTAACG
GTTTTGAAAGAAGAATGTTAAGTAATTTTTATACACAATTAGTTTGGACTCCAATTTCAACAATCACAGG
ACAAATTGTGAAGAAAAACAAAGGGGGACCGTCTGGCCAGCCTTCAACCGTCGTAGACAATACCATGA
TGTTGATGATAGCAGTTGA

>NC_018572.1_Caladenia_virus_A_complete_genome

GAAGGGAAAATGGGCGTGTGGAATGCTTCGCTAAAGGCAGAGTTGAGGCCAATTGAAAAAGTGCAAC
AACACAAAACCAGGGTTTTTATGGCCGCACCATTCTGTACGCTAATTGCTGGCAAATGCTACGTCGACA
ATTTCAACAAGTTATTTTATACCAGGCAACAAGGAAGCCGATGGACAGTTGGCATCAATAAATTCAATT
GTGGTTGGCACGAACTAGCAACAAGGTTCAATCATAACTGGAAATTTCTTGACGCAGATGGCTCCCAGT
ATGATAGCAGCCTAACACCGCTTCTCTTTGATGCTGTGTACCAGATACGCGCATATTTTTTGCAAGCTGA
AGAGGACGATTTGCAGTGTTTGAGAAATTTATATACACAATATGTCTGGACCCCAGTTGCACTTTCAACT
GGTCAGATAATTAAGAAGAACAAAGGTGGACCAAGTGGGCAACCCTCAACAGTCGTGGATAACACCTT
AATGCTAATGATCACAGTGGA

>NC_005904.1_Hordeum_mosaic_virus_complete_genome

AATGGCAAGCTAGGAGTTTGGAACGGATCGCTCAAAGCAGAGTTGAGGCCCAACGAAAAGGTGGAAG
CGAATAAAACAAGAGTATTTACAGCTGCTCCACTTGATACGCTACTAGCAGCTAAAGGGTGCGTGGAC
GATTTCAATAACCAATTTTATGACGCACATCTTAAGGGCCCATGGACTGTTGGTATAACCAAATTTAAAG
GCAGGTGGAACGACTTTCTACGATTACTGCCAGATGGATGGGTGTATTGCGATGCTGACGGTTCACAA
TTCGATAGTTCACTCACGCCTTATCTGATAAACGCAGTGTTAAATTTGCGATTACAATTCATGGAGGATT
GGGCCATTGGGAAGGAGTGTCTCGCTAACTTGTACACTGAAATTGTATACACTCCTATAGCAACACCTG
ATGGATCAGTGGTTAAGAAGTACCGGGGAAACAACAGCGGTCAACCGTCAACAGTGGTTGACAACAC
ATTAATGGTGGTGTTGGCGATGCA

>NC_005903.1_Agropyron_mosaic_virus_complete_genome

GAAGGAAAGTTTGGTGTATGGAACGGATCGTTGAAAGCTGAGCTTAGACCAAATGCAAAGGTTGAAG
CGAACAAAACCCGAGTCTTCACAGCAGCACCTCTGGACACACTTCTTGCAGCGAAGGGTTGTGTTGACG
ACTTCAACAACCAATTCTATAGCAAGCACCTCGAAGGCCCGTGGACGGTGGGAATCACAAAATTCAAA
GGCCGATGGAACGATTTTCTTCGTCTCTTACCGGATGGGTGGATCTATTGCGATGCGGATGGTTCTCAA
TTTGATAGCTCATTAACTCCTTATCTCATAAACGCCATTCTCAATGTTCGATTGCAGTTCATGCAGGAATG
GAACATTGGAAAGAGATGTTTGGAGAACCTCTACACTGAAATTGTCTACACAGCCATAGCAACTCCAGA

TGGGTCAGTCATTAAGAAGTTCAGAGGGAACAATAGCGGACAGCCATCAACAGTCGTTGACAATACAT
TAATGGTTGTCTTAGCTATGCA

>NC_001814.1_Ryegrass_mosaic_virus_complete_genome

GAAGGAAAAATGGGAATTTGGAATGGATCTTTGAAAGCCGAGCTGAGATCGAAGGAGAAGGTTGAAG
CAAATAAAACACGCGTATTCACAGCAGCACCGCTCGATACACTATTGGCTGGCAAAGGATGCGTTGAT
GATTTTAACAATCAATTTTACGCGGCACACTTGAAAGGACCATGGACGGTTGGCATTACAAAGTTCTTT
GGACGCTGGAACGATTTCTTGAGCGAACTGCCACCTGGTTGGGATTACTTTGATGCTGATGGATCGCG
ATTTGATAGTTCCCTCACACCCTTTCTCCTAAACGCTGTTCTTAACATTCGCAAGAAATTCATGATCAATT
GGGCTTTTGGTCAGCGGTGTTTAGGAAATTTATACACTGAAATCATTTACACACCGATAGCAACTCCAG
ATGGTTCTGTAGTCAAGAAAATGCGTGGAAACAATAGCGGACAGCCATCCACCGTCGTCGATAACACA
ATTATGGTCATAATAGCAATGCA

>NC_009805.1_Wheat_eqlid_mosaic_virus_complete_genome

AAGAATGGACATGGAGTTTGGTCAGCTTTGCTGAAAGCTGAACTCAGGCCTGCAGCCAAAGTGGTGGC
CCAGAAGACACGGACTTTCACGTCCGCACCTATCGACACTTTGCTTGGTGCGAAAATTGTGGTGGACGA
CTTTAACAAGAAGTTCTATTCCCTGCACCTGAAAGGTCCGTGGACAGTCGGAATTAATAAATTCAATGC
AGGATGGAACATTTTGGCTGAGAGCTTGTCGCACTTCACTCATTACATAGACGCGGATGGCTCGCAGTT
TGATAGCTCAATCACGCCTTTGTTAATGAATGCTGTGCTCAACATTCGATTGTATTTCTTAGAGCGTGAT
GATGAAGCTGAGTGTATGCTCAAGAATCTCTACACGCAGATTATCCACACTTGCATTCTCATTGGCGAT
GGTACTATTGTTCAGAAGTTCCGTGGAAACAATAGCGGACAGCCTGGCACAGTGGTAGATAACACTCT
GTGTTTGATGATCGCTGTTGA

>NC_005136.1_Oat_necrotic_mottle_virus_complete_genome

GGAAATGGACATGGCGTGTGGTCAGGATTGCTGAAAGCTGAGCTCAGACCGAAAGCAAAAGTGGTGG
CAAACAAGACGCGCACTTTCACTTCAGCACCAGTTGATATTCTAATGGGAGCCAAGGCGGTCGTGGAT
GAGTTCAATAAATTTTTCTATACGAAACACCTCCGAGGCCCGTGGACTGTTGGGATTAACAAATTCAAC
TGTGGATGGAATCTTCTGGCAGAGAGCCTGATGGTGCATGAGTGGTTTATCGATGCAGACGGGTCGCA
ATTTGATAGCTCGATAACACCACTCCTTATGAATGCTGTTCTGAACATCAGACAATATTTCATGGCGGAC
GAAGAAGAGGCCCAAACGATGCTTGCAAACCTGTACACGCACATCATAAACACATGCATACTCATAGA
AGATGGCACAATTGTACAGAAATTCAGAGGCAACAACAGTGGTCAGCCGAGTACTGTTGTCGATAATA
CGCTGTGCCTAATCATGGCAATGGA

>NC_003501.1_Brome_streak_mosaic_virus_complete_genome

GCAAATGGGCACGGAGTGTGGTCAGCTCTCCTGAAGGCTGAGTTACGTCCAGCTGAGAAGGTTGCAGC
CAACAAGACGAGAACATTCACATCAGCGCCCATCGACATCTTATTCGGAGCAAAGGCTGTGGTAGACG
ATTTCAATAAGCAATTTTACAAGCGACATCTACTAGGTCCTTGGACTGTTGGTATAAACAAGTTCAACAA
GGGCTGGGACTTACTTGCACGATCGTTGATGCGCTATGAATGGTTTATTGATGCAGACGGATCACAATT
CGACAGCTCAATAACGCCGTTGCTCATGAATGCTGTTCTAACAATAAGGTTGTACTTCATGGAGCGAGA
CGATATCACTGAGCTCATGTTGAGGAATTTGTACACTCAAATCATCAGTACATGCATGCTCGCAGAGGA

TGGCTTAATAGTGCAAAAGCATCGAGGAAACAATAGTGGCCAACCAAGCACAGTTGTGGATAATACTC
TGTGCTTGATGATAGCAATGGA

>NC_024471.1_Yellow_oat-grass_mosaic_virus_isolate_YOgMV-Sb_complete_genome

GGAAATGGACATGGTGTATGGTCGGGTTTACTAAAAGCTGAACTCAGGCCAAAAGCAAAGGTATCCCA
AGGGAAGACGCGGACTTTCACTTCAGCACCTGTTGACATACTAATGGGGGCAAAAAGCGTTGTGGATG
ATTTTAATAAGTTGTTCTATTCCCGACACCTACGAGGACCTTGGACAGTAGGAATAAACAAATTTAATG
GTGGGTGGAACTTACTCGCAGGGAGCCTCACTAAGCACGAGTGGTATATAGGTGCGGATGGGTCGCA
GTTTGACAGTTCGATCACACCATTGCTCATGAATGCCATTCTCAATATACGGCAATACTTCATGGAGGAT
GACGAGGACGCAAACACTATGTTGGCCAACTTGTACACACAGATCATAAACACATGCATCCTCATTGAA
GACGGCACCATAGTCCAGAAGTACAGAGGTAACAACAGTGGCCAACCTAGCACAGTCGTAGACAACAC
AATGTGCCTCATCATTGCAATGGA

>NC_022745.1_Tall_oatgrass_mosaic_virus_isolate_Benesov_complete_genome

AGCAATGGACATGGTGTGTGGTCAGGGTTATTGAAAGCGGAACTAAGGCCAAAAGCTAAGGTAGATG
CCAACAAGACTCGAACTTTCACGTCAGCGCCTGCTGATATACTTATGGGAGCAAAGGCGGTAGTGGAT
GAGTTCAACAAGAAGTTCTACACGCAGCACCTAAAAGGCCCGTGGACTGTAGGAATTAACAAGTTTAA
TAGAGGGTGGGACCTACTAGCGAAGAATCTGCAAGAGCATGAATGGTACATAGATGCAGATGGTTCA
CAATTCGATAGTTCAATCACACCTCTCCTGATGAATGCAGTTCTTAATATAAGATTATATTTCTTAGAGG
AGGATAATGTGGGCGAAACCATGCTGAAAAATCTATACACCCAAATAATAAATACGTGCATATTAATAG
AGGACGGAACTATAGTGCAAAAATATAGAGGTAATAATAGTGGACAACCTAGTACAGTTGTTGATAAT
ACTATGTGTTTAATAATTGCTATGGA

>NC_001886.1_Wheat_streak_mosaic_virus_complete_genome

AGTAACGGACATGGAGTATGGTCTGGTTTACTCAAAGCTGAGTTGAGACCGAAGGCAAAGGTCGTGG
CGAACAAAACGCGAACATTCACATCAGCACCAATTGATATACTCATGGGTGCCAAAGCTGTGGTTGATG
AGTTCAACAAATTCTTCTACACAAAGCATTTGCGCGGACCATGGACTGTCGGAATCAATAAGTTCAACG
GAGGTTGGGATTTGTTGGCCAAAAATTTAATGGTGCACGAGTGGTTCATTGACGCTGATGGTTCGCAA
TTCGACAGTTCAATCACTCCACTTCTCATGAATGCAATTCTTAACATACGGCAATACTTCATGGCAGAAG
ATGATGAAGCTGAACAAATGCTGGCAAATTTGTATACGCAGATTATAAACACATGCATTTTAATTGAAG
ATGGAACGATTGTGCAGAAGTTTCGAGGTAATAACAGTGGCCAACCAAGCACAGTTGTTGACAACACG
ATGTGTTTAATCATAGCAATGGA

	LMV	PPV	PVMV	PVY	SPFMV	TEV	WMV	Genus
gi|189009878|ref|NC 010736.1| Algerian watermelon mosaic virus	68.5	70.5	65.3	67.3	69.1	67.5	64.7	*Potyvirus*
gi|318054196|ref|NC 014905.1| Apium virus Y	72.1	73.9	68.5	64.5	73.1	66.9	66.1	*Potyvirus*
gi|396587253|ref|NC 018176.1| Arracacha mottle virus	67.7	70.3	67.7	68.5	69.9	67.1	63.7	*Potyvirus*
gi|156447513|ref|NC 009745.1| Banana bract mosaic virus	69.7	67.7	60.6	68.5	70.1	69.5	64.1	*Potyvirus*
gi|156447515|ref|NC 009741.1| Basella rugose mosaic virus	68.5	68.9	67.1	68.9	70.5	65.9	62.2	*Potyvirus*
gi|21553928|ref|NC 004047.1| Bean common mosaic necrosis virus	70.1	71.7	66.3	66.7	71.7	68.1	71.7	*Potyvirus*
gi|18677787|ref|NC 003397.1| Bean common mosaic virus	68.1	69.9	63.7	65.5	71.7	68.1	70.9	*Potyvirus*
gi|19881394|ref|NC 003492.1| Bean yellow mosaic virus	71.7	71.9	67.7	68.1	71.7	69.1	68.1	*Potyvirus*
gi|40254027|ref|NC 005304.1| Beet mosaic virus	71.7	71.5	68.5	67.1	70.9	69.3	64.3	*Potyvirus*
gi|564614857|ref|NC 023014.1| Bidens mosaic virus	70.1	71.1	67.5	74.9	69.7	67.1	65.5	*Potyvirus*
gi|301173441|ref|NC 014325.1| Bidens mottle virus	69.1	69.3	65.9	71.5	70.3	69.3	64.7	*Potyvirus*
gi|414090072|ref|NC 019415.1| Blue squill virus A	69.1	69.7	65.7	66.1	71.7	69.5	72.5	*Potyvirus*
gi|307563838|ref|NC 014536.1| Brugmansia suaveolens mottle virus	70.9	69.9	66.9	71.5	70.3	67.3	65.5	*Potyvirus*
gi|259120449|ref|NC 013261.1| Canna Yellow Streak Virus	68.5	71.9	67.3	68.1	68.9	70.1	67.1	*Potyvirus*
gi|330370639|ref|NC 015393.1| Celery mosaic virus	72.5	74.1	66.7	68.1	69.3	71.1	66.7	*Potyvirus*
gi|349641625|ref|NC 016044.1| Chilli ringspot virus	69.1	71.3	70.1	64.9	70.7	68.7	65.1	*Potyvirus*
gi|45004654|ref|NC 005778.1| Chilli veinal mottle virus	68.5	69.1	72.9	64.5	66.3	65.9	62.3	*Potyvirus*
gi|20087030|ref|NC 003536.1| Clover yellow vein virus	72.1	73.1	66.9	67.3	70.3	71.1	67.3	*Potyvirus*
gi|20428636|ref|NC 003742.1| Cocksfoot streak virus	70.3	68.9	64.9	67.5	66.9	67.3	62.0	*Potyvirus*
gi|440382952|ref|NC 020072.1| Colombian datura virus	67.5	70.3	64.1	65.5	68.1	72.3	65.5	*Potyvirus*
gi|21427633|ref|NC 004013.1| Cowpea aphid-borne mosaic virus	69.1	72.3	65.5	65.7	69.7	69.3	71.9	*Potyvirus*
gi|96980660|ref|NC 008028.1| Daphne mosaic virus	68.1	68.5	66.5	65.3	66.3	66.1	66.1	*Potyvirus*
gi|20087054|ref|NC 003537.1| Dasheen mosaic virus	68.1	70.3	63.7	65.7	69.7	66.9	70.7	*Potyvirus*
gi|85677473|ref|NC 007728.1| East Asian Passiflora virus	68.9	70.9	66.3	66.5	71.1	68.1	71.5	*Potyvirus*
gi|298388366|ref|NC 014064.1| Freesia mosaic virus	48.9	50.5	52.0	47.6	49.5	50.4	48.0	*Potyvirus*
gi|190336494|ref|NC 010954.1| Fritillary virus Y	68.9	72.3	66.1	66.1	71.3	67.7	73.9	*Potyvirus*
gi|526118368|ref|NC 021786.1| Habenaria mosaic virus	66.3	69.1	68.3	64.1	68.7	67.3	63.3	*Potyvirus*
gi|335352402|ref|NC 015394.2| Hardenbergia mosaic virus	69.3	68.7	63.1	64.5	71.5	68.3	70.9	*Potyvirus*
gi|388570304|ref|NC 017967.1| Hippeastrum mosaic virus	68.7	71.3	65.1	62.4	70.7	70.3	63.5	*Potyvirus*
gi|408905828|ref|NC 018833.1| Iranian johnsongrass mosaic virus	71.1	69.5	67.1	67.5	68.7	69.5	66.1	*Potyvirus*
gi|9633628|ref|NC 000947.1| Japanese yam mosaic virus	70.3	71.1	67.7	66.9	71.1	72.3	65.7	*Potyvirus*
gi|20153407|ref|NC 003606.1| Johnsongrass mosaic virus	71.1	70.7	67.1	67.9	69.3	70.1	66.7	*Potyvirus*
gi|358356468|ref|NC 016159.1| Keunjorong mosaic virus	68.7	68.9	63.5	65.1	68.7	69.5	66.9	*Potyvirus*
gi|90093251|ref|NC 007913.1| Konjac mosaic virus	68.3	71.3	65.9	66.7	70.5	69.5	60.8	*Potyvirus*
gi|21427635|ref|NC 004011.1| Leek yellow stripe virus	71.1	72.7	65.3	65.9	70.9	68.7	66.7	*Potyvirus*
gi|20153339|ref|NC 003605.1| Lettuce mosaic virus	94.0	70.3	66.5	65.1	69.5	68.1	65.1	*Potyvirus*
gi|39163614|ref|NC 005288.1| Lily mottle virus	67.7	71.7	65.3	67.9	70.9	70.3	64.9	*Potyvirus*
gi|319774833|ref|NC 014898.1| Lupine mosaic virus	66.3	70.3	65.7	63.9	68.1	66.1	64.3	*Potyvirus*
gi|18490052|ref|NC 003377.1| Maize dwarf mosaic virus	68.9	73.1	67.3	65.5	70.9	69.9	66.5	*Potyvirus*
gi|160700540|ref|NC 009995.1| Moroccan watermelon mosaic virus	69.9	70.9	65.1	66.7	69.9	65.7	66.1	*Potyvirus*
gi|124249189|ref|NC 008824.1| Narcissus degeneration virus	67.3	69.9	64.7	64.3	70.3	68.1	65.1	*Potyvirus*
gi|589875219|ref|NC 023628.1| Narcissus late season yellows virus isolate	72.3	73.7	66.9	67.1	69.5	69.9	65.5	*Potyvirus*
gi|212499141|ref|NC 011541.1| Narcissus yellow stripe virus	71.7	74.1	67.9	65.7	72.5	69.5	66.5	*Potyvirus*
gi|32490546|ref|NC 005029.1| Onion yellow dwarf virus	64.3	69.3	65.1	65.5	67.7	67.3	63.3	*Potyvirus*
gi|414089216|ref|NC 019409.1| Ornithogalum mosaic virus	68.9	69.3	67.3	63.1	67.7	69.3	62.0	*Potyvirus*
gi|298531304|ref|NC 014252.1| Panax virus Y	69.3	71.1	68.7	65.5	69.9	69.9	65.1	*Potyvirus*
gi|32490548|ref|NC 005028.1| Papaya leaf-distortion mosaic virus	67.5	67.5	65.7	66.9	69.3	70.3	68.5	*Potyvirus*
gi|9629244|ref|NC 001785.1| Papaya ringspot virus	70.1	69.7	65.7	66.5	67.7	65.1	65.7	*Potyvirus*
gi|448261108|ref|NC 014790.2| Passion fruit woodiness virus	68.1	70.7	65.3	65.5	68.5	68.9	70.5	*Potyvirus*
gi|9628429|ref|NC 001671.1| Pea seed-borne mosaic virus	69.7	69.3	65.5	65.7	71.3	68.9	65.1	*Potyvirus*
gi|11072108|ref|NC 002600.1| Peanut mottle virus	70.1	69.3	65.7	66.3	72.1	68.3	66.5	*Potyvirus*
gi|68299603|ref|NC 007147.1| Pennisetum mosaic virus	70.7	73.5	66.3	67.3	68.7	69.7	64.5	*Potyvirus*
gi|9627034|ref|NC 001517.1| Pepper mottle virus	70.5	70.3	66.5	69.9	71.1	67.9	63.9	*Potyvirus*
gi|115357968|ref|NC 008393.1| Pepper severe mosaic virus	70.5	71.7	68.3	70.1	69.5	65.3	67.7	*Potyvirus*
gi|221048141|ref|NC 011918.1| Pepper veinal mottle virus	69.5	68.1	96.4	65.5	66.9	64.3	63.9	*Potyvirus*
gi|301173451|ref|NC 014327.1| Pepper yellow mosaic virus	69.9	70.9	66.1	72.5	71.7	70.7	65.3	*Potyvirus*
gi|28492878|ref|NC 004573.1| Peru tomato mosaic virus	71.1	72.9	65.1	70.9	67.1	70.9	65.9	*Potyvirus*
gi|9626508|ref|NC 001445.1| Plum pox virus	70.3	98.4	65.9	66.3	72.1	69.7	66.3	*Potyvirus*
gi|554967333|ref|NC 018872.2| Pokeweed mosaic virus	73.9	73.5	67.1	67.1	70.3	67.5	66.5	*Potyvirus*
gi|21492611|ref|NC 004039.1| Potato virus A	70.9	70.7	67.1	65.9	71.7	67.7	65.1	*Potyvirus*
gi|21431571|ref|NC 004010.1| Potato virus V	71.5	74.3	67.5	69.5	69.1	69.5	66.9	*Potyvirus*
gi|9627728|ref|NC 001616.1| Potato virus Y	68.1	70.5	65.5	83.1	69.5	67.7	65.9	*Potyvirus*
gi|18652416|ref|NC 003399.1| Scallion mosaic virus	70.5	73.1	70.5	65.9	71.9	71.1	67.1	*Potyvirus*
gi|76803354|ref|NC 007433.1| Shallot yellow stripe virus	69.7	70.3	67.7	64.5	68.3	68.5	67.5	*Potyvirus*
gi|21449930|ref|NC 004035.1| Sorghum mosaic virus	71.5	69.7	69.1	65.5	69.1	66.5	64.9	*Potyvirus*
gi|12018225|ref|NC 002634.1| Soybean mosaic virus	67.5	73.3	66.5	65.1	71.1	69.3	76.7	*Potyvirus*
gi|18652414|ref|NC 003398.1| Sugarcane mosaic virus	70.9	69.9	66.5	68.3	66.9	70.1	65.3	*Potyvirus*
gi|294872884|ref|NC 014038.1| Sunflower chlorotic mottle virus	71.3	69.5	65.1	72.7	71.1	68.9	65.7	*Potyvirus*
gi|9629730|ref|NC 001841.1| Sweet potato feathery mottle virus	69.1	71.9	65.7	67.9	90.0	68.3	67.1	*Potyvirus*
gi|475155116|ref|NC 020896.1| Sweet potato latent virus	69.7	73.7	66.7	67.1	71.3	72.9	64.7	*Potyvirus*
gi|388570521|ref|NC 017970.1| Sweet potato virus 2	70.3	74.9	66.1	66.5	74.3	69.9	66.1	*Potyvirus*
gi|313139317|ref|NC 014742.1| Sweet potato virus C	70.9	71.9	66.3	66.9	79.3	68.9	65.7	*Potyvirus*
gi|393248211|ref|NC 018093.1| Sweet potato virus G	70.9	74.1	68.9	68.3	74.5	70.9	65.3	*Potyvirus*
gi|156447517|ref|NC 009742.1| Telosma mosaic virus	69.9	70.7	67.3	65.1	69.9	67.5	73.3	*Potyvirus*
gi|68989216|ref|NC 007180.1| Thunberg fritillary virus	68.9	73.7	62.4	66.7	68.5	69.1	66.1	*Potyvirus*
gi|9790340|ref|NC 001555.1| Tobacco etch virus	69.7	71.9	64.3	67.1	68.9	96.0	68.3	*Potyvirus*
gi|160700528|ref|NC 009994.1| Tobacco vein banding mosaic virus	68.9	71.3	69.1	64.5	66.1	71.9	61.8	*Potyvirus*
gi|9629179|ref|NC 001768.1| Tobacco vein mottling virus	74.3	73.3	67.1	68.7	70.1	67.9	67.3	*Potyvirus*
gi|386522667|ref|NC 017824.1| Tomato necrotic stunt virus	72.1	72.7	68.7	70.1	72.5	70.1	68.1	*Potyvirus*
gi|56407093|ref|NC 002509.2| Turnip mosaic virus	70.5	73.1	67.1	69.1	69.5	72.5	67.1	*Potyvirus*
gi|388570618|ref|NC 017977.1| Vallota speciosa virus	66.5	68.3	66.7	65.1	69.5	66.9	63.3	*Potyvirus*
gi|189009876|ref|NC 010735.1| Verbena virus Y	69.9	71.3	69.5	70.3	69.3	68.1	62.7	*Potyvirus*
gi|51949945|ref|NC 006262.1| Watermelon mosaic virus	69.1	71.1	65.7	66.9	71.3	69.1	92.2	*Potyvirus*
gi|25140980|ref|NC 004426.1| Wild potato mosaic virus	71.3	70.9	65.5	72.1	66.3	68.9	64.5	*Potyvirus*
gi|156447521|ref|NC 009744.1| Wild tomato mosaic virus	67.9	71.7	74.5	63.9	67.3	65.7	63.5	*Potyvirus*
gi|71647082|ref|NC 007216.1| Wisteria vein mosaic virus	68.9	70.5	67.7	67.5	73.5	70.1	74.5	*Potyvirus*
gi|360040872|ref|NC 016441.1| Yam bean mosaic virus	68.9	69.9	64.9	67.3	73.3	67.1	72.5	*Potyvirus*
gi|414089934|ref|NC 019412.1| Yam mild mosaic virus	67.5	68.1	69.7	66.9	70.7	68.5	65.9	*Potyvirus*
gi|30146781|ref|NC 004752.1| Yam mosaic virus	70.7	73.3	67.7	68.7	72.3	70.1	68.7	*Potyvirus*
gi|212525937|ref|NC 011560.1| Zantedeschia mild mosaic virus	70.5	70.1	65.9	66.5	69.1	67.3	69.9	*Potyvirus*
gi|570364799|ref|NC 023175.1| Zucchini tigre mosaic virus	67.9	69.3	64.5	65.5	71.1	66.3	64.9	*Potyvirus*
gi|17059637|ref|NC 003224.1| Zucchini yellow mosaic virus	68.7	68.9	63.7	64.1	68.9	67.7	72.3	*Potyvirus*
NC 008558.1 Blackberry virus Y	61.2	60.2	55.3	57.1	59.6	59.8	56.1	*Brambyvirus*
AY994084.1 Blackberry virus Y	61.2	60.2	55.3	57.1	59.6	59.8	56.1	*Brambyvirus*
NC 002350.1 Wheat yellow mosaic virus	56.6	53.6	58.2	56.2	58.6	56.0	54.4	*Bymovirus*
NC 004016.1 Oat mosaic virus	56.2	60.0	56.6	57.2	58.8	58.8	55.0	*Bymovirus*
NC 002990.1 Barley yellow mosaic virus	57.1	57.1	56.5	54.3	56.7	59.6	56.7	*Bymovirus*
NC 028144.1 Rice necrosis mosaic virus	59.6	57.4	58.8	54.4	59.6	60.0	56.8	*Bymovirus*
NC 003483.1 Barley mild mosaic virus	57.2	55.0	58.0	55.4	57.0	58.6	55.4	*Bymovirus*
NC 030840.1 Coccinia mottle virus	63.1	61.1	62.9	60.5	58.9	62.5	58.1	*Ipomovirus*
NC 010521.1 Squash vein yellowing virus	60.7	62.9	58.5	56.3	63.3	60.7	56.3	*Ipomovirus*
NC 014791.1 Ugandan cassava brown streak virus	58.7	58.9	58.9	57.9	62.5	60.3	56.9	*Ipomovirus*
NC 006941.1 Cucumber vein yellowing virus	62.7	60.5	62.7	60.3	62.7	60.9	56.7	*Ipomovirus*
NC 003797.1 Sweet potato mild mottle virus	61.9	63.3	60.7	56.9	61.5	64.5	59.9	*Ipomovirus*
NC 012698.2 Cassava brown streak virus	59.1	60.1	60.7	55.8	63.5	61.7	57.1	*Ipomovirus*
NC 026759.1 Artichoke latent virus	58.0	58.4	59.2	55.7	56.6	58.6	55.1	*Macluravirus*
NC 018455.1 Chinese yam necrotic mosaic virus	57.8	57.8	59.4	55.3	56.3	58.8	56.8	*Macluravirus*
NC 014037.1 Sugarcane streak mosaic virus	59.6	58.6	57.1	58.8	58.6	57.9	57.7	*Poacevirus*
NC 012799.1 Triticum mosaic virus	59.6	58.4	57.5	57.1	58.1	56.3	57.1	*Poacevirus*
NC 018572.1 Caladenia virus A	58.4	57.5	56.1	55.9	56.9	59.2	56.5	*Poacevirus*
NC 005904.1 Hordeum mosaic virus	68.2	69.6	64.0	66.0	69.0	68.2	62.8	*Rymovirus*
NC 005903.1 Agropyron mosaic virus	70.0	69.4	65.0	62.6	68.6	66.4	62.8	*Rymovirus*
NC 001814.1 Ryegrass mosaic virus	68.8	67.2	62.2	66.0	65.6	65.8	60.6	*Rymovirus*
NC 009805.1 Wheat eqlid mosaic virus	61.8	61.4	57.7	58.6	59.4	58.8	58.6	*Tritimovirus*
NC 005136.1 Oat necrotic mottle virus	61.4	62.2	60.2	59.6	61.6	58.6	58.4	*Tritimovirus*
NC 003501.1 Brome streak mosaic virus	61.6	62.2	59.2	60.4	61.8	63.8	59.0	*Tritimovirus*
NC 024471.1 Yellow oat-grass mosaic virus	61.8	61.2	55.1	60.8	59.0	59.2	55.9	*Tritimovirus*
NC 022745.1 Tall oatgrass mosaic virus	61.0	63.2	58.6	61.6	62.2	59.2	59.4	*Tritimovirus*
NC 001886.1 Wheat streak mosaic virus	63.4	64.8	61.2	62.4	62.8	62.8	60.4	*Tritimovirus*