This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

**Part 1:** **TITLE, AUTHORS, etc**

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| **Code assigned:** | ***2019.016P*** |  |
| **Short title:** Create eight new species in the genus *Potyvirus* |
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| **Author(s) and email address(es):** |
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 |
| **Corresponding author** |
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| **List the ICTV study group(s) that have seen this proposal:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ***Potyviridae*** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
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| Date first submitted to ICTV: |       |
| Date of this revision (if different to above): |       |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
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**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2019.016P.A.v1.Potyvirus\_8sp.xlxs |

Eight proposed new species within genus *Potyvirus* are described below. Phylogenetic placement is indicated in Figure 1.

**Dendrobium chlorotic mosaic virus**

A newly-described virus, tentatively named dendrobium chlorotic mosaic virus (DeCMV), was detected in plants of *Dendrobium smillieae* showing chlorotic and mosaic symptoms. DeCMV isolate 98-De-31 was found in an infected plant growing in an orchid farm located in Puli Township of Nantou County, Taiwan (Huang *et al*., 2019). The isolate was transmitted to dendrobium orchids by grafting and mechanical inoculation. The vector was not identified. Potyvirus-like, flexuous filamentous particles were observed under an electron microscope, measuring approximately 700-800 nm in length and 11-12 nm in diameter.

Total RNA was prepared from symptomatic dendrobium leaves, and then the reverse transcription-polymerase chain reaction (RT-PCR) was carried out using degenerate potyvirid primer pairs. The full-length sequence of DeCMV-98-De-31 was assembled from nine overlapping fragments independently amplified by RT-PCR.

The entire nucleotide sequences of the genome were obtained using the Sanger sequencing method. The genome was 10,041 nucleotides in length and assigned GenBank accession MK241979. It was predicted to encode a polyprotein of 3,189 amino acid residues, which is predicted to be cleaved into 10 polypeptides *via* proteolysis at specific cleavage sites. It displayed organizational features typical of viruses in genus *Potyvirus*.

Sequence analyses revealed that the DeCMV-98-De-3 coat protein gene shared 59.6-66.0% nucleotide sequence identities and its deduced amino acid sequence shared 57.6-66.0% identities with CPs of other potyviruses. The complete genome shared 54.1-57.3% nucleotide sequence identities and 43.7-49.5% amino acid sequence identities with other known potyviruses. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities based upon the large ORF, which suggests dendrobium chlorotic mosaic virus represents a novel species in genus *Potyvirus*.

Thus,the *Potyviridae* study group proposes that dendrobium chlorotic mosaic virus represents a new species, named *Dendrobium chlorotic mosaic virus*, within the genus *Potyvirus*, with ’98-De-31” (DeCMV-98-De-31) being the exemplar isolate.

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**Dioscorea mosaic virus**

A newly-described virus, tentatively named Dioscorea mosaic virus (DiMV) isolate FL, was detected in air potato (*Dioscorea bulbifera*) showing foliar mosaic symptoms. DiMV isolate FL (Florida) isolate was found in plants growing in the Florida Department of Agriculture and Consumer Services Division of Plant Industry Biological Control Laboratory II in Alachua County, Florida, U.S.A. (Dey *et al*., 2019). The DiMV-infected plant was co-infected with an ampelovirus. The vector was not identified.

Double-stranded (ds) RNAs of approximately 15 kbp in size were isolated from plant tissue. A library was prepared for high-throughput sequencing. The 5′ terminal sequence was determined using RLM-RACE, and the 3’ terminal sequence was determined with an oligo-dT(15) primer targeting the poly(A) terminus.

The complete genome sequence of a DiMV-FL isolate was 9,550 nucleotides in length and assigned GenBank accession MH206616. It was predicted to encode a polyprotein of 3,054 amino acid residues, and displayed the organization of a typical potyvirus.

The DiMV-FL polyprotein was most similar to that of the potyvirus yam mild mosaic virus (YMMV), with 62% nucleotide identity and 52% amino acid identity. The CP gene shared greatest nucleotide identity with that of the potyvirus sweet potato latent virus isolate HN76 (72%). The nucleotide identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities based upon the large ORF, which suggests DiMV represents a novel species.

Thus, the *Potyviridae* study group proposes that Dioscorea mosaic virus represents a new species, named *Dioscorea mosaic virus*, within the genus *Potyvirus*, with DMV-FL being the exemplar isolate.

**East Asian passiflora distortion virus**

A newly-described virus, tentatively named East Asian passiflora distortion virus (EAPDV), was detected in passionfruit plants (*Passiflora edulis* x *P. edulis* f. *flavicarpa*) showing foliar mosaic, leaf curl and fruit malformation. Four isolates were characterized, EAPDV-AK from Akita Prefecture (2013, nursery shop), EAPDV-OK from Okinawa Prefecture (2014, Agriculture Research Center), EAPDV-SA from Satsuma Prefecture and EAPDV-YO from Yoron Island, the last two in Kagoshima Prefecture (2015, fields) (Riska *et al*., 2019).

The four isolates were characterized and the complete genome sequenced: PV-AK (LC379162), PV-OK (LC373083), PY-YO (LC377302), and PV-SA (LC375413). The virus can be transmitted mechanically, producing local lesions in *Chenopodium amaranticolor*, *Phaseolus vulgaris* cvs. Canario, Pinto 111, Red Kidney, Sujinashi-Edogawa, Taisho-Kintoki, Rico 23, and Rosinha; producing local lesions, and leaf curling and mosaic in *P. foetida*; local lesions, and leaf curling and systemic necrosis in *P. vulgaris* cvs. Hon-Kintoki, Kairyo-Ohtebou; local lesions and a latent infection in *P. vulgaris* cv. Masterpiece; local lesions and mosaic in *Vigna unguiculata* cv. Kurodane sanjaku; a latent local lesion in *C. quinoa, Nicotiana tabacum* cv. Bright Yellow; a latent infection in *N. benthamiana* and *P. vulgaris* cv. Black Eye; and systemic infection (after grafting) in *P. edulis*, *P. edulis* x *P. edulis* f. *flavicarpa,* and *P. foetida* with leaf curling and mosaic. Virions were visualized as flexuous rods of 780-754 nm at TEM.

RNA preparations were purified from infected leaves of passiflora plants, and used to amplify the genome of EAPDV by RT-PCR using primers designed based on viruses of the bean common mosaic virus group. A total of 8 PCR fragments were amplified, cloned and sequenced (Sanger). The complete genome sequence of the four EAPDV isolates was assembled. The genomes were 9,973-9,974 nucleotides in length. The genome sequences of EAPDV was assigned GenBank accession LC379162, LC375413, LC373083, and LC377302 (see above). Genomes were predicted to encode a polyprotein of 3217 amino acid residues, with 129-130 nt at the 5'UTR, and 193 nt at the 3' UTR. It displayed the organization of a typical potyvirus.

The genome sequence of EAPDV-AK shared a maximum of 68.1% nucleotide identity with watermelon mosaic virus (DQ399708), and 66.3% with bean common mosaic virus (AJ312437). The deduced amino acid sequence of the EAPDV-AK polyprotein shared 70.1% and 65.6% identity, respectively, with these viruses. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities.

Therefore, the *Potyviridae* study group proposes that East Asian passiflora distortion virus represents a new species, *East Asian passiflora distortion virus*, within the genus *Potyvirus*, with EAPDV-AK being the exemplar isolate.

**Gomphocarpus mosaic virus**

A newly-described virus, tentatively named Gomphocarpus mosaic virus (GoMV), was detected in *Gomphocarpus physocarpus* showing mosaic, mottling and crinking. GoMV isolate CM532 was found in infected plants in southwestern Taiwan (Tainan) in 2015 (Chang and Chen, 2018). The virus was transmitted to experimental host species by means of mechanical inoculation, and caused local lesions in *Chenopodium quinoa*, and infected systemically *G. fruticosus* and *Nicotiana benthamiana*. Virions were visualized as flexuous rods (800x12 nm) by TEM, together with pinwheel-shaped and laminated inclusion bodies.

The complete genome sequence of GoMV-CM532 was determined after RT-PCR, cloning and Sanger sequencing. The genome was 9,998 nucleotides in length excluding the poly-A tract. The genome sequence of GoMV-CM532 was assigned GenBank accession LC228573. It was predicted to encode a polyprotein of 3196 amino acid residues. It displayed the organization of a typical potyvirus.

The genome sequence shared a maximum of 68.4% nucleotide identity with the potyvirus Keunjorong mosaic virus (KjMV). The deduced amino acid sequence of the polyprotein shared 75.8% identity with KjMV. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities, which suggests Gomphocarpus mosaic virus represents a novel taxon.

Gomphocarpus mosaic virus shares 99% identity with the sequence of allamanda mosaic virus (LC271190-LC271192), a virus found in allamanda plants in Taiwan (Chao, Wu, Chen). These sequences are partial with only 1670 nt of the 3' genome termini. The date of submission to the sequence database is almost the same as GoMV, August of 2018. It is most likely that the two groups were inadvertently working with the same virus from distinct hosts in the same country. The study of allamanda virus was not published. As GoMV is completely sequenced and its description published, we propose that Gomphocarpus mosaic virus is preferred for this virus.

The *Potyviridae* study group proposes that Gomphocarpus mosaic virus isolate CM532 (GoMV-CM532) represents a novel species, *Gomphocarpus mosaic virus,* within genus *Potyvirus*.

**Lily virus Y**

A newly-described virus, tentatively named lily yellow mosaic virus (LYMV), isolate lily-bua, was detected in lily plants (*Lilium* sp.) showing leaf yellowing, twisting and brownish necrotic spots in 2016 (Li et al., 2018). LYMV-lily-bua was collected in the experimental field of Beijing Agricultural University infecting plants under natural conditions. The virus was identified from an unknown number of plants, at least one of which was co-infected with cucumber mosaic virus (genus *Cucumovirus,* family *Bromoviridae*) and lily symptomless virus (genus *Carlavirus,* family *Betaflexiviridae*). Specific symptoms induced by LYMV in lily plants are not known, and as such the name given to the virus is not based on observed symptoms of yellow mosaic.

Small RNA molecules were purified and sequenced using an Illumina HiSeq2000 platform. The complete genome sequence of LYMV was reported to be assembled from 53 contigs assembled *de novo* from 16-30 nucleotide fragments. If there were gaps between contigs and how they were filled was not reported. Depth of sequence coverage was not discussed. RT-PCR was done with two species-specific primers (LYMV-F and -R) that annealed 1388 nucleotides apart in the HC-Pro cistron, but no sequence analysis was reported from this amplication. The paper also states that RT-PCR with primer pairs targeting different protein regions was carried out, but none of the primer sequences were provided, the purpose of this work was not given, nor was sequence analysis of the amplicons discussed. The 5' and 3' sequence termini were determined by RACE.

The genome was 9811 nucleotides in length. The genome sequence of LYMV-lily-bua was assigned GenBank accession MF543013. The large ORF was flanked by 5’UTR and 3’UTR of 217 and 219 nucleotides, respectively. The predicted large polyprotein was of 3124 amino acid residues. It displayed genome and polyprotein organization of a typical potyvirus, with all of the expected motifs in the expected places.

The genome sequence shared 55% and 60% nucleotide identities (52% amino acid identities) with the potyvirus thunberg fritillary mosaic virus and the proposed potyvirus Platycodon mild mosaic virus, respectively. The coat protein shared greatest identity (71%) with that of pepper veinal mottle virus. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide identity and <82% amino acid identity for the genome and large ORF sequences, respectively, which suggests lily yellow mosaic virus represents a novel taxon.

Although the genome sequence of lily yellow mosaic virus isolate lily-bua appears to have been assembled solely (or mainly) from sequences derived from small (16-30 nucleotide) cDNA fragments to unknown depth, the genome and ORFs exhibit the size, peptide motifs and phylogeny of a typical member of genus *Potyvirus*, and it is accepted as such.

The *Potyviridae* Study Group proposes lily yellow mosaic virus as a member of a new species in the genus *Potyvirus*. The name of the new species is proposed as *Lily virus Y*, since the symptoms induced by the virus in lily are actually unknown.

**Mashua virus Y**

A virus, tentatively named mashua virus Y (MasVY) isolate Cam, was detected in 1984 from a plant of mashua (*Tropaeolum tuberosum*), an Andean tuber crop, exhibiting mosaic symptoms. At the time, the virus was transmitted to *Nicotiana clevelandii* plants, where the virus induced mosaic symptoms; also, flexuous filamentous particles of about 750 nm were observed by TEM. Other reports of mosaic diseases of mashua came from Bolivia (Delhey and Monasterios, 1977) and Ecuador (Soria et al., 1998), and in the latter case the disease was associated to a potyvirus named Tropaeolum mosaic virus (TropMV). Also, two potyviruses named Tropaeolum 1 and 2 viruses, originated in samples from Peru were found in plants growing from imported mashua tubers (Brunt et al., 1999). However, until now no sequences were available for the different viruses mentioned.

Leaf samples of the above described *N. clevelandii* plants infected with the virus from mashua have been maintained as lyophilized samples until now. These samples were used to extract total RNA and to generate an indexed sequencing library for NGS (Illumina). A contig representing the complete genome sequence of MasVY was obtained, being 9,769 nucleotides in length, excluding the poly (A) tail. The sequence was assigned GenBank accession MH680824. It was predicted to encode a polyprotein of 3,074 amino acid residues, structurally displaying the organization of a typical potyvirus, including PIPO within the P3 region (Adams et al., 2018).

Although at this point there are no data about distribution of the virus, at least a partial sequence (GeneBank accession MH680823) of a different isolate with 96% amino acid identity in the CP region was detected in a mashua tuber from Europe. It is unclear if any of the previously described virus isolates described from *Tropaeolum tuberosum* plants are isolates of the same species.

The genome sequence of MasVY-Cam shared a maximum of 70% nucleotide identity with Verbena virus Y sequences (Kraus et al., 2010), within the potato virus *Y* subclade.This percentage of identity is below the ICTV-accepted demarcation limits of <76% (Adams et al. 2005).

Based upon above-reported data, the *Potyviridae* study group proposes that masha virus Y (MasVY) distortion virus represents a new species, *Masha virus Y*, within the genus *Potyvirus*, with MasVY-Cam being the exemplar isolate.

**Platycodon mild mottle virus**

A newly described virus, tentatively named Platycodon mild mottle virus (PlaMMV) isolate Okcheon, was detected from a plant of Platycodon grandiflorum plants in Okcheon county, Korea, exhibiting ‘virus disease-like symptoms in 2013 (Lim *et al*., 2018). The virus was not reported to be transmitted to experimental host plants.

An RNA preparation was used to construct a cDNA library that was sequenced using an Illumina high-throughput sequencing platform, and the sequence was confirmed by RT-PCR using specific and random primers. Rapid amplification of cDNA ends (RACE) was used to confirm the 5’ and 3’ termini of the genome sequence.

The complete genome sequence of PlaMMV-Okcheon was determined/assembled. The genome was 9556 nucleotides in length. The genome sequence of PlaMMV-Okcheon was assigned GenBank accession MH779625. It was predicted to encode a polyprotein of 3079 amino acid residues. It displayed the genome organization and motifs of a typical potyvirus.

The genome sequence shared a maximum of 70% nucleotide identity (40% query coverage) with

with carrot thin leaf virus (JX156434) and that the complete amino acid sequence of the PlaMMV polyprotein shared 54% sequence identity (98% query coverage) with thunberg fritillary mosaic virus (CAI59123) in genus *Potyvirus*. The coat protein (amino acid) sequence most closely matched that of turnip mosaic virus (68% identity). These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities.

Therefore, the *Potyviridae* study group proposes that Platycodon mild mottle virus (PlaMMV) represents a new species, *Platycodon mild mottle virus*, within the genus *Potyvirus*, with PlaMMV-Okcheon being the exemplar isolate.

**Potato yellow blotch virus**

A newly-described virus, tentatively named potato yellow blotch virus (PYBV) isolate QV276, was detected from a plant of *Solanum tuberosum* (potato) breeding line 99m-022-026 in Scotland (Nisbet *et al*., 2019). The infected plants showed isolated yellow blotches on the leaves. The virus was successfully transmitted to a range of solanaceous and non-solanaceous experimental host plants, including species of *Chenopodium*, *Datura*, *Nicandra*, *Nicotiana*, and *Solanum*. The virus cross-reacted with potato virus A (PVA) anti-serum.

Amplicons were generated by RT-PCR using primers based on the PVA genome, and the complete genome was obtained after alignment of overlapping amplicons. Rapid amplification of cDNA ends (RACE) was used to confirm the 5’ and 3’ termini of the genome sequence.

The complete genome sequence of PYBV-QV276 was 9518 nucleotides in length. The genome sequence of PYBV-QV276 was assigned GenBank accession JX294310. It was predicted to encode a polyprotein of 3054 amino acid residues (AFS28882, where it is referred to as potato virus B). It displayed the genome organization and motifs of a typical potyvirus.

The genome sequence shared <72% nucleotide identity with genomes of PVA isolates (e.g. KF977085), and <78% amino acid identities over the complete polyprotein. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities.

Therefore, the *Potyviridae* study group proposes that potato yellow blotch virus (PYBV) represents a new species, *Potato yellow blotch virus*, within the genus *Potyvirus*, with PYBV-QV276 being the exemplar isolate.

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**Figure 1** Estimated phylogeny of deduced polyprotein sequences of completely sequenced representative viruses of species in genera *Arepavirus*, *Bevemovirus*, *Brambyvirus, Bymovirus, Celavirus, Ipomovirus, Macluravirus, Poacevirus, Potyvirus, Roymovirus*, *Rymovirus,* and *Tritimovirus* in the family *Potyviridae*. Proposed new species in genera *Arepavirus* (proposed new genus), *Celavirus* (proposed new genus), *Macluravirus*, *Potyvirus,* and *Roymovirus* are indicated by a red dot. The tree was deduced in Mega v7.0.26 after alignment in Muscle using Neighbor-joining with 1000 bootstrap replications. Bootstrap support for branches is shown at the junctions of branches where it was >60%. Evolutionary distances were calculated using the Poisson correction method and branch lengths are proportional to genetic distance in units of amino acid substitutions per site.

Accession codes corresponding to the nucleotide sequence of each virus genome sequence used in the tree are: African eggplant mosaic virus, MF997470; Agropyron mosaic virus, AY623626; Algerian watermelon mosaic virus, EU410442; Alpinia oxyphylla mosaic virus, MG978107; Apium virus Y, HM363516; Areca palm necrotic ringspot virus, MH395371; Areca palm necrotic spindle-spot virus, MH330686; Arracacha mottle virus, DQ925486; artichoke latent virus, KP405232; Asparagus virus 1, KJ830760; banana bract mosaic virus, HM131454; Barbacena virus Y, KU685505; barley mild mosaic virus (RNA1), D83408; Basella rugose mosaic virus, DQ821939; bean common mosaic necrosis virus, U19287; bean common mosaic virus, U19287; bean yellow mosaic virus, D83749; beet mosaic virus, AY206394; bellflower veinal mottle virus, KY491536; Bidens mosaic virus, KF649336; Bidens mottle virus, AF538686; blackberry virus Y, AY994084; blue squill virus A, JQ807999; broad-leafed dock virus A, KU053507; brome streak mosaic virus, Z48506; Brugmansia mosaic virus, JX867236; Brugmansia suaveolens mottle virus, AB551370; Caladenia virus A, JX156425; calla lily latent virus, EF105297; Callistephus mottle virus, KX013584; Canna yellow streak virus, GQ421689; carrot thin leaf virus, JX156434; Catharanthus mosaic virus, KP742991; cassava brown streak virus, FN434437; celery latent virus, MH932227; celery mosaic virus, HQ676607; chilli ringspot virus, JQ234922; chilli veinal mottle virus, GQ981316; Chinese yam necrotic mosaic virus, AB710145; clover yellow vein virus, AB011819; Coccinia mottle virus, KU935732; cocksfoot streak virus, AF499738; Colombian datura virus; JQ801448; common reed chlorotic stripe virus, KY612317; cowpea aphid-borne mosaic virus, KM655833; cucumber vein yellowing virus, AY578085; cucurbit vein banding virus, KY657266; Cyrtanthus elatus virus A, JQ723475.; Daphne mosaic virus, DQ299908; Daphne virus Y, KU556609; dasheen mosaic virus, AB219545; Dendrobium chlorotic mosaic virus, MK241979; Dioscerea mosaic virus, MH206616; donkey orchid virus A, JX156422; East Asian Passiflora virus, AB246773; East Asian Passiflora distortion virus, LC379162; Freesia mosaic virus, FM206346; fritillary virus Y, AM039800; Gloriosa stripe mosaic virus, EF427894; Gomphocarpus mosaic virus, LC228573; Habenaria mosaic virus, EF427894; Hardenbergia mosaic virus, HQ161081; Hippeastrum mosaic virus, JQ395040; Hordeum mosaic virus, AY623627; Impatiens flower break virus, KU981084; Japanese yam mosaic virus, AB027007; Jasmine virus T, KT222674; johnsongrass mosaic virus, Z26920; Keunjorong mosaic virus, JF838187; konjac mosaic virus, AB219545; leek yellow stripe virus, KP258216; lettuce Italian necrotic virus; KP769852; lettuce mosaic virus, KF268954; lily mottle virus, AB570195; lily virus Y, MF543013; longan witches’ broom-associated virus, KY649478; Lupinus mosaic virus, EU847625; maize dwarf mosaic virus, AM110758; Mashua virus Y, MH680824; Mediterranean ruda virus, MF953305; Moroccan watermelon mosaic virus, EF579955.; Narcissus degeneration virus, AM182028; Narcissus late season yellows virus, KC691259; Narcissus yellow stripe virus, KC691259; oat mosaic virus (RNA1), AJ306718; oat necrotic mottle virus, AY377938; onion yellow dwarf virus, KJ451436; Ornithogalum mosaic virus, JQ807995; Panax virus Y, GQ916624; papaya leaf distortion mosaic virus, AB088221; papaya ringspot virus, KC345607; Paris mosaic necrosis virus, MF509898; Passiflora edulis symptomless virus, MH379332; passion fruit woodiness virus, HQ122652; pea seed-borne mosaic virus, AJ252242; peanut mottle virus, AF023848; pecan mosaic-associated virus, KT633868; Pennisetum mosaic virus, AY642590; pepper severe mosaic virus, AM181350; pepper veinal mottle virus, DQ645484; pepper yellow mosaic virus, AB541985; Peru tomato mosaic virus, AJ437280; Platycodon mild mottle virus, MH779625; plum pox virus, AY953267; pokeweed mosaic virus, JQ609095; potato virus A, Z21670; potato virus V, KP849483; potato virus Y, U09509; potato yellow blotch virus, JX294310; rose yellow mosaic virus, JF280796; ryegrass mosaic virus, Y09854; saffron latent virus, KY562565; scallion mosaic virus, AJ316084; shallot yellow stripe virus, AJ865076; sorghum mosaic virus, U57358; soybean mosaic virus, S42280; squash vein yellowing virus, EU259611; Sudan watermelon mosaic virus, KY623505; sugarcane mosaic virus, GU474635; sugarcane streak mosaic virus, GQ388116; sunflower chlorotic mottle virus, GU181199; sunflower mild mosaic virus, JQ350738; sunflower ring blotch virus, KX856009; sweet potato feathery mottle virus, AB439206; sweet potato latent virus, KC443039; sweet potato mild mottle virus, Z73124; sweet potato virus 2, JN613807; sweet potato virus C; GU207957; sweet potato virus G, JQ824374; tamarillo leaf malformation virus, KM523548.; Telosma mosaic virus, DQ851493; Thunberg fritillary mosaic virus, AJ851866; tobacco etch virus, DQ986288; tobacco mosqueado virus, KT834407; tobacco vein banding mosaic virus, EF219408; tobacco vein mottling virus, U38621; tomato necrotic stunt virus, JQ314463; Triticum mosaic virus, FJ669487; turnip mosaic virus, AF169561; Vanilla distortion mosaic virus, KF906523; Verbena virus Y, EU564817; wheat yellow mosaic virus (RNA1), FJ361765; wild melon vein banding virus, KY623506; wild onion symptomless virus, LC159494; wild potato mosaic virus, AJ437279; wild tomato mosaic virus, DQ851495; Wisteria vein mosaic virus, AY656816; yambean mosaic virus, JN190431; yam chlorotic mosaic virus, KT724961; yam chlorotic necrosis virus, MG755240; yam mild mosaic virus, JX470965; yam mosaic virus, U42596; Zantedeschia mild mosaic virus, AY626825; Zea mosaic virus, JQ692088; zucchini shoestring virus, KU355553; zucchini tigre mosaic virus, KC345607; zucchini yellow mosaic virus, L31350.