

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

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| **Code assigned:** | **2020.024P** |  |
| **Short title:** Create seven new species in the genus *Potyvirus* (*Patatavirales*: *Potyviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | July 4, 2020 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.024P.R.Potyviridae\_7nsp.xlxs |

**Abstract**

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| The complete genome sequences of seven novel viruses is presented. Each has a genome architecture typical of viruses within genus *Potyvirus*, family *Potyviridae*. The particles of several have been visualized by TEM and these are typical of members of the genus. In some cases, transmission has been shown experimentally. Pairwise comparisons of the genome sequences with other potyviruses shows that all meet the criteria for their classification into seven newly created species. |

**Text of proposal**

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| |  | | --- | | **1. Virus**: Begonia flower breaking virus (BFBV) isolate YN-Tiger  **Proposed species name**: *Begonia flower breaking virus*  **Genus**: *Potyvirus*  **NCBI accession**: MN592680  **Authors**: Wu et al. (2016) and Tang et al. (2020)  **Author location**: Yunnan Agricultural University, Kunming, China  **Publication**: Tang et al. (2020)  **Original hosts**: *Begonia species. BFBV-*YN-Tiger host is *B. bowerae* cv. Tiger  **Symptoms of infection**: *In Begonia semperflorens* (Bouwen and van der Vlugt 2005) and *B. bowerae* (Wu et al. 2016), the infected plants exhibited flower color-breaking symptoms. In *B. odorata* ‘White Angel’, no color-breaking symptoms were observed, but some plants displayed chlorotic ring symptoms on foliage (Dey et al., 2019).  **Country of isolation**: Netherlands, USA, China  **Sequencing approach(es)**: High-throughput RNA-Seq. Sequence confirmed by RT-PCR with overlapping virus-specific primers.  **Genome sequence**: 9540 nucleotides  **Nucleotide sequence identity**: BFBV isolate YN-Tiger shared >95% identity with partial sequences of two different isolates of BFBV, one named isolate F10 from the Netherlands reported in 2008 (Accession number FJ539085), and other named isolate Alachua from Florida, USA (Accession number MK567882), in this case with a preliminary description published in 2019 (Dey et al., 2019).  BLAST searches performed with the complete genome sequence of BFBV isolate YN-Tiger suggest that closest relatives are isolates of peanut mottle virus at around 65% nucleotide identity.  **Polyprotein sequence**: 3073 amino acids  **Polyprotein identity**: Shares about 55% amino acid identity with isolates of beet mosaic virus (e.g. ABG74927), Basella rugose mosaic virus (ABH10135) and peanut mottle virus (QFO46835).  **Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites were present in the BFBV polyprotein. Predicted that the BFBV polyprotein is proteolytically cleaved into 10 mature peptides (and PIPO) and that BFBV has similar cleavage sites to other viruses in the genus *Potyvirus*. Most of the conserved motifs found in members of the genus *Potyvirus*, including those associated with aphid transmission, were also found in BFBV YN-Tiger.  **Natural transmission**: Unknown, but probably aphids.  **Experimental transmission**: Bouwen and Vlugt (2005) were able to mechanically transmit the virus to virus-free *B. semperflorens* plants. BFBV YN-Tiger was mechanically inoculated to *Nicotiana glutinosa*, *N. tabacum*, *Chenopodium quinoa*, *B. bowerae*, *B. semperflorens*, and 19 other species or varieties of *Begonia.* No abnormal symptoms were observed in all inoculated plants. Thirty days post inoculation, the inoculated plants were tested by RT-PCR using the potyvirus group primers, and results showed that only the *B. bowerae* plants were infected (Wu et al., 2016).  **Other host**s: No described. May be restricted to *Begonia* spp.  **Additional information**:  The virus was first described in the Netherlands in 2005 (Bouwen and Vlugt, 2005) in *B. semperflorens;* the virus exhibited a positive reaction in ELISA with a general monoclonal directed against potyviruses. The sequence of BFBV isolate YN-Tiger coincides with a partial fragment of 669 nucleotides (GenBank accession number KT275858.1) corresponding to part of the CP and 3'UTR of a virus isolate with the same name that was reported by the same team in the same location from infected *B. bowerae* cv. Tiger plants, exhibiting swelling or deformation of leaves (Wu et al., 2016). The isolate was collected in 2009.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that Begonia flower breaking virus isolate YN-Tiger be considered as representative of a new species.  **2. Virus**: Costus stripe mosaic virus (CoSMV) isolate BR1  **Proposed species name**: *Costus stripe mosaic virus*  **Genus**: *Potyvirus*  **NCBI accession**: MK286375  **Authors**: Alexandre et al.  **Author location**: Instituto Biológico, Av. Cons. Rodrigues Alves 1252, São Paulo, SP, Brazil, 04014-002.  **Original host**: *Costus spiralis*  **Symptoms of infection**: Dark green leaf stripes and mosaic  **Country of isolation**: Brazil  **Particle**: Elongated, flexuous filamentous virus particles (700-750 nm long and ca. 13 nm wide) were consistently detected in leaf extracts of naturally infected *Costus* plants.  **Sequencing approach(es)**: RT-PCR and high throughput sequencing (Illumina HiSeq 2500).  **Genome sequence**: 9446 nucleotides  **Nucleotide sequence identity**: Greatest identity was 52% with onion yellow dwarf virus isolates.  **Polyprotein sequence**: 3046 amino acids  **Polyprotein identity**: Greatest identity was 43% with Ornithogalum mosaic virus isolates.  **Proteins and motifs**: Amino acid sequence analyses of CoSMV deduced polyprotein showed conserved motifs typical of potyviruses. Motifs KITC and PTK in HC-Pro involved in aphid transmission are modified [329LTTC332 and 585PIK587]. However, a 604PTK606 sequence can also be found, albeit not aligned to the PTK domains of other potyviruses. Polyprotein cleavage site analysis showed an unusual aa sequence (MTHC/S) in the P1/HC-Pro border, where the presence of Cys prior to the cleavage point is distinct to all other potyvirids.  **Natural transmission**: No transmission by aphids *Aphis solanella*, *Myzus persicae* and *Uroleucon sonchi* was detected.  **Experimental transmission**: Systemic infection of *Costus comosus* and *C. spiralis.*  **Other hosts**: None identified  **Additional information**:  Phylogenetic analysis places this virus basal to other potyviruses. The virus is detected in ELISA with potyvirus group antisera.  **Study Group recommendation**: The *Potyviridae* Study Group recommends that Costus stripe mosaic virus isolate BR1 be considered as representative of a new potyvirus species.  3. **Virus**: noni mosaic virus (NoMV) isolate NoMV-YJh, noni mosaic virus isolate Yunnan  **Proposed species name**: *Noni mosaic virus*  **Genus**: *Potyvirus*  **NCBI accession**: MN114634 (isolate NoMV-YJh), MN158696 (isolate Yunnan)  **Authors**: Lan et al. (2019) (isolate NoMV-YJh); Yu et al. (2020) (isolate Yunnan).  **Author location**: Lan et al., 2019: Molecular Virology, Institute of Tropical Bioscience and Biotechnology, CATAS, No. 4 Xueyuan Road, Longhua District, Haikou, Hainan 571101, China; Yu et al., 2020: Yunnan Agricultural University, College of Plant Protection, 452 Fengyuan Rd., Kunming, Yunnan 650201, China  **Original host**: *Morinda citrifolia*  **Symptoms of infection**: Chlorosis and mosaic symptoms. Yu et al 2020 showed in field surveys that 100% of symptomatic samples and 29% of asymptomatic samples were infected with this potyvirus.  **Country of isolation**: Yunnan province, China  **Particle**: Viral particles with flexuous filaments about 800 nm in length and 12-20 nm in width were found.  **Sequencing approach(es)**: The Illumina HiSeq X-ten platform was used for high-throughput sequencing of isolate NoMV-YJh. The complete genome of isolate Yunnan was obtained by Sanger sequencing of eight amplicons generated by RT-PCR and 5′ and 3’ RACE.  **Genome sequence**: 9645 nucleotides (isolate NoMV-YJh), 9659 (isolate Yunnan)  **Nucleotide sequence identity**: The complete genome shared 49 – 59% (isolate NoMV-YJh) or 47- 51% (isolate Yunnan) nucleotide sequence identity with those other known potyviruses. Highest sequence identities in the polyprotein region were with jasmine virus T and tobacco vein banding virus.  **Polyprotein sequence**: 3077 amino acids (isolate NoMV-YJh); 3026 amino acids (isolate Yunnan)  **Polyprotein identity**: The complete polyprotein shared 39-53% amino acid sequence identity with those other known potyviruses. Highest sequence identity was with kalanchoe mosaic virus.  **Proteins and motifs**: Predicted to encode 10 mature proteins. Most conserved motifs that are typical of potyviruses were present. Three motifs involved in aphid transmission, 52K-I-T-C55 and 310P-T-K312 in HC-Pro and 7D-A-G9 in CP, were found to be present in the polyprotein of NoMV-YJh.  **Natural transmission**: Yu et al. (2020) found that aphids collected from diseased leaves were detected carrying the virus and aphid transmission tests confirmed aphids are able to transmit the virus.  **Experimental transmission:** Not described  **Other hosts**: Not described  **Additional information**: The two isolates of NoMV share 99.6% nucleotide sequence identity. The apparent differences in polyprotein sizes between them are due to different interpretations of which of two possible start codons is the correct one, not differences in sequence. Alignment with the 5’ regions of other potyviruses suggests that the AUG predicted for NoMV-YJh is likely to be the correct one.  A likely recombination site predicted by five programs was detected that suggests recombination between tobacco vein mottle virus (accession number U38621, major parent) and tobacco etch virus (accession number NC\_001555, minor parent). Two or three other possible recombination sites were also identified. These results suggest that interspecies recombination occurred during the evolutionary history of NoMV-YJh.  The sequence of NoMV isolate NoMV-YJh was described first, and this sequence should be considered as the type (exemplar) isolate for this new species.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that Noni mosaic virus isolate NoMV-YJh be considered as the representative of a new species in genus *Potyvirus.*  4. **Virus**: Paris virus 1 (ParV1) isolate KM  **Proposed species name**: *Paris virus 1*  **Genus**: *Potyvirus*  **NCBI accession**: MN549985  **Authors**: Chen et al. (2020)  **Author location**: Yunnan Agricultural University, State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, 452 Fengyuan Rd, Kunming, Yunnan 650201, China  **Original host**: *Paris polyphylla* var. yunnanensis  **Symptoms of infection**: Yellow mosaic symptoms on foliage  **Country of isolation**: Yunnan Province, China  **Particle**: Filamentous viral particles of 700-1000 nm in length and 13 nm in width  **Sequencing approach(es)**: Illumina high-troughput sequencing using a paired-end strategy.  **Genome sequence**: 10,066 nucleotides  **Nucleotide sequence identity**: The complete genome shares up to 65% nucleotide sequence identity with its closest known relative, Thunberg fritillary mosaic virus.  **Polyprotein sequence**: 3240 amino acids  **Polyprotein identity**: The complete polyprotein shared 50-69% amino acid sequence identity with those of other known potyviruses. The closest known relative is thunberg fritillary mosaic virus.  **Proteins and motifs**: Nine cleavage sites and conserved motifs that are typical features of potyviruses.  **Natural transmission**: Not described  **Experimental transmission:**  Not described  **Other hosts**: Not described  **Additional information**: None.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that Paris virus 1 be considered as representative of a new species in genus *Potyvirus.*  5. **Virus**: passionfruit Vietnam virus (PVV) isolate DakNong  **Proposed species name**: *Passiflora mottle virus*  **Genus**: *Potyvirus*  **NCBI accession**: MH286883  **Authors**: Chong et al. (2018) (unpublished)  **Author location**: Chong et al: Department of Plant Pathology, National Chung Hsing University, No. 145, Xingda Road, South District, Taichung City 402, Taiwan  **Original host**: *Passiflora edulis*  **Symptoms of infection**: Chlorosis and mosaic symptoms  **Country of isolation**: Vietnam  **Particle**: Potyvirus-like particles measuring approximately 770 nm in length were observed in crude sap from the plant with diseased fruit (isolate FJ).  **Sequencing approach(es)**: Small RNA high-throughput sequencing using a HiSeq XTen sequencer to generate contigs. To obtain the complete viral genome sequence, RT-PCR was carried out using two pairs of potyvirus-specific degenerate primers and four virus-specific primer pairs that were designed based on the contig sequences.  **Genome sequence**: 10071 (isolate DakNong)  **Nucleotide sequence identity**: The complete genome of FJ shares 70–72% nucleotide sequence with closely-related potyviruses, the nearest being telosma mosaic virus, East Asian passiflora virus, soybean mosaic virus and others.  **Polyprotein sequence**: 3209 amino acids (both isolates)  **Polyprotein identity**: The complete polyprotein shares 69–74% amino acid sequence identity with isolates of closely-related potyviruses telosma mosaic virus and East Asian passiflora virus  **Proteins and motifs**: Predicted to encode 10 mature proteins plus PIPO.  **Natural transmission**: Not described  **Experimental transmission:** Not described  **Other hosts**: Not described  **Additional information**:  A number of virus isolates representing a new potyvirus from passion fruit have been identified from Vietnam and China since 2018. There has been some confusion over this virus' identity because different groups have proposed different names. The Study Group has considered these data and has made a decision on the name based on the first sequences of this virus made available in NCBI databases.  Partial sequences of this potyvirus from *P. edulis* plants in Vietnam were named Passiflora mottle virus isolates Nghean10 (MG087836, 2223 nt), Nghean13 (MG087835, 602 nt) and Lamdong1 (MG087833, 603 nt). These were submitted to NCBI by a group from Vietnam lead by Ha in Aug 2018. Isolate Nghean10 was transmitted mechanically to *Chenopodium amaranticolor* plants. These partial sequences shared 99% nt identities with those of isolates Daknong and FJ (described below). A full description has not been published yet.  The first complete genome sequence of this potyvirus was isolated from *P. edulis* plants in Vietnam by a group from Taiwan (Chong et al.) was named passionfruit Vietnam virus isolate PVV-DakNong (MH286883, 10,071 nt). The sequence was deposited in GenBank in Dec 2018. A full description has not been published yet.  Another complete genome sequence of this potyvirus was named passionfruit severe mottle virus isolate FJ (MK449340, 9974 nt). It was deposited in GenBank Feb 2020 by a group from China (Xie et al., 2020) that isolated it from *P. edulis* plants in Fujian. A comprehensive description of the isolate was published in 2020. The authors referred to passionfruit Vietnam virus isolate PVV-DakNong as an ‘unreported virus’, the genome and polyprotein of which shared 89% nt and 91% aa identities with isolate FJ, respectively. These identities are above the species demarcation limits suggested for potyviruses, yet Xie and colleagues chose a new name for the virus.  Note: the deduced polyprotein sequences of isolates DakNong and FJ are identical sizes (3209 aa), the size differences between the two genome sequences being found in the untranslated regions.  A fragment of the same virus, this time named passion fruit woodiness virus isolate GX1 (MN549399, 819 nt), was submitted to NCBI in Feb 2020. It was isolated from *P. edulis* plants in Nanning, China by Jiang and colleagues. This partial sequence shares 92% nt identity with isolate DakNong.  Note: passionfruit woodiness virus (*sensu stricto*) is a distinct virus found only in Australia. The partial (coat protein, CP) sequence of isolate GX1 shares ~72% nt identity with CPs of isolates of passionfruit woodiness virus, below the suggested potyvirid species demarcation limit for CP sequences.  The first isolates (described with partial sequences) of this new virus were named Passiflora mottle virus, and the Potyvirus Study Group considers that this name should be ascribed to the new species. The isolate from which the first complete genome was obtained, passionfruit Vietnam virus isolate DakNong, should be considered as the exemplar isolate for this new species. Furthermore, all isolates of differently named viruses listed in this proposal belong to the same proposed new species .  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that passionfruit Vietnam virus isolate DakNong represent a new species, *Passiflora mottle virus*, in genus *Potyvirus.*  6. **Virus**: Pleione flower breaking virus (PlFBV) isolate CZ-Wharf1  **Proposed species name**: *Pleione flower breaking virus*  **Genus**: *Potyvirus*  **NCBI accession**: NC\_040650  **Authors**: Kominek et al. (2019)  **Author location**: Plant Virology and Phytoplasmatology, Crop Research Institute, Drnovska 507, Praha 16106, Czech Republic  **Original host**: *Pleione humilis,* also *P. formosana and Pleione* hybrids  **Symptoms of infection**: Symptoms included leaf mosaic and flower color-breaking  **Country of isolation**: Czech Republic and The Netherlands  **Particle**: Filamentous particles with modal length of 720 nm were observed in the sap of symptomatic Pleione plants by TEM.  **Sequencing approach(es)**: The complete genome sequence was generated from RNA isolated from symptomatic plants using a mirVana miRNA isolation kit; ribosomal RNA was removed using a RiboMinus Plant Kit for RNA-Seq; total RNA libraries were prepared using a simplified protocol (no enrichment in poly-A RNA) with a TrueSeq Stranded mRNA kit; and, libraries were sequenced using an Illumina Nextseq 500 platform with PE 2×150 nt. Rapid amplification of cDNA ends (RACE) strategies were used to confirm the 5’ and 3’ termini of the genome sequence.  **Genome sequence**: 9952 nucleotides  **Nucleotide sequence identity**: The genomic nucleotide sequence shared 56-65% nucleotide identities with those of other potyviruses, with the closest relative being keunjorong mosaic virus.  **Polyprotein sequence**: 3226 amino acids  **Polyprotein identity**: The complete polyprotein amino acid sequence shared 45-70% amino acid identities with those of other potyviruses, with the closest relative being keunjorong mosaic virus.  **Proteins and motifs**: The genome and its 10 predicted protein products resembled the genome organization and shared motifs of a typical potyvirus. The P1/HC-Pro cleavage site was identified in a position similar to other species of the genus *Potyvirus* but presented an unusual protease-recognition sequence (TRHF/S). The putative PIPO ORF was located within the P3 cistron and predicted to be translated by +2 frameshift at the conserved GAAAAAA, as seen in most potyvirids.  **Natural transmission**: Not described.  **Experimental transmission:**  The virus was experimentally transmitted by aphids to *Pleione* and *Chenopodium quinoa* plants.  **Other hosts**: Not described.  **Additional information**:  Another PlFBV sequence (isolate 052013) exists in GenBank (KF360240) from 2013; it is 1367 nt in length and was derived from an RT-PCR amplicon from the 3’ end of the genome generated using potyvirus-specific degenerate primers in combination with an oligo-dT reverse primer from RNA from a Dutch Pleione sample exhibiting flower color-break symptoms. The 392 aa deduced protein sequence shares 99% identity with that of isolate CZ-Wharf1.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that Pleione flower breaking virus isolate CZ-Wharf1 be considered as representative of a new species in genus *Potyvirus.*  **7. Virus**: Ugandan passiflora virus (UPV) isolate KH7-1  **Proposed species name**: *Ugandan passiflora virus*  **Genus**: *Potyvirus*  **NCBI accession**: MK110656  **Authors**: Mbeyagala et al.  **Author location**: Dryland Legume Research Program, National Semi Arid Agricultural Research Institute and National Agricultural Research Organization, Lugard Avenue, Entebbe +256, Uganda  **Original host**: *Passiflora edulis* cv KH7  **Symptoms of infection**: Leaf mosaic, crinkle, distortion in foliage, fruit woodiness and malformations.  **Country of isolation**: Uganda  **Particle**: Flexuous, filamentous particles were observed under an electron microscope, measuring approximately 700 to 800 nm in length and 11 to 12 nm in diameter.  **Sequencing approach(es)**: High-throughput sequencing  **Genome sequence**: 9651 nucleotides  **Nucleotide sequence identity**: The complete genome shared 70% nucleotide sequence identity with the most closely-related relative, bean common mosaic necrosis virus.  **Polyprotein sequence**: 3087 amino acids  **Polyprotein identity**: The complete polyprotein shared 71% amino acid sequence identity with that of isolates of bean common mosaic virus.  **Proteins and motifs**: Predicted to encode 10 mature proteins typical of other potyviruses  **Natural transmission**: Not described  **Experimental transmission:** Not described  **Other hosts**: Not described  **Additional information**:  The name Ugandan passiflora virus was proposed by Ochwo-Ssemakula et al. (2012). These researchers sequenced ~1700 nt of the partial NIb and CP regions of UPV isolates UGM-19a (FJ896000) and UGM-17 (FJ896003) from plants of *Passiflora edulis* in Uganda. Isolates UGM-58 (FJ896001) and UGM-73 (FJ896002) were from plants of *P. edulis edulis x P. edulis flavicarpa*. Bancy et al. (2018) identified the virus in *P. edulis* plants in Rwanda. Sequences of ~650 nt were submitted to NCBI from isolates RW10 (MK132862), RW23 (MK132863), RW104 (MK132864), RW140 (MK132865). In Rwanda the incidence of virus infection was highest in *P. edulis p*lants in North Province at 45.8% and lowest in West Province at 18.7%.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that Ugandan passiflora virus isolate KH7-1 be considered as representative of a new species in genus *Potyvirus.* | |

**Supporting evidence**

**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 genus *Potyvirus* 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; Begonia flower breaking virus, MN592680; 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; Costus stripe mosaic virus, MK286375; 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; noni mosaic virus, MN114634; 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; Paris virus 1, MN549985; Passiflora edulis symptomless virus, MH379332; passionfruit Vietnam virus (species *Passiflora mottle virus*), MH286883; 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; Pleione flower breaking virus, NC\_040650; 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; Ugandan passiflora virus, MK110656; 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.

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