This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2016.008a,bP***	(to be completed by ICTV officers)

Short title: Create three species in genus *Potyvirus* and abolish five species in genus *Potyvirus*

(e.g. 6 new species in the genus *Zetavirus*)

Modules attached
(modules 1 and 11 are required)

2 ☒ **3** ☐ **4** ☐ **5** ☐
6 ☐ **7** ☐ **8** ☒ **9** ☐ **10** ☐

Author(s):

Wylie, Stephen (Chair)	s.wylie@murdoch.edu.au
Adams, Michael J.	mike.adams.ictv@gmail.com
Chalam, Celia	mailcelia@gmail.com
Kreuze, Jan F.	j.kreuze@cgiar.org
Lopez-Moya, Juan Jose	juanjose.lopez@cragenomica.es
Ohshima, Kazusato	ohshimak@cc.saga-u.ac.jp
Praveen, Shelly	shellypraveen@hotmail.com
Rabenstein, Frank	frank.rabenstein@jki.bund.de
Stenger, Drake C.	dstenger@fresno.ars.usda.gov
Wang, Aiming	aiming.wang@agr.gc.ca
Zerbini, F. Murilo	zerbini@ufv.br

Corresponding author with e-mail address:

Stephen Wylie s.wylie@murdoch.edu.au

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	*Potyviridae*

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

EC comment: SG response:

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2016.008aP***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Potyvirus***
Subfamily:	
Family:	***Potyviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of species	**Exemplar Isolate**		**Genbank Accession no.**
Lettuce Italian necrotic virus	lettuce Italian necrotic virus isolate I234		KP769852
Jasmine virus T	jasmine virus T isolate FZ		KT222674
Zucchini shoestring virus	zucchini shoestring virus isolate RSA Patty Pan		KU355553

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The family *Potyviridae* consists of plant viruses with a single stranded, positive sense RNA genome and flexuous, filamentous particles. Genomes have a VPg covalently linked to the 5'-end and the 3'-terminus is polyadenylated. Genomes encode a large precursor polyprotein (except in the case of genus *Bymovirus*, which is bipartite and encodes two polyproteins) that is self-cleaved into a set of functional proteins that is strongly conserved throughout the family.

According to criteria published in the ICTV 9th Report (Adams *et al*., 2011), species are distinguished by the following criteria:

- Genome sequence relatedness: different species have CP aa sequence identity less than ca. 80%; and nt sequence identity less than 76% either in the CP or over the whole genome. There are also differences in polyprotein cleavage sites.
- Host range and key host reactions; lack of cross protection.
- Different inclusion body morphology.
- Antigenic properties: serological relatedness may help in distinguishing species.

The viruses described below represent new species in the genus *Potyvirus*. For each, there is at least one complete genome sequence in the public domain and this shows the expected ORFs, conserved motifs and cleavage sites. The molecular criteria to create new species have been satisfied.

Phylogenetic analysis of the complete polyprotein coding sequences (Annex Figure 1) supports the placement of these viruses as distinct species within genus *Potyvirus*.

Jasmine virus T

The name jasmine virus T (JaVT) was first proposed by Lin *et al*., (2004) who provided 1.2 kb (EF535842) of its sequence from the 3’ region of the genome of isolate jasmine from Taiwan. A virus isolated from India and named jasmine yellow mosaic potyvirus was partially sequenced (1.6 kb partial NIb-CP-3'UTR, FJ543110; Sudheera *et al*., 2014). The CP sequence of JaYMV-India shares 89% aa identity (83% nt) with the Taiwanese isolate of JaVT. The complete genome sequence of jasmine virus T isolate FZ was recovered from a plant of *Jasminum sambac* L. showing yellow ringspot symptoms in Fuzhou, China (Tang *et al*., 2016). The authors of the paper name it jasmine virus T in the title and throughout the paper until the last sentence of the discussion, where they suggest the alternative name jasmine ringspot virus for consideration. Although jasmine ringspot virus is the name given to its sequence lodged at NCBI (GenBank accession KT222674), we see no convincing reason to abandon the name first used. The JaVT-FZ coat protein (CP) sequence shares 97% aa identity with JaVT-Jasmine, and 90% aa identity with JaYMV-India, showing that all three isolates are likely to belong to the same taxon. The complete genome (9590 nt) and polyprotein of jasmine virus T isolate FZ shares 66-70% nucleotide and 52-56% amino acid identities, respectively, with seven other potyvirus genomes, all members of the plum pox virus subgroup.

Lettuce Italian necrotic virus

A virus causing necrosis and leaf distortion on lettuce (*Lactuca sativa* cv. Romana) was found in the Lazio region of Italy. Electron microscopy suggested the presence of a potyvirus but antibodies to lettuce mosaic virus (a common potyvirus on this host) did not recognise it. Host range analysis (by sap inoculation) showed its ability to infect only *Chenopodium quinoa* and *C. amaranticolor* in addition to some lettuce cultivars. Symptoms were invariably correlated with the presence of virus particles in inoculated plants. The virus could also be transmitted by aphids of the species *Myzus persicae*. The complete genome sequence of isolate I234 (9829 nt) was then determined by Sanger sequencing of overlapping RT-PCR clones using total RNA extracted from inoculated *C. quinoa* plants (KP769852; Ciuffo *et al.*, 2016). The complete polyprotein sequence shares 50-52% identity with isolates of a number of potyviruses including lettuce mosaic virus, sweet potato feathery mottle virus, sweet potato virus C, sweet potato latent virus, asparagus virus 1, celery mosaic virus, turnip mosaic virus, and others. In our analysis (Annex Fig. 1) using a complete sequence to represent each of the current species, lettuce Italian necrotic virus does not fall into any of the recognised sub-groups within genus *Potyvirus* but Ciuffo *et al*., (2016), using a smaller number of sequences, report a distant clustering with *Lettuce mosaic virus*.

Zucchini shoestring virus

Zucchini shoestring virus (ZSSV) is a virus in the papaya ringspot virus subgroup within *Potyvirus* (Ibaba *et al*., 2016). ZSSV was associated with disease of zucchini (*Cucurbita pepo* L.) in the Republic of South Africa where severe leaf filiformy and fruit deformation on zucchini occurred. Losses up to 100 % were recorded in cases when the infection occurred before fruit formation. No transmission studies were reported and Koch’s postulates were not satisfied. The genome sequence of ZSSV was determined by next-generation sequencing of total RNA. The ZSSV isolate RSA Patty Pan genome is 10,295 nucleotides long excluding the poly(A) tail and displays a typical potyvirus organization. Algerian watermelon mosaic virus (AWMV; EU410442) was identified as the closest relative of ZSSV, sharing the highest genome sequence identity of 66% and complete polyprotein identity of 72%.

MODULE 8: **REMOVE (ABOLISH)**

Use this module if an existing taxon needs to be completely removed (abolished). Use module 9 if there is simply a change of name.

removing (abolishing a taxon)

Code	***2016.008bP***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Cowpea green vein banding virus, Groundnut eyespot virus, Guinea grass mosaic virus, Helenium virus Y, Tropaeolum mosaic virus

The present taxonomic position of these taxon/taxa:

Genus:	***Potyvirus***	Fill in all that apply.
Subfamily:		
Family:	***Potyviridae***	
Order:		

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

The species listed below do not have nucleotide sequence data supporting their differentiation, there are no known cultures, in some cases no known antibodies, and they have not been worked on for some years. Although they are currently listed as belonging to *Potyvirus*, in some cases there is no strong evidence supporting their inclusion in this genus.

Cowpea green vein banding virus. Two known publications support the existence of this virus (Lin, 1979; Lin *et al.*, 1979). Murilo Zerbini contacted co-author E. Kitajima who indicated there is probably no source of CGVBV in existence. In the absence of an isolate that could be sequenced and compared to known/recognized viruses it was decided to remove this taxon.

Groundnut eyespot virus. Two publications (Dubern and Dollet, 1980; Dubern, 1981) describe this legume-infecting virus. No work has been published on it since. A polyclonal antibody was raised (Dubern and Dollet, 1980), but its whereabouts is unknown. Mike Adams contacted M. Dollet who said he did not think it would be possible to locate the original source. In the absence of an isolate that could be sequenced and compared to known/recognized viruses it was decided to remove this taxon.

Guinea grass mosaic virus. It appears likely that isolates of guinea grass mosaic virus (GGMV) can be placed with isolates of johnsongrass mosaic virus (JGMV). There are six publications describing GGMV (Thouvenel et al, 1976; Lamy et al, 1979; Kukla et al, 1984; Fauquet & Thouvenel, 1987; Thottappilly et al, 1993; Morales et al, 1996). An antiserum was raised against an isolate of GGMV. A brief summary of information about GGMV is given below:

1. GGMV appears to be widespread in the Ivory Coast where three strains are distinguished based on host range in guinea grass, pearl millet and maize.
2. JGMV-Brac was detected using a GGMV antiserum raised against the virus in West Africa. A partial sequence (~900 nt) of JGMV-Brac confirmed it to be JGMV

3 Morales *et al.,* (1996) showed that antisera raised against JGMV-Brac from Colombia, South America and against GGMV from Ivory Coast, West Africa both reacted to seven infected *Bracharia* spp plants in Columbia, suggesting that GGMV and JGMV are closely related viruses.

4 The GGMV antiserum reacted against 12 of 30 Johnsongrass samples that the JGMV-Brac serum did not react against.

5 Morales *et al.,* (1996) were cautious in proposing GGMV as a strain of JGMV. They wrote "…in view of the serological differences between GGMV and JGMV-Brac, the possible relationship of the West African strains of GGMV to JGMV and other species of the sugarcane mosaic subgroup of potyviruses remains to be determined."

6 Both JGMV and GGMV infect guinea grass (*Panicum maximum*) and both are found in West Africa. A Brazilian strain of JGMV found infecting *P. maximum* was recently characterized by Camelo-Garcia *et al.,* (2016). The complete genome sequence of this strain showed 82 % amino acid sequence identity in the polyprotein to that of an isolate of JGMV from Australia. Besides that, a further strain of JGMV (JGMV-CNPGL) was recently isolated from elephant grass (*Pennisetum purpureum*) in Brazil (Silva *et al.,* 2016). Comparison of the JGMV-CNPGL genome sequence with those of other potyviruses revealed also highest nucleotide sequence identity (80 % nt and 86 % aa) to a JGMV isolate from Australia (NC-003606). Interestingly, the N-terminal region of CP from JGMV-CNPGL is highly divergent. These observations underline that JGMV strains may be highly divergent regarding host range and serological properties.

Because there is a strong likelihood that guinea grass mosaic virus is a strain of Johnsongrass mosaic virus, it was decided to remove this taxon.

Helenium virus Y. One publication describes a virus representing this species (Kuschki *et al.,* 1978) and no one has worked on it since publication. Juan Jose Lopez-Moya contacted Renate Koening and Katja Richert-Poggeler, but neither of them has done any further characterization work, nor kept cultures of the virus. In the absence of an isolate that could be further characterized and compared to recognized viruses it was decided to remove this taxon.

Tropaeolum mosaic virus. Nasturtium mosaic virus is listed as a synonym http://www.dpvweb.net/notes/showgenusmembers.php?genus=potyvirus (see e.g. Berger & Parrish, 2011, http://link.springer.com/referenceworkentry/10.1007%2F978-0-387-95919-1_235). One paper describes an isolate of this species (Guimarães & Flores, 2005), in which a monoclonal antibody is reported. Efforts to contact the authors were unsuccessful. In the absence of an isolate that could be sequenced it was decided to remove this taxon.

MODULE 11: **APPENDIX**: supporting material

Additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Fauquet CM (2005). Molecular criteria for genus and species discrimination within the family *Potyviridae*. *Arch Virol* 150:459–479

Adams MJ, Zerbini FM, French R, Rabenstein F, Stenger DC, Valkonen JPT (2011). Family *Potyviridae*. In: Virus Taxonomy, Ninth Report of the International Committee on Taxonomy of Viruses (A.M.Q. King, M.J. Adams, E.B. Carstens & E.J. Lefkowitz, eds), pp. 1069-1089. Elsevier Academic Press, London.

Dubern J, Dollet M (1980). Groundnut eyespot virus, a new member of the potyvirus group. *Annals of Applied Biology* 96.2: 193-200.

Dubern J (1981). *Physalis floridana*, a natural host of groundnut eyespot virus. *J Phytopathol* 100: 237-241

Camelo-García VM, da Silva Andrade SC, Geering AD, Kitajima EW, Rezende JA (2016). Genome organization and host range of a Brazilian isolate of johnsongrass mosaic virus. *Arch Virol* 161:1335-1341.

Ciuffo M, Mammella,M, Vallino M, Caciagli P, Turina M (2016). Molecular identification and biological characterization of a new potyvirus in lettuce. *Arch. Virol*. DOI 10.1007/s00705-016-2920-x

Fauquet C, Thouvenel JC (1987). Plant Viral Diseases in the Ivory Coast, Paris: ORSTOM; Institut Francais de Recherche Scientifique pour le Developpement en Cooperation, Collection Initiations-Documentations Techniques no. 46, pp 243.

Guimarães RL, Flores HE (2005). Tropaeolum mosaic potyvirus (TropMV) reduces yield of Andean mashua (*Tropaeolum tuberosum*) accessions. *HortScience* 40: 1405-1407.

Ibaba JD, Laing MD, Gubba A (2016). Zucchini shoestring virus: a distinct potyvirus in the papaya ringspot virus cluster. *Arch Virol* 2016 DOI: 10.1007/s00705-016-2899-3

Kukla B, Thourenel JC, Fauquet C (1984). A strain of guinea grass mosaic virus from pearl millet in the Ivory Coast. *Phytopathologische Zeitschrift* 109:65-73.

Kuschki GH, Koenig R, Duvel D, Kuhne H (1978). Helenium virus S and Y-Two new viruses from commercially grown *Helenium* hybrids. *Phytopathol* 68: 1407-1411.

Lamy D, Thouvenel JC, Fauquet C (1979). A strain of guinea grass mosaic virus naturally occurring on maize in the Ivory Coast. *Annals of Applied Biology* 93: 37-40.

Lin MT (1979). Purification and serology of legume and corn viruses in Brazil. *Fitopatologia Brasileira* 4:203-213.

Lin MT, Anjos JRN, Kitajima EW, Rios GP (1979). A new potyvirus isolated from cowpea, potentially important for Brazilian bean crops (in Portuguese). *Fitopatologia Brasileira* 4:120-121.

Lin YY, Chen TH, Chang CA (2004). Characterization of a new potyvirus isolated from jasmine (*Jasminum sambac* (L.) Ait) in Taiwan. *Plant Pathology Bulletin 13:*69-84.

Morales FJ, Ospina MD, Castano M, Calvert LA (1996). Sequence analysis of the genomic RNA 30-terminal region of a potyvirus from *Brachiaria* spp. related to Guineagrass mosaic virus. *J Phytopathol* 144:485–489.

Silva KN, Melo FL, Orílio AF, Nagata T, Silva MS, Fernandes CD, Fragoso RR, Dessaune SN, Resende RO (2016). Biological and molecular characterization of a highly divergent johnsongrass mosaic virus isolate from *Pennisetum purpureum*. *Arch Virol* 161:1981-1986.

Sudheera Y, Vishnu Vardhan GP, Hema M, Krishna Reddy M, Sreenivasulu, P (2014). Characterization of a

Additional material in support of this proposal

References:

potyvirus associated with yellow mosaic disease of jasmine (*Jasminum sambac* L.) in Andhra Pradesh, India. *Virus Dis*. 25:394-397.

Tang Y, Gao F, Yang Z, Wu Z, Yang L (2016). Complete genome analysis of jasmine virus T from *Jasminum sambac* in China. *Arch Virol*. doi: 10.1007/s00705-016-2811-1

Thottappilly G, Bosque-Pérez NA, Rossel HW (1993). Viruses and virus diseases of maize in tropical Africa. *Plant Pathol* 42: 494-509.

Thouvenel JC, Givord L, Pfeiffer P (1976). Guinea grass mosaic virus, a new member of the potato virus Y group. *Phytopathol* 66: 954-957.

Annex:

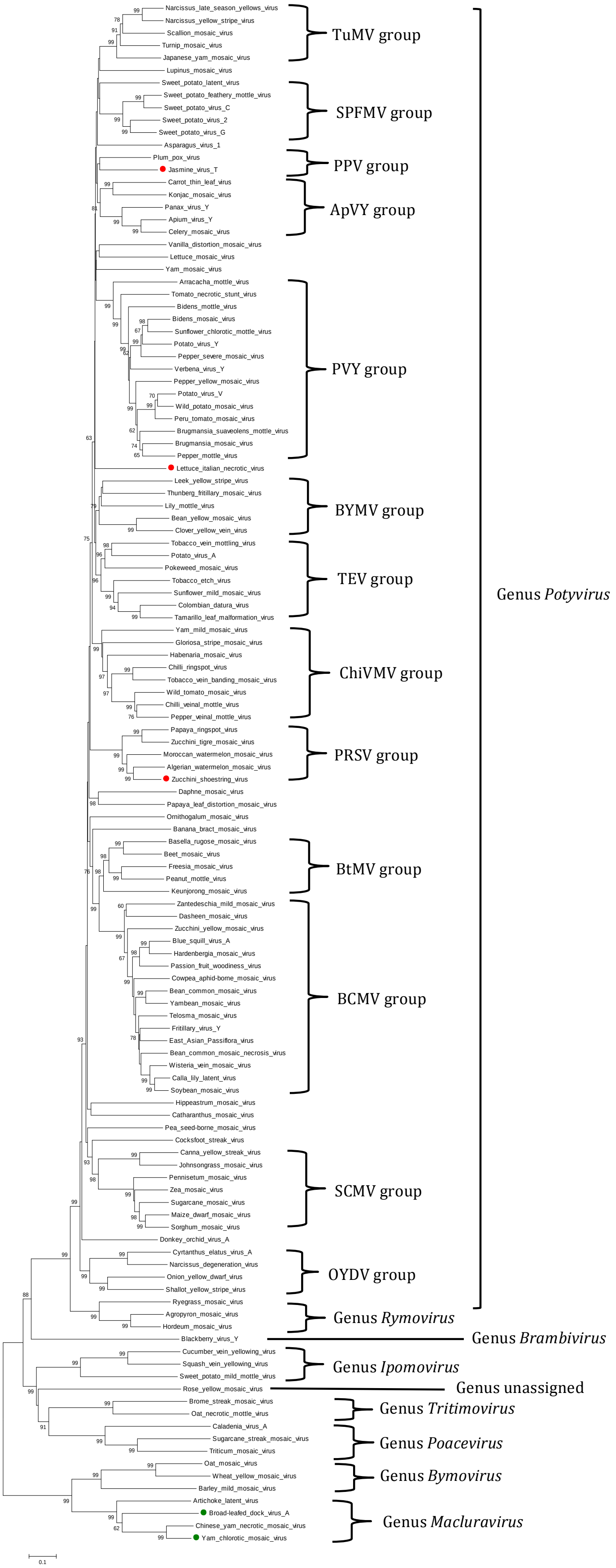
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Figure 1.

Neighbor-joining tree generated from an alignment of complete polyprotein sequences showing estimated phylogeny of polyprotein amino acid sequences deduced from completely sequenced isolates of representative members of the family *Potyviridae*. Representative members of genera *Brambyvirus, Bymovirus, Ipomovirus, Macluravirus, Poacevirus, Potyvirus, Rymovirus, Tritimovirus*, and one virus, rose yellow mosaic virus, for which a genus is currently unassigned, were used. The three new members of genus *Potyvirus* proposed here are indicated with a red dot, and two new members of genus *Macluravirus* (see separate proposal) are indicated with a green dot. The tree was deduced in Mega v6.06 after alignment by Muscle using Neighbor-joining based on the Poisson model with 1,000 bootstrap replicates. Branch lengths are proportional to genetic distance in units of amino acid substitutions per site. Bootstrap support for branches >60% is shown at the junctions of branches.

Accession codes corresponding to the nucleotide sequence of each virus genome sequence used in the tree are: Agropyron mosaic virus, NC_005903; Algerian watermelon mosaic virus, NC_010736; Apium virus Y, NC_014905; arracacha mottle virus, NC_018176; artichoke latent virus, NC_026759; Asparagus virus 1, NC_025821; banana bract mosaic virus, NC_009745; barley mild mosaic virus (RNA1), D83408; Basella rugose mosaic virus, NC_009741; bean common mosaic necrosis virus, NC_004047; bean common mosaic virus, NC_004047; bean yellow mosaic virus, NC_003492; beet mosaic virus, NC_005304; bidens mosaic virus, NC_023014; bidens mottle virus, NC_014325; blackberry virus Y, NC_008558; blue squill virus A, NC_019415; broad-leafed dock virus A, KU053507; brome streak mosaic virus, NC_003501; Brugmansia mosaic virus, NC_020105; Brugmansia suaveolens mottle virus, NC_014536;

Caladenia virus A, NC_018572; calla lily latent virus, NC_021196; Canna yellow streak virus, NC_013261; carrot thin leaf virus, NC_025254; Catharanthus mosaic virus, KP742991; celery mosaic virus, NC_015393; chilli ringspot virus, NC_016044; chilli veinal mottle virus, NC_005778; Chinese yam necrotic mosaic virus, NC_018455; clover yellow vein virus, NC_003536; cocksfoot streak virus, NC_003742; Colombian datura virus; NC_020072; cowpea aphid-borne mosaic virus, NC_004013; Cyrtanthus elatus virus A, NC_017977; Daphne mosaic virus, NC_008028; Dasheen mosaic virus, NC_003537; donkey orchid virus A, NC_021197; East Asian Passiflora virus, NC_007728; Freesia mosaic virus, NC_014064; fritillary virus Y, NC_010954; Gloriosa stripe mosaic virus, EF427894; habenaria mosaic virus, EF427894; Hardenbergia mosaic virus, NC_015394; Hippeastrum mosaic virus, NC_017967; Hordeum mosaic virus, NC_005904; Japanese yam mosaic virus, NC_000947; jasmine virus T, KT222674; johnsongrass mosaic virus, NC_003606; keunjorong mosaic virus, NC_016159; konjac mosaic virus, NC_007913; leek yellow stripe virus, NC_004011; lettuce Italian necrotic virus; KP769852; lettuce mosaic virus, NC_003605; lily mottle virus, NC_005288; Lupinus mosaic virus, NC_014898; maize dwarf mosaic virus, NC_003377; Moroccan watermelon mosaic virus, NC_009995; Narcissus degeneration virus, NC_008824; Narcissus late season yellows virus, NC_023628; Narcissus yellow stripe virus, NC_011541; oat mosaic virus (RNA1), NC_004016; oat necrotic mottle virus, NC_005136; onion yellow dwarf virus, NC_005029; Ornithogalum mosaic virus, NC_019409; Panax virus Y, NC_014252; papaya leaf distortion mosaic virus, NC_005028; papaya ringspot virus, NC_001785; passion fruit woodiness virus, NC_014790; pea seed-borne mosaic virus, NC_001671; peanut mottle virus, NC_002600; Pennisetum mosaic virus, NC_007147; pepper severe mosaic virus, NC_008393; pepper veinal mottle virus, NC_011918; pepper yellow mosaic virus, NC_014327; Peru tomato mosaic virus, NC_004573; plum pox virus, NC_001445; pokeweed mosaic virus, NC_018872; potato virus A, NC_004039; potato virus V, NC_004010; potato virus Y, NC_001616; rose yellow mosaic virus, NC_019031; ryegrass mosaic virus, NC_001814; scallion mosaic virus, NC_003399; shallot yellow stripe virus, NC_007433; sorghum mosaic virus, NC_004035; soybean mosaic virus, NC_002634; squash vein yellowing virus, NC_010521; sugarcane mosaic virus, NC_003398; sugarcane streak mosaic virus, NC_014037; sunflower chlorotic mottle virus, NC_014038; sunflower mild mosaic virus, NC_021065; sweet potato feathery mottle virus, NC_001841; sweet potato latent virus, NC_020896; sweet potato mild mottle virus, NC_003797; sweet potato virus 2, NC_017970; sweet potato virus C; NC_014742; sweet potato virus G, NC_018093; tamarillo leaf malformation virus, NC_026615; Telosma mosaic virus, NC_009742; thunberg fritillary mosaic virus, NC_007180; tobacco etch virus, NC_001555; tobacco vein banding mosaic virus, NC_009994; tobacco vein mottling virus, NC_001768; tomato necrotic stunt virus, NC_017824; Triticum mosaic virus, NC_012799; turnip mosaic virus, NC_002509; vanilla distortion mosaic virus, NC_025250; Verbena virus Y, NC_010735; wheat yellow mosaic virus (RNA1), FJ361765; wild potato mosaic virus, NC_004426; wild tomato mosaic virus, NC_009744; Wisteria vein mosaic virus, NC_007216; yambean mosaic virus, NC_016441; yam chlorotic mosaic virus, KT724961; yam mild mosaic virus, NC_019412; yam mosaic virus, NC_004752; Zantedeschia mild mosaic virus, NC_011560; Zea mosaic virus, NC_018833; zucchini shoestring virus, KU355553; zucchini tigre mosaic virus, NC_023175; zucchini yellow mosaic virus, NC_003224.


Narcissus_late_season_yellows_virus
Narcissus_yellow_stripe_virus
Scallion_mosaic_virus
Turnip_mosaic_virus
Japanese_yam_mosaic_virus
TuMV group
Lupinus_mosaic_virus
Sweet_potato_latent_virus
Sweet_potato_feathery_mottle_virus
Sweet_potato_virus_C
Sweet_potato_virus_2
Sweet_potato_virus_G
SPFMV group
Asparagus_virus_1
Plum_pox_virus
Jasmine_virus_T
PPV group
Carrot_thin_leaf_virus
Konjac_mosaic_virus
Panax_virus_Y
Apium_virus_Y
Celery_mosaic_virus
ApVY group
Vanilla_distortion_mosaic_virus
Lettuce_mosaic_virus
Yam_mosaic_virus
Arracacha_mottle_virus
Tomato_necrotic_stunt_virus
Bidens_mottle_virus
Bidens_mosaic_virus
Sunflower_chlorotic_mottle_virus
Potato_virus_Y
Pepper_severe_mosaic_virus
Verbena_virus_Y
Pepper_yellow_mosaic_virus
Potato_virus_V
Wild_potato_mosaic_virus
Peru_tomato_mosaic_virus
Brugmansia_suaveolens_mottle_virus
Brugmansia_mosaic_virus
Pepper_mottle_virus
PVY group
Lettuce_italian_necrotic_virus
Leek_yellow_stripe_virus
Thunberg_fritillary_mosaic_virus
Lily_mottle_virus
Bean_yellow_mosaic_virus
Clover_yellow_vein_virus
BYMV group
Tobacco_vein_mottling_virus
Potato_virus_A
Pokeweed_mosaic_virus
Tobacco_etch_virus
Sunflower_mild_mosaic_virus
Colombian_datura_virus
Tamarillo_leaf_malformation_virus
TEV group
Yam_mild_mosaic_virus
Gloriosa_stripe_mosaic_virus
Habenaria_mosaic_virus
Chilli_ringspot_virus
Tobacco_vein_banding_mosaic_virus
Wild_tomato_mosaic_virus
Chilli_veinal_mottle_virus
Pepper_veinal_mottle_virus
ChiVMV group
Papaya_ringspot_virus
Zucchini_tigre_mosaic_virus
Moroccan_watermelon_mosaic_virus
Algerian_watermelon_mosaic_virus
Zucchini_shoestring_virus
PRSV group
Daphne_mosaic_virus
Papaya_leaf_distortion_mosaic_virus
Ornithogalum_mosaic_virus
Banana_bract_mosaic_virus
Basella_rugose_mosaic_virus
Beet_mosaic_virus
Freesia_mosaic_virus
Peanut_mottle_virus
Keunjorong_mosaic_virus
BtMV group
Zantedeschia_mild_mosaic_virus
Dasheen_mosaic_virus
Zucchini_yellow_mosaic_virus
Blue_squill_virus_A
Hardenbergia_mosaic_virus
Passion_fruit_woodiness_virus
Cowpea_aphid-borne_mosaic_virus
Bean_common_mosaic_virus
Yambean_mosaic_virus
Telosma_mosaic_virus
Fritillary_virus_Y
East_Asian_Passiflora_virus
Bean_common_mosaic_necrosis_virus
Wisteria_vein_mosaic_virus
Calla_lily_latent_virus
Soybean_mosaic_virus
BCMV group
Hippeastrum_mosaic_virus
Catharanthus_mosaic_virus
Pea_seed-borne_mosaic_virus
Cocksfoot_streak_virus
Canna_yellow_streak_virus
Johnsongrass_mosaic_virus
Pennisetum_mosaic_virus
Zea_mosaic_virus
Sugarcane_mosaic_virus
Maize_dwarf_mosaic_virus
Sorghum_mosaic_virus
SCMV group
Donkey_orchid_virus_A
Cyrtanthus_elatus_virus_A
Narcissus_degeneration_virus
Onion_yellow_dwarf_virus
Shallot_yellow_stripe_virus
OYDV group
Genus *Potyvirus*
Ryegrass_mosaic_virus
Agropyron_mosaic_virus
Hordeum_mosaic_virus
Genus *Rymovirus*
Blackberry_virus_Y
Genus *Brambivirus*
Cucumber_vein_yellowing_virus
Squash_vein_yellowing_virus
Sweet_potato_mild_mottle_virus
Genus *Ipomovirus*
Rose_yellow_mosaic_virus
Genus unassigned
Brome_streak_mosaic_virus
Oat_necrotic_mottle_virus
Genus *Tritimovirus*
Caladenia_virus_A
Sugarcane_streak_mosaic_virus
Triticum_mosaic_virus
Genus *Poacevirus*
Oat_mosaic_virus
Wheat_yellow_mosaic_virus
Barley_mild_mosaic_virus
Genus *Bymovirus*
Artichoke_latent_virus
Broad-leafed_dock_virus_A
Chinese_yam_necrotic_mosaic_virus
Yam_chlorotic_mosaic_virus
Genus *Macluravirus*
0.1