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: *2009.004a-iP* (to be completed by ICTV officers)

Short title: New species and genus in the family Potyviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

Roy French and Satyanarayana Tatineni Roy.French@ars.usda.gov
Satyanarayana.Tatineni@ars.usda.gov

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	May 2009
Date of this revision (if different to above):	May 2010

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.004aP***	(assigned by ICTV officers)

To create 1 new species with the name(s):

Triticum mosaic virus

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.004bP***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***Poacevirus*** **(new genus)**
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.

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

The virus is transmitted by an eriophyid mite and causes a disease in wheat. The complete genome sequence (FJ669487) shows it to have the genome organization of a member of the family *Potyviridae* with some unique characteristics. It has a much longer 5'-UTR than any other known member of the family and it is only distantly related to other fully sequenced members (always <45% amino acid identity even in the NIb cistron, the most conserved region of the genome). See Appendix, Fig. 1 and Table 1).

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.004cP***	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Code	***2009.004dP***	(assigned by ICTV officers)

To name the new genus: *Poacevirus*

assigning a new genus to higher taxa

Code	***2009.004eP***	(assigned by ICTV officers)

To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

Subfamily:	
Family:	***Potyviridae***
Order:	

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

Code	***2009.004fP***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Triticum mosaic virus

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Code	***2009.004gP***	(assigned by ICTV officers)

To assign the following as additional species of the new genus:

***Sugarcane streak mosaic virus* (previously an unassigned species in the family)**

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Phylogenetic analysis of complete genome sequences indicates that ***Triticum mosaic virus*** does not cluster with any existing genus in the ***Potyviridae.*** *Triticum mosaic virus* is transmitted by an eriophyid mite but is not closely related to other mite-transmitted potyvirids in the genera ***Tritimovirus*** and ***Rymovirus***. See the appendix Table 1 and Fig. 2 for more details.

Origin of the new genus name:

Derived from the plant family Poaceae; all known hosts for two proposed members of this genus (*Triticum mosaic virus* and *Sugarcane streak mosaic virus*) belong to this plant family.

Reasons to justify the choice of type species:

Triticum mosaic virus was the first virus species belonging to the proposed genus to be completely sequenced.

Species demarcation criteria in the new genus:

- If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

Suggested species demarcation criteria are those for the family in general and include:
Genome sequence relatedness.
- CP aa sequence identity less than ca. 80%,
- nt sequence identity of less than 85% over whole genome,
- nt sequence identity of less than 75% in the 3’ non-coding region
- different polyprotein cleavage sites.

The proposed two species have <50% CP aa sequence identity (see Appendix, Table 1). All NIa proteinase cleavage sites of TriMV and SCMV have an H in the -1 position (see Appendix, Table 2). This is based on the accessions: *Triticum mosaic virus* FJ669487 and *Sugarcane streak mosaic virus* GQ388116.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2009.004hP***	(assigned by ICTV officers)

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

Sugarcane streak mosaic virus

The present taxonomic position of these taxon/taxa:

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

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	

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

Allocation to (new) genus within the family.

Part (b) re-assign to a higher taxon

Code	***2009.004iP***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Poacevirus* (new)**	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:		
Family:	***Potyviridae***	
Order:		

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Only the 3'-half of the genome has been sequenced but in this region the polyprotein has about 50% aa identity to the complete sequence of Triticum mosaic virus (the type member of the proposed new genus). The two viruses group convincingly in phylogenetic analyses.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Tatineni, S., Ziems, A. D., Wegulo, S. N., French, R. 2009. Triticum mosaic virus: A Distinct Member of the Family Potyviridae with an Unusually Long Leader Sequence, Phytopathology 99:943-950.

Seifers, D. L., Martin, T. J., Harvey, T. L., Fellers, J. P., Stack, J. P., Ryba-White, M., Haber, S., Krokhin, O., Spicer, V., Lovat, N., Yamchuk, A., and Standing, K. G. 2008. Triticum mosaic virus: A new virus isolated from wheat in Kansas. Plant Dis. 92:808-817.

Seifers, D. L., Martin, T. J., Harvey, T. L., Fellers, J. P., and Michaud, J. P. 2009. Identification of the wheat curl mite as the vector of Triticum mosaic virus. Plant Dis. 93:25-29.

Xu, D. -L., Zhou, G. -H., Xie, Y. -J.,Mock,R., Li, R. 2010. Complete nucleotide sequence and taxonomy of Sugarcane streak mosaic virus, member of a novel genus in the family Potyviridae. Virus Genes 40:432–439.

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.

ABSTRACT

Tatineni, S., Ziems, A. D., Wegulo, S. N., and French, R. 2009. *Triticum mosaic virus*: a distinct member of the family *Potyviridae* with an unusually long leader sequence. Phytopathology 99: 0000-0000.

The complete genome sequence of *Triticum mosaic virus* (TriMV), a member in the family *Potyviridae*, has been determined to be 10,266 nucleotides (nt) excluding the 3’-polyadenylated tail. The genome encodes a large polyprotein of 3,112 amino acids with the ‘hall-mark proteins’ of potyviruses including a small overlapping gene, PIPO, in the P3 cistron. The genome of TriMV has an unusually long 5’-nontranslated region of 739 nts with 12 translation initiation codons and three small open reading frames, which resemble those of the internal ribosome entry site containing 5’-leader sequences of the members of *Picornaviridae*. Pair-wise comparison of 10 putative mature proteins of TriMV with those of representative members of genera in the family *Potyviridae* revealed 33-44% amino acid identity within the highly conserved NIb protein sequence, and 15-29% amino acid identity within the least conserved P1 protein, suggesting that TriMV is a distinct member in the family *Potyviridae*. In contrast, TriMV displayed 47-65% amino acid sequence identity with available sequences of mature proteins of *Sugarcane streak mosaic virus* (SCSMV), an unassigned member of the *Potyviridae*. Phylogenetic analyses of the complete polyprotein, NIa-Pro, NIb and CP sequences of representative species of six genera and unassigned members of the *Potyviridae* suggested TriMV and SCSMV are sister taxa and share a most recent common ancestor with tritimoviruses or ipomoviruses. These results suggest that TriMV and SCSMV should be classified in a new genus, and we propose the genus *Poacevirus* in the family *Potyviridae* with TriMV as the type member.

Table 1. Percent amino acid sequence identities of TriMV proteins compared to selected members of other genera and unassigned members in the family *Potyviridae*.
[a]Sequence data not available; [b]Compared with P1a; [c]Compared TriMV P1 with CVYV P1b; [d]HC-Pro cistron is not present; Virus names for abbreviations and GenBank accession numbers of sequences used for sequence comparison are given in the legend for Figure 2.

Cistron	*Potyvirus*		*Rymovirus*		*Macluravirus*	*Ipomovirus*		*Tritimovirus*		*Bymovirus*	Unassigned	
	PYV	SCMV	RGMV	AgMV	MacMV	CVYV	SPMMV	WSMV	BrSMV	BaYMV	BlVY	SCSMV
P1	17.6	16.5	17.1	16.3	-[a]	18.5[b]	15.0	26.9	28.7	17.4	15.0	40.2
HC-Pro	20.4	19.0	21.8	20.5	-	20.9[c]	20.4	21.1	19.5	-[d]	20.4	45.4
P3	17.3	19.5	19.3	19.2	-	17.6	18.4	19.7	19.9	20.1	20.1	35.3
6K1	19.3	14.9	21.1	19.6	-	19.3	12.5	17.9	22.8	17.9	17.5	60.7
CI	25.5	26.1	29.0	27.6	-	24.8	24.3	29.2	25.6	24.5	23.4	60.6
6K2	13.5	22.6	18.3	17.0	-	21.8	26.4	21.6	33.3	10.7	20.6	54.0
NIa-VPg	22.7	22.0	21.4	21.3	-	24.8	24.5	22.9	17.7	21.6	20.9	49.0
NIa-Pro	20.2	22.1	22.4	23.0	-	31.1	24.4	25.4	24.2	19.2	23.0	46.9
NIb	37.9	38.7	39.4	38.7	-	43.7	40.7	41.3	43.1	32.6	38.4	66.9
CP	22.9	22.0	23.6	20.4	19.0	24.7	25.8	25.6	29.6	21.0	18.7	48.3

Table 2. Putative proteinase cleavage sites in *Triticum mosaic virus* and *Sugarcane streak mosaic virus* polyproteins.

		Triticum mosaic virus	*Sugarcane streak mosaic virus*
Proteinase	Peptide junction	Amino acid sequence	Amino acid sequence
P1	P1/HC-Pro	EGLTYY/S	EEIVFY/T
HC-Pro	HC-Pro/P3	KDYRIG/G	MKYRIG/G
NIa	P3/6K1	EDYVLH/A	ESLIHH/A
NIa	6K1/CI	DSFVFH/A	ESLVFH/A
NIa	CI/6K2	DCLVFH/G	ECLIYH/G
NIa	6K2/NIa-VPg	EKYVMH/G	ETLIMH/A
NIa	NIa-VPg/NIa-Pro	DNYVPH/S	ETIVMH/A
NIa	NIa-Pro/NIb	SEFIFH/N	TELIFH/G
NIa	NIb/CP	DEFVFH/S	EALIYH/A

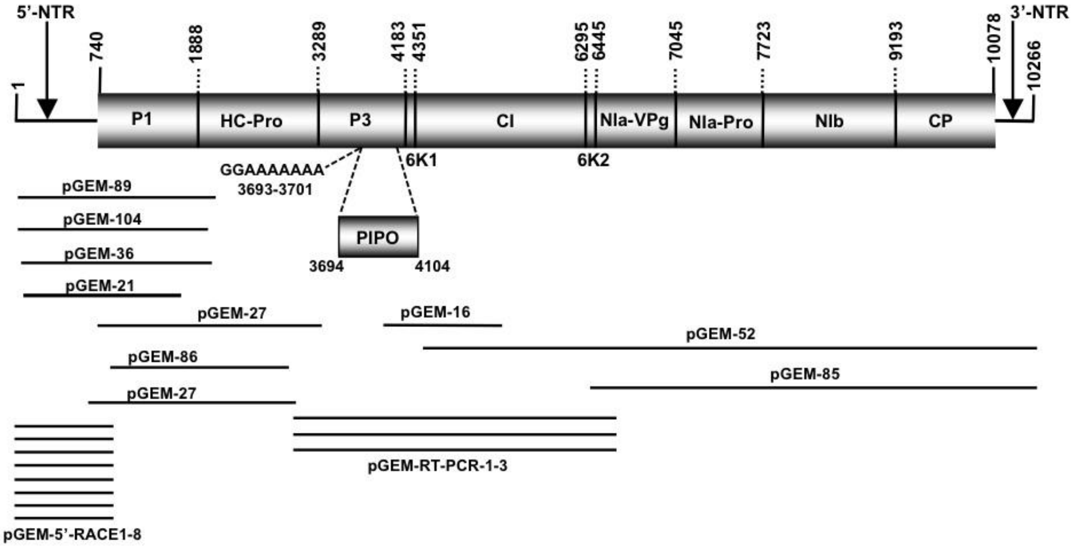
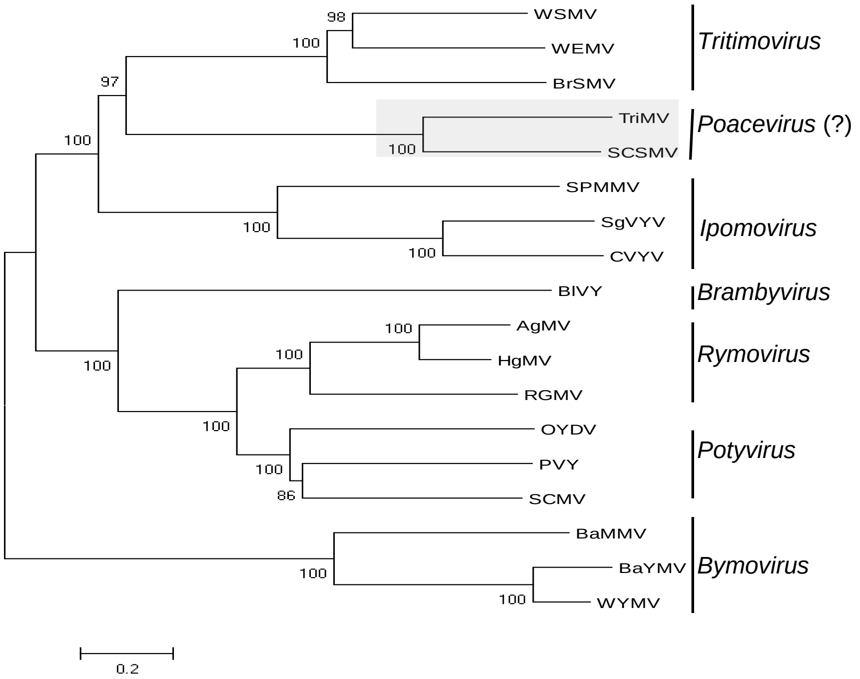
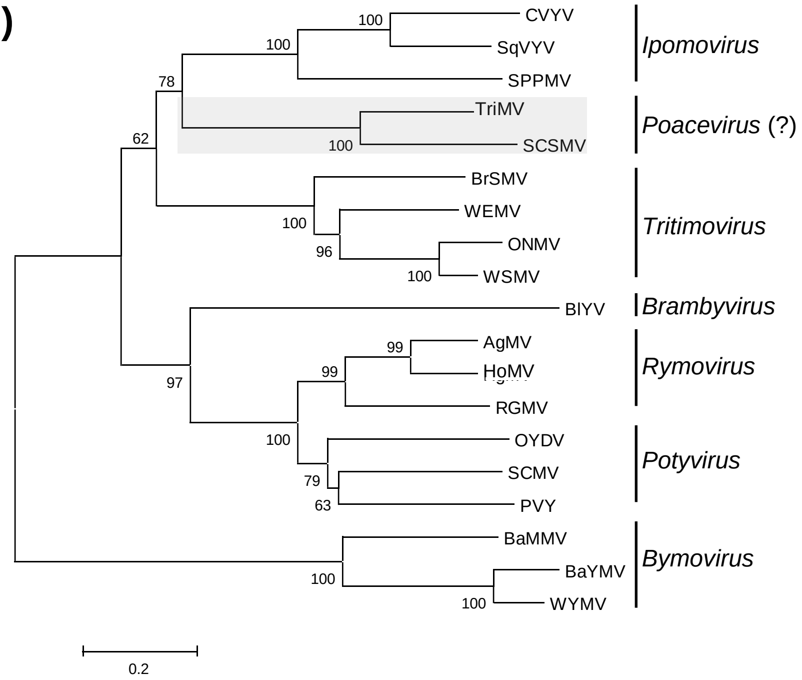


Figure 1. Schematic representation of the genome organization of TriMV depicting coding proteins in cistrons and the location of cleavage sites (dotted lines). The solid lines on either side of the genome organization represent nontranslated regions (NTR). The location of a small open reading frame (ORF), pretty interesting potyvirus ORF (PIPO) (7), in P3 is shown below the genomic organization as an enlarged view. The location of the conserved motif (G2A7) at the 5' end of PIPO is indicated. Horizontal lines below the genomic organization represent the location of overlapping cDNA, RT-PCR and 5'RACE clones used to obtain the complete genome sequence of TriMV. Note that several independent clones covering the 5' end of genomic RNA were sequenced to obtain an unambiguous 5' end sequence.

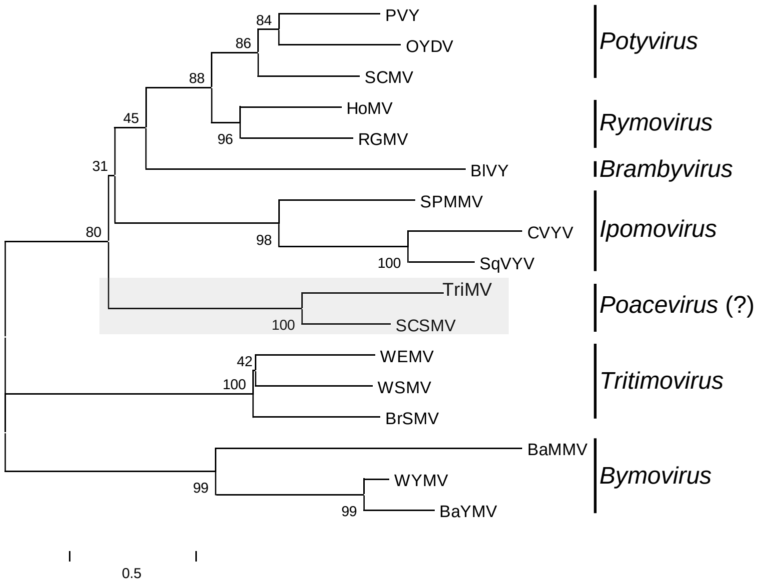
(A)


98
100
97
100
WSMV
WEMV
BrSMV
Tritimovirus
TriMV
100
SCSMV
Poacevirus (?)
SPMMV
100
SgVYV
100
CVYV
Ipomovirus
BlVY
Brambyvirus
100
AgMV
100
HgMV
100
RGMV
Rymovirus
100
OYDV
100
PVY
86
SCMV
Potyvirus
BaMMV
100
BaYMV
100
WYMV
Bymovirus
0.2

(B)


100
CVYV
100
SqVYV
SPPMV
Ipomovirus
78
62
TriMV
100
SCSMV
Poacevirus (?)
BrSMV
100
WEMV
96
ONMV
100
WSMV
Tritimovirus
BlYV
Brambyvirus
99
AgMV
99
HoMV
RGMV
Rymovirus
97
100
OYDV
79
SCMV
63
PVY
Potyvirus
BaMMV
100
BaYMV
100
WYMV
Bymovirus
0.2

(C) NIa-VPg



(D) CP

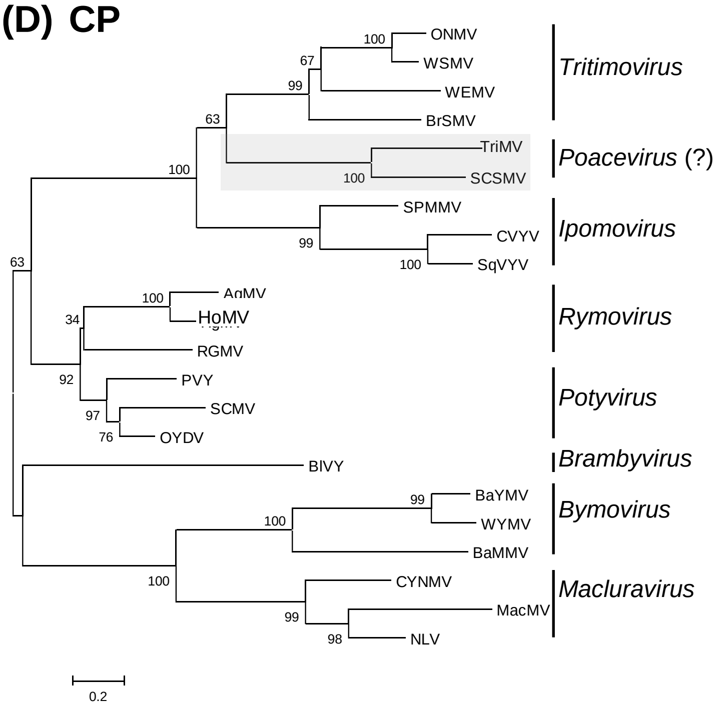


Figure. 2. Unrooted bootstrap consensus phylogenetic trees derived from the amino acid sequences of polyprotein (A), NIb (B), NIa-VPg (C), and CP (D) of TriMV, unassigned and representative species of various genera of the family Potyviridae. Phylogenetic trees were constructed by the neighbor-joining method using the JTT matrix and pair-wise gap deletion with 1,000 bootstrap replicates; and bootstrap support is indicated at branch points. The bar represents the number of amino acid replacements per site. The recognized genera with representative members are indicated on the right side of the phylogenetic trees, and TriMV and SCSMV are indicated with shade. GenBank accession numbers of potyviruses used in phylogenetic tree analysis are Agropyron mosaic virus (AgMV, AY623626), Barley mild mosaic virus (BaMMV, Y10973), Barley yellow mosaic virus (BaYMV, AJ132688), Blackberry virus Y (BlVY, AY994084), Brome streak mosaic virus (BrSMV, Z48506), Chinese yam necrotic mosaic virus (CYNMV, AB044386), Cucumber vein yellowing virus (CVYV, AY578085), Hordeum mosaic virus (HoMV, AY623627), Maclura mosaic virus, MacMV, U58771), Narcissus latent virus (NLV, DQ450199), Oat necrotic mottle virus (ONMV, AY377983), Onion yellow dwarf virus (OYDV, AJ510223), Potato virus Y (PVY, X12456), Ryegrass mosaic virus (RGMV, Y09854), Squash vein yellowing virus (SqVYV, EU259611), Sugarcane mosaic virus (SCMV,

AJ297628), Sugarcane streak mosaic virus (SCSMV, GQ388116), Sweet potato mild mottle virus (SPMMV, Z73124), Triticum mosaic virus (TriMV, FJ669487), Wheat eqlid mosaic virus (WEMV, EF608612), Wheat streak mosaic virus (WSMV, AF057533), and Wheat yellow mosaic virus (WYMV, D86634).