**Virus Taxonomy**
The ICTV Report on Virus Classification and Taxon Nomenclature
*Potyviridae* Chapter

**Potyviridae**

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**Summary**

Members of family *Potyviridae* (termed potyvirids) consist of monopartite and bipartite plant viruses with a single-stranded, positive-sense RNA genome and flexuous, filamentous particles (Table 1. *Potyviridae*). Genomes have a VPg covalently linked to the 5′-end and the 3′-terminus is polyadenylated. Genomes encode a large polyprotein that is self-cleaved into a set of functional proteins. Gene order is generally conserved throughout the family (Adams et al., 2005b).

**Table 1. Potyviridae.** Characteristics of members of the family *Potyviridae.*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td>potato virus Y-O (U09509), species <em>Potato virus Y</em>, genus <em>Potyvirus</em></td>
</tr>
<tr>
<td>Virion</td>
<td>Non-enveloped, flexuous and filamentous capsid, 680–900 nm long and 11–20 nm in diameter with a single core capsid protein</td>
</tr>
<tr>
<td>Genome</td>
<td>8–11 kb of positive-sense, single-stranded, usually monopartite RNA (bipartite in genus <em>Bymovirus</em>)</td>
</tr>
<tr>
<td>Replication</td>
<td>Cytoplasmic, initiated in virus replication complexes on membranous vesicles at ER exit sites. Replication initiates at 6K2-induced ER-originated vesicles</td>
</tr>
<tr>
<td>Translation</td>
<td>Directly from genomic RNA.</td>
</tr>
<tr>
<td>Host range</td>
<td>Plants (all virus genera). Most members are arthropod-borne but those of genus <em>Bymovirus</em> are transmitted by plasmodiophorids</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>10 genera including over 200 species</td>
</tr>
</tbody>
</table>

**Virion**

**Morphology**

Virions are flexuous filaments with no envelope and are 11–20 nm in diameter, with a helical pitch of about 3.4 nm (Figure 1. *Potyviridae*). Particle lengths of members of some of the ten genera differ. Members of the genera *Potyvirus*, *Poaecivirus*, *Ipomovirus*, *Macluravirus*, *Rymovirus*, *Tritimovirus*, *Brambyvirus*, *Bevemovirus*, *Roymovirus* and of the unassigned virus species *Spartina mottle virus* are monopartite with particle modal lengths of 650–950 nm. Members of the genus *Bymovirus* are bipartite with particles of two modal lengths of 250–300 and 500–600 nm.
Physicochemical and physical properties

Virions of viruses in the genera Potyvirus and Rymovirus have a density in CsCl of about 1.31 g cm\(^{-3}\) and Sedimentation coefficient \(S_{20,w}\) of 137–160S. Those of the genus Bymovirus have a density in CsCl of about 1.29 g cm\(^{-3}\).

Nucleic acid

Viruses in all genera except Bymovirus have a single molecule of positive-sense, ssRNA, 8.2 kb (bellflower veinal mottle virus-SW) to 11.0 kb (sweet potato feathery mottle virus-Piu3) in size. Virions are infectious. A VPg of about 24 kDa is covalently linked to the 5′-terminal nucleotide. A polyadenylate tract (20 to 160 adenosines) is present at the 3′-terminus. Bymoviruses have two positive-sense, ssRNA molecules; RNA1 is 7.3–7.6 kb and RNA2 is 3.5–3.7 kb. Both RNAs have 3′-terminal polyadenylate tracts and probably a VPg at the 5′-termini.

Proteins

Virions contain one type of coat (capsid) protein (CP) of 28.5–47 kDa. N- and C-terminal residues are positioned on the exterior of the virion. Mild trypsin treatment removes N- and C-terminal segments, leaving a trypsin-resistant core of about 24 kDa. Plant proteases may degrade the CP \(in\ vivo\), as occurs \(in\ vitro\) during purification using some procedures or from certain hosts. All potyvirus CPs display significant aa sequence identity in the trypsin-resistant core, but little identity in their N and C-terminal segments.

Genome organization and replication

The genomic RNA (two RNAs for members of the genus Bymovirus) encodes a single major polyprotein. This then undergoes co- and post-translational proteolytic processing by three viral-encoded proteinases to form the mature proteins. Genomic RNA replicates via the production of a full-length negative-sense RNA. While there are exceptions noted in the relevant genus descriptions, the polyprotein of the majority of monopartite viruses in the family is cleaved into ten products, which show conservation of sequence and organisation (Kekarainen et al., 2002). As shown in Figure 2. Potyviridae, these products are:

- **P1** (Protein 1): Of all the potyvirid proteins, P1 is the least conserved in sequence and the most variable in size. It plays a significant role in virus replication probably due to the stimulation of the gene silencing suppressor HC-Pro. A serine protease domain towards the C-terminus cleaves the P1 from the polyprotein, typically at Tyr/Phe-Ser (Valli et al., 2007).
- **HC-Pro** (Helper Component-Protease): the HC-Pro protein has roles in suppression of gene silencing and in vector transmission. A cysteine protease domain towards the C-terminus cleaves it from the remainder of the downstream polyprotein, typically at Gly-Gly.
- **P3** (Protein 3): Involved in virus replication and appears to be significant in host range and symptom development.
- **6K1** (6-kDa peptide 1): Although it is present in the replication complex and required for replication, the function of this small protein is not known.
- **CI** (Cylindrical Inclusion protein): This protein has helicase activity and accumulates in inclusion bodies in the cytoplasm of infected plant cells.
- **6K2** (6-kDa peptide 2): A small transmembrane protein probably anchoring the replication complex to the ER.
- **VPg** (Viral Protein genome-linked): Attached to the 5′-terminus of the genome and belongs to a class of intrinsically disordered proteins. It is essential for virus replication and translation, interacting with one or several isoforms of the eIF4E translation initiation factor, and is also involved in suppression of RNA silencing.
- **Nla-Pro** (Nuclear inclusion A-protease): Serine-like cysteine protease responsible for cleavage of most sites in the polyprotein, typically at Gin/Glu-Ser/Gly/Ala (Adams et al., 2005a).
- **Nlb** (Nuclear inclusion B): The RNA-dependent RNA polymerase.
- **CP** (Coat (capsid) protein): Viral coat protein that also has roles in virus movement, genome amplification and vector transmission.
- **PIPO** (Pretty Interesting Potyvirus ORF): A short ORF embedded within the P3 cistron expressed as the trans-frame P3N-PIPO protein.
by a polymerase slippage mechanism (Chung et al., 2008, Olspert et al., 2015, Rodamilans et al., 2015). PIPO has been identified throughout the family and has been shown to be essential for the intercellular movement of viruses.

The polymerase slippage model for the production of P3N-PIPO is consistent with the theory that potyvirus intercellular movement is coupled to active virus genome replication and translation. Potyvirus replication initiates at the 6K2-induced ER-originated vesicles. The cellular COPI and COPII coating machineries are involved in the biogenesis of the potyvirus 6K2 vesicles (Wei and Wang 2008). The ER-derived 6K2 vesicles also target and are associated with chloroplasts for virus replication.

Figure 2. Potyviridae. Genomic map of a typical member of the genus Potyvirus. The ssRNA genome is represented by a line and the polyprotein ORF by an open box with the mature proteolytic products named. VPg (viral protein genome-linked), the genome-linked viral protein covalently attached to the 5′-terminal nucleotide is represented by a hexagon; P1-Pro (protein 1 protease), a protein with serine proteolytic activity responsible for cleavage at typically Tyr/Phe-Ser (O); HC-Pro (helper component protease), a protein with aphid transmission helper-component activity and cysteine proteolytic activity responsible for cleavage at typically Gly-Gly (◆); P3 (protein 3); PIPO (pretty interesting Potyviridae ORF); 6K (six kilodalton peptide); CI (cytoplasmic inclusion); Nla-Pro (nuclear inclusion A protease), cysteine-like proteolytic activity responsible for cleavage at Gln/Glu-(Ser/Gly/Ala) (↓); Nib (nuclear inclusion B), RNA-dependent RNA polymerase; CP (coat protein). Cleavage sites of P1-Pro, (O), HC-Pro (◆) and Nla-Pro (↓) are indicated.

Biology

Inclusion body formation

All members of the family Potyviridae form cytoplasmic cylindrical inclusion (CI) bodies during infection. The CI is an array of a 70 kDa viral protein that possesses ATPase and helicase activities. Some potyviruses induce nuclear inclusion bodies that are co-crystals of two viral-encoded proteins – Nla and Nib – that are present in equimolar amounts. The small nuclear inclusion (Nia) protein (49 kDa) is a polyprotein consisting of VPg and Nia-Pro. Amorphous inclusion bodies are also evident in the cytoplasm during certain potyvirus infections and represent aggregations of HC-Pro and perhaps other non-structural proteins.

Host range

Some members have a narrow host range, most members infect an intermediate number of plants, and a few members infect species in up to 30 families. Transmission to most hosts is readily accomplished by mechanical inoculation. Many viruses are widely distributed. Distribution is aided by seed transmission in some cases.

Transmission

Potyvirids are vectored by a variety of organisms. Members of the genera Potyvirus and Macluravirus have aphid vectors that transmit in a non-persistent, non-circulative manner. Two helper component protease aa motifs (R/KITC and PTK) and a CP motif (DAG for many potyviruses) are highly conserved and required for aphid transmission. Viruses in other genera in the Potyviridae lacking these motifs are not transmitted by aphids, and include rymoviruses, poaceviruses and tritimoviruses which are transmitted by eriophyid mites in a semi-persistent manner. The vector of rose yellow mosaic virus (RoYMV), the type species of the monotypic genus Roymovirus, has not been identified. The conserved potyvirus HC-Pro motifs are not present. Instead, a putative C-2x-C eriophyid mite transmission motif occurs at the N-terminus of the HC-Pro. The DAG motif of the CP is lacking. Together this information suggests RoYMV may also be transmitted by eriophyid mites, but this has not been proven experimentally. Bymoviruses are transmitted by root-infecting vectors in the order Plasmodiophorales, once described as fungi but now classified as Cercozoa. Ipomoviruses appear to be transmitted by whiteflies, and the vector of the one species within Brambyvirus is unknown. The HC-Pro of BVMV lacks the conserved potyvirus aphid transmission motifs, but the CP has a DTG near its N-terminus, possibly analogous to the DAG motif involved in aphid transmission.

Antigenicity

An epitope of the CP in the conserved internal trypsin-resistant core has been identified that is similar in most members of the family.

Derivation of names

Potyviridae: from the type species of the genus Potyvirus, Potato virus Y.

Genus demarcation criteria

The ten genera are differentiated by biological criteria, mainly transmission by specific vectors, and by molecular data (Figure 3. Potyviridae) (Adams et al., 2005b, Gibbs and Ohshima 2010). For the entire open reading frame, genus demarcation criteria are <46% nucleotide identity.
but this does not separate rymoviruses from potyviruses, which have different vectors.

**Figure 3. Potyviridae.** Pairwise unrooted neighbor-joining tree of complete polyprotein sequences of representative viruses within the family *Potyviridae*. The tree was produced in MEGA 7 (Kumar et al., 2016) using the JTT and gamma rate variation options from a CLUSTAL (Larkin et al., 2007) alignment of polyprotein sequences. Branches supported by >70% of 100 bootstrap replicates are indicated. This phylogenetic tree and corresponding sequence alignment are available to download from the Resources page.

**Species demarcation criteria**

Species demarcation criteria for the complete ORF are <76% nucleotide identity and <82% amino acid identity. The thresholds for species demarcation using nucleotide identity values for the individual coding regions range from 58% for the P1 coding region to 74–78% for other regions. For the coat protein, the optimal species demarcation criterion is 76–77% nucleotide and 80% amino acid identity (Adams et al., 2005b).

**Relationships with other taxa**
Members of the family Potyviridae are related to viruses in the order Picornavirales in their genome structure, in particular the presence of a single ORF translated into a polyprotein and the block of replication genes (helicase, VPg, 3C-like protease and polymerase). However, they differ from picornaviruses in virion morphology, the size of VPg and the type of helicase.
Genus: Bevemovirus

Distinguishing features

Like macluraviruses, members of the type species, Bellflower veinal mottle virus, lack the P1 region of most potyvirids. The HC-Pro lacks the conserved potyvirus aphid transmission motifs R/KITC and PTK. Isolates of bellflower veinal mottle virus share low (22–27%) nucleotide and amino acid sequence identities to macluraviruses.

Virion

Nucleic acid

Bellflower veinal mottle virus has a positive-sense RNA genome of 8,259 nt.

Genome organization and replication

Genome organization resembles that of members of the genus Macluravirus.

Biology

Isolates of Bellflower veinal mottle virus were obtained from bellflower (Campanula takesimana) that exhibited veinal mottle symptoms in South Korea. The virus is probably not aphid transmitted because the HC-Pro lacks the conserved potyvirus aphid transmission motifs R/KITC and PTK.

Derivation of names

Bevemovirus: from bellflower veinal mottle virus

Species demarcation criteria

See discussion under family description.

Member species

★ Exemplar isolate of the species

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
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<td>bellflower veinal mottle virus SW</td>
<td>KY491536</td>
<td>NC_039002</td>
<td>Complete genome</td>
<td>BVMoV</td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
Genus: Brambyvirus

Distinguishing features

The genus includes a single species, members of which are distinguished from all other members of the family in that they encode a very large P1 protein (83.6 k Da) containing an AlkB domain, and are also phylogenetically distinct (Susaimuthu et al., 2008).

Virion

Morphology

Virions are flexuous filaments 800×11–15 nm in size.

Nucleic acid

Virions contain a single molecule of linear, positive-sense ssRNA of about 11 kb.

Proteins

There is a single coat (capsid) protein of 40.9 kDa.

Genome organization and replication

Apart from the size of the P1 coding region, the genome organization is identical to that of most monopartite viruses in the family Potyviridae (Figure 2.Potyviridae).

Biology

Host range

The virus has been reported only from wild and cultivated blackberry (Rubus sp.) where it is often symptomless but is also a component of a complex of viruses. It is not known to cause symptoms in any herbaceous test host.

Transmission

The virus is presumed to be transmitted by an aerial vector that has not yet been identified.

Antigenicity

The virus could not be detected by a universal potyvirus monoclonal antibody but there are no additional data.

Derivation of names

Brambyvirus: from bramble, the host of blackberry virus Y, a member of the type species Blackberry virus Y

Species demarcation criteria

See discussion under family description.

Member species

<table>
<thead>
<tr>
<th>★ Exemplar isolate of the species</th>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
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<tr>
<td>blackberry virus Y</td>
<td>Blackberry virus Y</td>
<td>Ark3</td>
<td>AF499638</td>
<td>NC_008558</td>
<td>Complete genome</td>
<td>BlVY</td>
<td></td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
Genus: Bymovirus

Distinguishing features

Compared with other viruses in the family, members of the genus Bymovirus are distinct in having a divided (bipartite) genome and in being transmitted by the root-infesting parasite, Polymyxa graminis (Plasmodiophorales) a fungoid protist.

Virion

Morphology

Virions are flexuous filaments of two modal lengths, 250–300 nm and 500-600 nm; both are 13 nm in width (Figure 1. Bymovirus).

![Image of virions](image)

Figure 1. Bymovirus. Virions of an isolate of barley yellow mosaic virus, stained with 1% PTA, pH 7.0. The bar represents 200 nm (from D. Lesemann).

Physicochemical and physical properties

Virion density in CsCl is 1.28–1.30 g cm$^{-3}$.

Nucleic acid

Virions contain two molecules of linear positive-sense, ssRNA. RNA1 is 7.5–8.0 kb and RNA2 is 3.5–4.0 kb; RNA makes up 5% by weight of particles. There is little sequence identity between the two RNAs except in the 5′-untranslated region.

Proteins

Virions have a single coat (capsid) protein (CP) of 28.5–33 kDa. The CP of barley yellow mosaic virus isolates has 297 aa.

Genome organization and replication

The two RNA molecules are translated initially into precursor polypeptides from which functional proteins are derived by proteolytic processing (Figure 2. Bymovirus). The organization of RNA1 is similar to that of other potyviruses but without the P1 and HC-Pro proteins. The RNA2 polyprotein is unique to bymoviruses although the first protein encoded by RNA2 (P1, ca. 28 kDa) has aa domains with sequence similarities to the potyvirus protein HC-Pro. The larger protein of RNA2 (P2) is believed to have a role in vector transmission (You and Shirako 2010).
barley yellow mosaic virus, BaYMV

RNA1 (7,637 nts)

<table>
<thead>
<tr>
<th>Protein</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>PIPO</td>
<td>(+2 fs)</td>
</tr>
</tbody>
</table>

RNA2 (3,582 nts)

Biology

Cytology

There are characteristic pinwheel-like inclusions and membranous network structures are formed in the cytoplasm of infected plant cells. No nuclear inclusions are found.

Host range

The host range of bymoviruses is narrow, restricted to the host family Gramineae. Each member has a very restricted host range; for example, the barley-infecting viruses do not infect wheat and vice versa.

Transmission

Bymoviruses are transmitted by Polymyxa graminis in a persistent manner, surviving in resting spores as long as these remain viable; they are transmissible experimentally by mechanical inoculation, sometimes with difficulty.

Antigenicity

The viral proteins are moderately immunogenic; apart from barley mild mosaic virus, most members of the genus are serologically related. The CP aa sequence identity among members is 35–74%.

Derivation of names

Bymovirus: from barley yellow mosaic virus

Species demarcation criteria

See discussion under family description.

Member species

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
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</thead>
<tbody>
<tr>
<td>★ Barley mild mosaic virus</td>
<td>barley mild mosaic virus</td>
<td>UK-F</td>
<td>RNA1: Y10973; RNA2: X90904</td>
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<td>Complete genome</td>
<td>BaMMV</td>
</tr>
<tr>
<td>★ Barley yellow mosaic virus</td>
<td>barley yellow mosaic virus</td>
<td>Yanchen g</td>
<td>RNA1: AJ132268; RNA2: AJ132269</td>
<td>RNA1: NC_002990; RNA2: NC_002991</td>
<td>Complete genome</td>
<td>BaYMV</td>
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<td>★ Oat mosaic virus</td>
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<td>Cranbrooke</td>
<td>RNA1: AJ108718; RNA2: AJ306719</td>
<td>RNA1: NC_003416; RNA2: NC_004017</td>
<td>Complete genome</td>
<td>OMV</td>
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<td>★ Rice necrosis mosaic virus</td>
<td>rice necrosis mosaic virus</td>
<td>Ka-1</td>
<td>RNA1: LC055681; RNA2: LC060925</td>
<td>RNA1: NC_028144; RNA2: NC_028145</td>
<td>Complete genome</td>
<td>RNMV</td>
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<td>★ Wheat spindle streak mosaic virus</td>
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<td>FR</td>
<td>X73883</td>
<td></td>
<td>Partial genome</td>
<td>WSSMV</td>
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</tbody>
</table>
Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.

### Related, unclassified viruses

<table>
<thead>
<tr>
<th>Virus name</th>
<th>Accession number</th>
<th>Virus abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Soybean leaf rugose mosaic virus</td>
<td>AB560671*</td>
<td>SLRMV</td>
</tr>
</tbody>
</table>

Virus names and virus abbreviations are not official ICTV designations.

* incomplete RNA1 genome sequence
Genus: Ipomovirus

Distinguishing features

Ipomoviruses are distinguished from members of other genera by their mode of transmission being by whiteflies, and by their separate branching on phylogenetic analyses.

Virion

Morphology

Virions are flexuous filaments 800–950 nm long.

Physicochemical and physical properties

Virion Sedimentation coefficient $S_{20,w}$ is 155S for sweet potato mild mottle virus (SPMMV).

Nucleic acid

Virions contain a single molecule of linear, positive-sense ssRNA of about 9.7 kb; virions contain 5% RNA by weight.

Proteins

The viral coat (capsid) protein (CP) is a single polypeptide of 302–378 aa (35–41 kDa).

Genome organization and replication

Ipomoviruses exhibit unusual structural variability. The structure and organization of the SPMMV genome is similar to that of members of the genus Potyvirus (Figure 2. Potyviridae), but some motifs of HC-Pro and CP characteristic of members of the genus Potyvirus are incomplete or missing, which may account for its vector relations. The unusually large P1 protein (83 kDa) of SPMMV contains no obvious AlkB domain and hence differs from that found in members of the genus Bramyvirus. Cucumber vein yellowing virus (CVYYV) and squash vein yellowing virus (SqVYV) differ from SPMMV by encoding two P1-like serine proteases (P1a and P1b) but no HC-Pro. P1b functions as a suppressor of RNA silencing (Li et al., 2008). Cassava brown streak virus (CBSV) differs from SPMMV by having no HC-Pro and differs from CVYYV and SqVYV by having only P1b which suppresses silencing (Figure 1. Ipomovirus). Additionally, cassava brown streak virus (CBSV) contains a Maf/HAM1-like sequence recombined into the Nb/CP junction, which can accommodate heterologous genes in engineered infectious potyvirus clones. Homology of HAM1h with cellular Maf/HAM1 NTP pyrophosphatases suggests that HAM1 might intercept non-canonical NTPs to reduce mutation rates of viral RNA.

sweet potato mild mottle virus, SPMMV (10,818 nts)

![Diagram of SPMMV genome organization](image1)

squash vein yellowing virus, SqVYV (9,836) nts

![Diagram of SqVYV genome organization](image2)

cassava brown streak virus, CBSV (9,069) nts

![Diagram of CBSV genome organization](image3)
**Figure 1. Ipomovirus.** Genomic maps of the ipomoviruses sweet potato mild mottle virus (SPMMV), squash vein yellowing virus (SqVYV) and cassava brown streak virus (CBSV). The ssRNA genome is represented by a line and the polyprotein ORF by an open box. Conventions are as for the potyvirus genome organization map (Figure 2. Potyviridae). Activities of most mature proteins are postulated by analogy with genus Potyvirus. CVYV and SqVYV contain two P1-like serine proteases (P1a and P1b), of which P1b functions as a suppressor of RNA silencing. CBSV also contain P1b which suppresses silencing and, additionally, carries a Maf/HAM1-like sequence recombined into the Nib/CP junction. HAMh1 might intercept non-canonical NTPs to reduce mutation rates of viral RNA.

**Biology**

**Host range**

The natural host range of SPMMV is wide, with more than nine families susceptible, whereas the host range of CBSV, CVYV and SqVYV is less known apart from the hosts which they have been found to infect in the field (Winter et al., 2010).

**Transmission**

CBSV, CVYV and SqVYV are transmitted by the whitefly *Bemisia tabaci* in a non-persistent manner. *B. tabaci* may also be the vector of SPMMV, but this is not fully confirmed. All ipomoviruses are transmissible experimentally by mechanical inoculation and by grafting.

**Antigenicity**

Moderately immunogenic. No serological relationships with other members of the family *Potyviridae* have been found.

**Derivation of names**

*Ipomovirus:* from *Ipomea* and *mosaic,* the symptoms induced on the host of members of the type species *Sweet potato mild mottle virus.*

**Species demarcation criteria**

See discussion under *family description.*

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
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<td>KU935732</td>
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<td>NC_006941</td>
<td>Complete genome</td>
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<td>EU259611</td>
<td>NC_010521</td>
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<td>SqVYV</td>
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<td>EA</td>
<td>JF74124</td>
<td>NC_002197</td>
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<td>SPMVV</td>
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<td>Ethiopia</td>
<td>HE800872</td>
<td>NC_038920</td>
<td>Complete genome</td>
<td>TMMLV</td>
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<td>eggplant mild leaf mottle virus</td>
<td>Israel</td>
<td>HQ840796</td>
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<td>EMLMV</td>
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Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
**Genus: Macluravirus**

Distinguishing features

Macluraviruses resemble members of the genus Potyvirus in their transmission by aphids but virions are slightly shorter. They form a distinct group in phylogenetic analyses and have different polyprotein consensus cleavage sites.

Virion

**Morphology**

Virions are flexuous filaments mostly 650–675 nm×13–16 nm.

**Physicochemical and physical properties**

Virion Sedimentation coefficient $S_{20,w}$ is 155–158S; density in CsCl is 1.31–1.33 g cm$^{-3}$.

**Nucleic acid**

Virions contain one molecule of linear positive-sense, ssRNA of about 8.0 kb.

**Proteins**

Macluraviruses have a single coat (capsid) protein (CP) species of 33–34 kDa.

**Genome organization and replication**

The complete genome sequences of four different macluraviruses are available. The aa sequences of macluravirus CPs show limited (14–23%) identity with CP sequences of some aphid-transmitted potyviruses. Macluraviruses show significant aa sequence identity in portions of the replicase protein with viruses in other genera of the family Potyviridae. The macluraviruses seem to have a genome organization and replication strategy typical of viruses in the family Potyviridae (Figure 2. Potyviridae).

**Biology**

**Host range**

Current information suggests that most viruses have a narrow host range, infecting species in up to nine host families.

**Transmission**

The viruses are transmitted by aphids in a non-persistent manner and experimentally by mechanical inoculation.

**Antigenicity**

Moderately immunogenic. No serological relationships to members of the genus Potyvirus have been found except for a weak reaction between maclura mosaic virus and bean yellow mosaic virus.

**Derivation of names**

*Macluravirus*: from the genus name of the host (*Maclura*) of members of the type species *Maclura mosaic virus*.

**Species demarcation criteria**

See discussion under family description.

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
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</table>

Virus names and virus abbreviations are not official ICTV designations.

* incomplete genome sequence
**Genus: Poacevirus**

**Distinguishing features**

Triticum mosaic virus (TriMV) is transmitted by the wheat curl mite and has an unusually long 5´-untranslated region. Vectors are unknown for the other members of the genus.

**Virion**

**Morphology**

Virions of sugarcane streak mosaic virus (SCSMV) are flexuous filaments 890 nm×15 nm in size.

**Nucleic acid**

Virions contain a positive-sense ssRNA of 9.7–10.2 kb with a 3´-poly(A) terminus.

**Proteins**

The TriMV coat (capsid) protein (CP) is a single peptide of 293 aa with a MW of about 32 kDa. For SCSMV the viral CP is 281 aa with the MW estimated to be 36 kDa. Caladenia virus A (CalVA) has a CP of 285 aa and MW of 31.

**Genome organization and replication**

The TriMV genome consists of 10,266 nt. The genome encodes a polyprotein of 3,122 aa. TriMV has an unusually long 5´-untranslated region, but this is not shared by members of the other two species. The order of coding regions is typical of that of the potyviruses (Figure 2. Potyviridae). Most known potyvirus motifs are present in the polyprotein of poaceviruses. The aphid transmission amino acid sequence motifs present in the HC-Pros (KITC, PTK) and CPs (DAG) of potyviruses are absent in poaceviruses. The zinc-finger-like motif H-(X₂)-C-(X₂₀)-C-(X₂)-C in the tritimovirus wheat streak mosaic virus (WSMV) HC-Pro is essential for its transmission by mites. A similar motif in the poacevirus CalVA (unknown vector) is present as H-(X₂)-H-(X₂₀)-C-(X₂)-C (Wylie et al., 2012). In TriMV (mite transmitted) and SCSMV (unknown vector), the C-(X₂₀)-C motif exists, but the remainder of the motif is incomplete. P1 rather than the HC-Pro suppresses the host RNA-suppression response in TriMV (Tatineni et al., 2012). Members of the genus Poacevirus are phylogenetically closest to those of another mite-transmitted genus, Tritimovirus.

**Biology**

**Host range**

TriMV and SCSMV only infect hosts in the Gramineae, while CalVA infects orchids (Wylie et al., 2012).

**Transmission**

TriMV is transmitted by the wheat curl mite (*Aceria tosichella*).

**Antigenicity**

A Western blot revealed that antiserum raised to SCSMV weakly cross-reacts with wheat streak mosaic virus capsid protein. SCSMV does not cross react with other sugarcane-infecting members of the *Potyviridae*.

**Derivation of names**

*Poacevirus*: from *Poaceae*, the family name of the hosts of members of two species in the genus.

**Species demarcation criteria**

See discussion under family description.

**Member species**

<table>
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<tr>
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Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
Genus: Potyvirus

Distinguishing features
The largest genus in the family contains viruses transmitted by aphids in a non-persistent manner.

Virion

Morphology
Virions are flexuous filaments, 680–900 nm long and 11–13 nm wide, with helical symmetry and a pitch of about 3.4 nm. Particles of some viruses are longer in the presence of divalent cations than in the presence of EDTA.

Physicochemical and physical properties
Virion Sedimentation coefficient $S_{20,w}$ is 137–160S; density in CsCl is 1.31 g cm$^{-3}$; Extinction coefficient $E^{0.1\%}_{1\text{cm}, 260\text{nm}}$=2.4–2.7.

Nucleic acid
Virions contain a single molecule of linear, positive-sense ssRNA of about 9.7 kb; virions contain 5% RNA by weight.

Proteins
Virions contain a single coat (capsid) protein (CP) of 30–47 kDa. The CP of most isolates of the type species, Potato virus Y, contains 267 aa.

Genome organization and replication
The genome is organized as described in Figure 2. Potyviridae.

Biology
Many individual viruses have a narrow host range, but a few infect plant species in up to 30 host families. The viruses are transmitted by aphids in a non-persistent manner and are transmissible experimentally by mechanical inoculation. Some isolates are inefficiently transmitted by aphids and others are not transmissible by aphids at all. This is apparently due to mutations within the helper component and/or CP cistrons. Some viruses are seed-transmitted.

Antigenicity
Virions are moderately immunogenic; there are serological relationships among many members. Some monoclonal antibodies react with most aphid-transmitted potyviruses. The CP aa sequence identity among aphid-transmitted viruses is 40–70%. Some viruses are serologically related to viruses in the genera Rymovirus and Bymovirus.

Derivation of names
Poty: from potato virus Y, an isolate of the type species Potato virus Y.

Species demarcation criteria
See discussion under family description.

Member species

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Lily mottle virus
Lettuce mosaic virus
Lettuce Italian necrotic virus
Keunjorong mosaic virus
Kalanchoe mosaic virus
Johnsongrass mosaic virus
Iris severe mosaic virus
Hippeastrum mosaic virus
Hibbertia virus Y
Habenaria mosaic virus
Gomphocarpus mosaic virus
Gloriosa stripe mosaic virus
Endive necrotic mosaic virus

Lycoris mild mottle virus
lily yellow mosaic virus
strain
lily mottle virus; tulip band breaking virus; tulip breaking virus
lettuce mosaic virus
johnsongrass mosaic virus; sugarcane mosaic virus
Japanese yam mosaic virus
iris mild mosaic virus

Cowpea aphid-borne mosaic virus; South African passiflora virus
Commelina mosaic virus
Columbian datura virus; Petunia flower mottle virus
cocksfoot streak virus
clover yellow vein virus
Chinese artichoke mosaic virus
Ceratobium mosaic virus
carrot virus Y
carrot thin leaf virus
carnation vein mottle virus
canna yellow streak virus
butterfly flower mosaic virus
Brugmansia mosaic virus
Bidens mosaic virus
white lupin mosaic virus
peanut stripe virus
serotype A

International	Committee	on	Taxonomy	of	Viruses	(ICTV)	-	www.ictv.global
International Committee on Taxonomy of Viruses (ICTV) - www.ictv.global
### Related, unclassified viruses

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</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
Virus names and virus abbreviations are not official ICTV designations.

* incomplete genome sequence
**Genus: Roymovirus**

**Distinguishing features**

The amino acid motifs KITC and PTK are not present in HC-Pro. Roymoviruses have low nucleotide and amino acid identities with other potyvirids. The nucleotide and deduced amino acid sequences of the polyprotein share greatest identities with other viruses in the family Potyviridae, but they are not clearly closer to members of any particular genera in the family. Comparison of the deduced amino acid sequence of the large ORF revealed identities with other viruses of the family to be low, ranging from 13% (some bymoviruses) to 23% (some potyviruses).

**Virion**

**Morphology**

Particles are 720 to 750 nm in size.

**Nucleic acid**

Rose yellow mosaic virus has a genome of 9,508 nt.

**Proteins**

The large polyprotein is probably processed in the same manner as potyviruses. PIPO is present.

**Genome organization and replication**

Genome organization resembles that of members of the genus *Potyvirus*.

**Biology**

Isolates of the type species, *Rose yellow mosaic virus*, were isolated from several rose cultivars in New York and Minnesota.

The conserved amino acid motifs KITC and PTK are not present in the HC-Pro of rose yellow mosaic virus. Instead, a putative C-2x-C eriophyd mite transmission motif is found at amino acid residues 48–51 at the N-terminus of the protein. The coat protein amino acid motif DAG found in most aphid-transmitted potyvirids is also lacking. Together this information suggests that rose yellow mosaic virus may be transmitted by eriophyid mites, although this has not been proven experimentally.

Phylogenetic analysis of the coat protein and ORF places rose yellow mosaic virus basal to viruses belonging to the genera *Tritimovirus*, *Poeacevirus* and *Ipomovirus* (Figure 3. Potyviridae).

**Derivation of names**

*Roymovirus* from *rose yellow mosaic virus*

**Species demarcation criteria**

See discussion under *family description*.

**Member species**

<table>
<thead>
<tr>
<th>★ Exemplar isolate of the species</th>
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<tr>
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Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
Genus: Rymovirus

Distinguishing features

This genus includes three species. Rymoviruses are presumably transmitted by host-adapted populations of eriophyid mite species in a semi-persistent manner. Rymoviruses share a reciprocal monophyletic relationship with members of the genus Potyvirus (French and Stenger 2005).

Virion

Morphology

Virions are flexuous filaments 690–720 nm×11–15 nm in size.

Physicochemical and physical properties

Virion density in CsCl is 1.325 g cm\(^{-3}\) (for ryegrass mosaic virus (RGMV)). Virion Sedimentation coefficient \(S_{20,w}\) is 165–166S for most members.

Nucleic acid

Virions contain a single molecule of linear positive-sense ssRNA of about 9.5 kb with a 3′-poly(A) terminus.

Proteins

Rymoviruses encode one type of coat (capsid) protein (CP), with a theoretical Mr of 35,482 Da and an apparent Mr estimated by Western blots of 45 kDa for RGMV.

Genome organization and replication

The complete genome sequences available for isolates of RGMV, Agropyron mosaic virus (AgMV), and Hordeum mosaic virus (HoMV) indicate that rymoviruses have a genome organization and replication strategy similar to other members of the Potyviridae with monopartite genomes (Figure 2. Potyviridae).

Biology

Host range

Most rymoviruses have limited but widespread host ranges within the family Gramineae but some have relatively narrow host ranges.

Transmission

Transmission by eriophyid mites and mechanical transmission have been reported for most members. The eriophyid mites transmitting rymoviruses are different from those transmitting tritimoviruses. The cereal rust mite Abacarus hystrix transmits both RGMV and AgMV, but only the former is efficiently transmitted. No vector is known for HoMV. Recent studies have revealed that host-associated populations of \(A. hystrix\) represent a species complex.

Antigenicity

Particles of most rymoviruses are moderately immunogenic. HoMV and AgMV are serologically related.

Derivation of names

Rymovirus: from ryegrass mosaic virus, a member of the type species Ryegrass mosaic virus.

Species demarcation criteria

See discussion under family description.

Member species
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Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
**Genus: Tritimovirus**

**Distinguishing features**

Tritimoviruses are transmitted by mites of a different species from those that transmit rymoviruses. They form a separate cluster in phylogenetic analyses.

**Virion**

**Morphology**

Virions are flexuous filaments 690–700 nm long.

**Physicochemical and physical properties**

Virion Sedimentation coefficient S\text{20, w} is 166S for wheat streak mosaic virus (WSMV).

**Nucleic acid**

Virions contain a positive-sense ssRNA of about 9.4–9.6 kb with a 3’-poly(A) terminus.

**Proteins**

The viral coat (capsid) protein (CP) is a single peptide of about 349 aa for WSMV and 320 aa for brome streak mosaic virus (BrSMV). The Mr estimated by electrophoresis is 42 kDa.

**Genome organization and replication**

The WSMV genome consists of 9,384 nt excluding the 3’-terminal poly(A) tail. Sequence analysis reveals an ORF of 3,035 aa. The structure and organization of the WSMV genome is similar to those of other members of the family Potyviridae except the bymoviruses (Figure 2. Potyviridae). Most known potyvirus motifs are present in the polyprotein of WSMV. However, motifs in the putative helper-component and CP of BrSMV are incomplete or missing, which may account for different vector relations of the tritimoviruses. The WSMV CP sequence shows limited (22-25%) identity with CP sequences of some aphid-transmitted potyviruses. WSMV shows significant aa sequence identity with aphid-transmitted potyviruses in the cylindrical inclusion protein and portions of the nuclear inclusion proteins. WSMV RNA is translated in vitro into several large proteins that can be immunoprecipitated with WSMV CP antiserum, suggesting that WSMV uses a proteolytic processing strategy to express functional proteins such as the CP. Antiserum to tobacco etch virus (TEV) 58 kDa nuclear inclusion protein also reacts with in vitro translation products of WSMV. An in vitro translation product is precipitated with antiserum to HC-Pro helper component of an isolate of the species Tobacco vein mottling virus (genus Potyvirus). Comparative sequence analyses show similarities with other members of the family Potyviridae, but these are limited to the nine mature proteins. WSMV is especially susceptible to proteinases in planta and has CP molecules of 42, 36 and 32 kDa; the two smaller proteins are parts of the 42 kDa protein.

**Biology**

**Host range**

The viruses only affect hosts in the Gramineae but while WSMV has a wide host range BrSMV and ONMV have narrow ones.

**Transmission**

WSMV and BrSMV are transmitted by eriophyid mites in a semi-persistent manner. The HC-Pro of WSMV is required for mite transmission. All tritimoviruses are transmissible experimentally by mechanical inoculation.

**Antigenicity**

Moderately immunogenic. WSMV and oat necrotic mottle virus (ONMV) are serologically related to each other, but not to the other members of the family Potyviridae.

**Derivation of names**

*Tritimovirus*: from the host genus (*Triticum*) and induced symptoms (mosaic) of isolates of the type species *Wheat streak mosaic virus*.

**Species demarcation criteria**
See discussion under family description.

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bromegrass mosaic virus</td>
<td>bromegrass mosaic virus</td>
<td>FR</td>
<td>Z48506</td>
<td>NC_003501</td>
<td>Complete coding genome</td>
<td>BrSMV</td>
</tr>
<tr>
<td>Oat necrotic mottle virus</td>
<td>oat necrotic mottle virus</td>
<td>Type-NE</td>
<td>AY377838</td>
<td>NC_005136</td>
<td>Complete genome</td>
<td>ONMV</td>
</tr>
<tr>
<td>Tall oatgrass mosaic virus</td>
<td>tall oatgrass mosaic virus</td>
<td>Benesov</td>
<td>KF600852</td>
<td>NC_022745</td>
<td>Complete genome</td>
<td>TOgMV</td>
</tr>
<tr>
<td>Wheat Eqlid mosaic virus</td>
<td>wheat Eqlid mosaic virus</td>
<td>IR</td>
<td>EF608612</td>
<td>NC_008805</td>
<td>Complete genome</td>
<td>WEqMV</td>
</tr>
<tr>
<td>Wheat streak mosaic virus</td>
<td>wheat streak mosaic virus</td>
<td>Sidney 81</td>
<td>AF057533</td>
<td>NC_001886</td>
<td>Complete genome</td>
<td>WSMV</td>
</tr>
<tr>
<td>Yellow oat grass mosaic virus</td>
<td>yellow oat grass mosaic virus</td>
<td>Sb</td>
<td>KF944546</td>
<td>NC_024471</td>
<td>Complete genome</td>
<td>YOGMV</td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
Summary

Strawberry mottle virus, black raspberry virus and chocolate lily virus A are related to satsuma dwarf virus (SDV) in phylogenetic trees using the conserved Pro-Pol region (Figure 4. Secoviridae). Dioscorea mosaic associated virus, recently isolated from yam, is most closely related to chocolate lily virus A (Hayashi et al., 2016). These viruses also have a bipartite genome. However, the nature of their capsid protein(s) and their genomic organization are not known. For this reason, they are unassigned species in the family Secoviridae. Strawberry latent ringspot virus was formerly considered a sadwavirus because it has two capsid proteins (CP) and some distant relation with SDV in phylogenetic trees using the Pro-Pol sequence (Figure 4. Secoviridae). However, its genomic organization is more related to that of cheraviruses (with the exception of the number of CPs, Figure 3. Secoviridae) and it branches more closely with cheraviruses than with sadwaviruses in the phylogenetic trees using the Pro-Pol sequence (Figure 4. Secoviridae). For these reasons, it is not considered a sadwavirus anymore, and is now an unassigned species in the family Secoviridae.

Unassigned species in family Secoviridae

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Strawberry latent ringspot</td>
<td>strawberry latent ringspot</td>
<td>NCGR MEN 454.001</td>
<td>RNA-1: AY860978;</td>
<td>RNA-1: NC_0068634; RNA-2:</td>
<td>Complete genome</td>
<td>SLRSV</td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
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Resources: *Potyviridae*

Sequence alignments and tree files:

**Figure 3.** *Potyviridae*

- Tree file (nexus format)
- Alignment file (fasta format)
References: Potyviridae


Citation: Potyviridae

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