Virus Taxonomy
The ICTV Report on Virus Classification and Taxon Nomenclature
Alphaflexiviridae Chapter

Alphaflexiviridae

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Summary

The family Alphaflexiviridae includes viruses with flexuous filamentous virions that are 470–800 nm long and 12–13 nm in diameter (Table 1. Alphaflexiviridae). Alphaflexiviruses have a single-stranded, positive-sense RNA genome of 5.4–9 kb. They infect plants and plant-infecting fungi. They share a distinct lineage of alphavirus-like replication proteins that is unusual in lacking any recognized protease domain. Cell-to-cell and long-distance movement is facilitated by triple gene block proteins in viruses that infect plants, except for members of the genus Platypuvirus.

Table 1. Alphaflexiviridae. Characteristics of members of the family Alphaflexiviridae

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td>shallot virus X, Kanyuka (M97264), species Shallot virus X, genus Allexivirus</td>
</tr>
<tr>
<td>Virion</td>
<td>Flexuous filaments, usually 12–13 nm in diameter and from 470 to about 800 nm in length</td>
</tr>
<tr>
<td>Genome</td>
<td>Single molecule of linear ss, positive sense RNA of about 5.5–9.0 kb</td>
</tr>
<tr>
<td>Replication</td>
<td>Cytoplasmic, virus-coded RdRP</td>
</tr>
<tr>
<td>Translation</td>
<td>Genome length and 3′-terminal subgenomic mRNAs; capped and polyadenylated</td>
</tr>
<tr>
<td>Host range</td>
<td>Plants and fungi</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Realm Riboviria, kingdom Orthornavirae, phylum Kitrinoviricota, class Alsuviricetes, order Tymovirales, seven genera with 56 species</td>
</tr>
</tbody>
</table>

Virion

Morphology

Virions are flexuous filaments, usually 12–13 nm in diameter (range 10–15 nm) and from 470 to about 800 nm in length. Alphaflexiviruses have helical capsid symmetry with a pitch of about 3.4 nm (range 3.3–3.7 nm) and in the members of some genera there is clearly visible cross-banding (Figure 1. Alphaflexiviridae).
Physicochemical and physical properties

Virions sediment as a single band (or occasionally two very close bands) with an $S_{20,w}$ of 92–176S.

Nucleic acid

Virions contain a single molecule of linear single-stranded RNA of 5.9–9.0 kb which is 5–6% by weight of the virion. Where studied, the RNA is capped at the 5′-terminus with m$\text{G}$ and has a polyadenylated tract at the 3′-terminus (Figure 2. Alphaflexiviridae). Open reading frames downstream from the large ORF encoding the replication-associated (Rep) protein are expressed from smaller 3′-co-terminal subgenomic RNAs (sgRNAs). These sgRNAs are encapsidated in some, but not all, members of the genus *Potexvirus*.

Proteins

The viral capsid is composed of a single polypeptide ranging in size from 18 to 43 kDa except for members of the genus *Lolavirus* which have two carboxy-coterminal capsid protein (CP) variants, and members of the genus *Sclerodarnavirus* in which no CP has been identified (Vaira et al., 2011). In allexiviruses, a 42 kDa polypeptide was also detected as a minor component of virions. In lolaviruses a shorter (ca. 28 kDa) carboxy co-terminal polypeptide forms an equimolar fraction of the virion with the polypeptide (ca. 32 kDa) originating from the first AUG of the CP-encoding ORF.

Lipids

None reported.

Carbohydrates

Usually none, but the capsid protein of some strains of the species *Potato virus X* (genus *Potexvirus*) and both forms of the lolavirus capsid protein are reported to be glycosylated.

Genome organization and replication

Most alphaflexviruses have five to seven genes, but members of the genus *Sclerodarnavirus* have a single gene encoding the Rep protein (Figure 2. Alphaflexiviridae). The ORF1-encoded product (encoded by ORF2 in members of the genus *Platypuvirus*), which follows a short 5′-UTR sequence, has homologies with replication-associated (Rep) proteins of the “alphavirus-like” supergroup of RNA viruses. This protein (150–195 kDa) contains conserved methyltransferase, helicase and RNA-directed RNA polymerase (RdRP) motifs (Batten et al., 2003); some also include an AlkB domain (alkylated DNA repair protein) (van den Born et al., 2008). In all plant-infecting alphaflexviruses, except members of the genus *Platypuvirus*, ORFs 2–4 encode the “triple gene block” (TGB) proteins involved in cell-to-cell movement and ORF5 is the viral capsid protein. In platypuviruses the CP is encoded by ORF 4 and a putative movement protein (MP) is found at ORF7. In members of some genera (*Allexivirus* except alfalfa virus S, *Lolavirus* and *Mandarivirus*) a final ORF encodes a protein with a zinc-finger motif and the ability to bind nucleic acids. ORFs downstream of the polymerase are translated from 3′-terminal sgRNAs that can often be found in infected tissue. Replication is known, or presumed to be, cytoplasmic and the product of ORF1 is the only virus-encoded protein known to be involved...
**Biology**

Alphaflexiviruses have been reported from a wide range of mono- and dicotyledonous plant species but the host range of members of individual species is usually limited. Many viruses have relatively mild effects on their host. All plant-infecting viruses can be transmitted by mechanical inoculation, often readily. Many viruses have no known invertebrate or fungal vectors; however, some alphaflexiviruses are mite-borne. Aggregates of virus particles accumulate in the cytoplasm but there are usually no specific cytopathic structures.

**Antigenicity**

Virions are usually highly immunogenic. Some viruses within genera are serologically related.

**Derivation of names**

*Alpha:* from Greek letter α

*Flexi:* from Latin flexus, meaning “bent”

**Genus demarcation criteria**

Members of different genera are distinguished by various features of genome organization (Figure 2. *Alphaflexiviridae*) and host (Table 2. *Alphaflexiviridae*). Viruses from different genera usually have less than 45% nt identity in the CP or polymerase genes.

**Table 2. Alphaflexiviridae.** Characteristics of members of the seven genera in the family *Alphaflexiviridae*

<table>
<thead>
<tr>
<th>Genus</th>
<th>Host</th>
<th>Virion length (nm)</th>
<th>ORFs</th>
<th>Rep (kDa)</th>
<th>MP</th>
<th>CP (kDa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Allexivirus</td>
<td>plants</td>
<td>ca. 800</td>
<td>5–6</td>
<td>170–195</td>
<td>TGB&lt;sup&gt;a&lt;/sup&gt;</td>
<td>25–32</td>
</tr>
<tr>
<td>Botrexvirus</td>
<td>fungi</td>
<td>ca.720</td>
<td>5</td>
<td>158</td>
<td>Absent</td>
<td>43</td>
</tr>
<tr>
<td>Lolavirus</td>
<td>plants</td>
<td>640</td>
<td>6</td>
<td>196</td>
<td>TGB</td>
<td>28, 32</td>
</tr>
<tr>
<td>Mandarinirus</td>
<td>plants</td>
<td>850</td>
<td>6</td>
<td>187</td>
<td>TGB</td>
<td>34</td>
</tr>
<tr>
<td>Platypuvirus</td>
<td>plants</td>
<td>No virions</td>
<td>7</td>
<td>157</td>
<td>3A-like</td>
<td>22</td>
</tr>
<tr>
<td>Potexvirus</td>
<td>plants</td>
<td>470–580</td>
<td>5</td>
<td>150–195</td>
<td>TGB</td>
<td>21–27</td>
</tr>
<tr>
<td>Sclerodarnavirus</td>
<td>fungi</td>
<td>No virions</td>
<td>1</td>
<td>193</td>
<td>Absent</td>
<td>Absent</td>
</tr>
</tbody>
</table>

<sup>a</sup>International Committee on Taxonomy of Viruses (ICTV) - www.ictv.global
TGB, triple gene block

Relationships within the family

In a phylogenetic analysis of the Rep protein of isolates for which a CP sequence was also available, members of most genera fall into well-supported clades, except for members of the genus Mandarivirus which group with members of the genus Potexvirus (Figure 3. Alphaflexiviridae). A similar tree is found based on CP sequences except that members of the genus Lolavirus group together with members of the genera Mandarivirus and Potexvirus (Figure 4. Alphaflexiviridae) and may be the result of modular recombination during evolution of viruses belonging to these genera.

Figure 3. Alphaflexiviridae. Unrooted phylogenetic (distance) tree based on the amino acid sequences of the entire Rep protein of members of the family Alphaflexiviridae. Virus genera are indicated to the right of their respective branches. Numbers on branches indicate percentage of bootstrap support out of 1000 bootstrap replications (when >60%). The scale indicates JTT amino acid distances. Tree produced in (Tamura et al., 2007). This phylogenetic tree and corresponding sequence alignment are available to download from the Resources page.
Figure 4. Alphaflexiviridae. Unrooted phylogenetic (distance) tree based on the amino acid sequences of the capsid protein of members of the family Alphaflexiviridae. Virus genera are indicated to the right of their respective branches. Numbers on branches indicate percentage of bootstrap support out of 1000 bootstrap replications (when >70%). The scale indicates JTT amino acid distances. Tree produced in MEGA7 (Kumar et al., 2016). This phylogenetic tree and corresponding sequence alignment are available to download from the Resources page.

Relationships with other taxa

The Rep proteins are members of the “alphavirus-like” supergroup of RNA viruses and are most closely related to those encoded by members of other families in the order, namely Betaflexiviridae, Gammaflexiviridae, Deltaflexiviridae and Tymoviridae. The TGB proteins are related to those of members of some genera in the family Betaflexiviridae and, more distantly, to those of rod-shaped viruses in the family Virgaviridae (genera Hordeiviruses, Pecluvirus and Pomovirus). In members of the genus Platypuvirus, ORF1 shows weak similarity to tymovirus movement proteins and the ORF7 movement protein shows similarity to those encoded by members of the families Tombusviridae and Virgaviridae.

Related, unclassified viruses

www.ictv.global/report/alphaflexiviridae
<table>
<thead>
<tr>
<th>Virus name</th>
<th>Accession number</th>
<th>Virus abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ambrosia asymptomatic virus 1</td>
<td>KF421905</td>
<td></td>
</tr>
<tr>
<td>cassava alphaflexivirus</td>
<td>KC505252</td>
<td></td>
</tr>
<tr>
<td>Escobaria virus</td>
<td>KF421919</td>
<td></td>
</tr>
<tr>
<td>Euonymus yellow mottle associated virus</td>
<td>MK572000</td>
<td>EuYMaV</td>
</tr>
<tr>
<td>grapevine associated alphaflexivirus-1</td>
<td>HM852918</td>
<td></td>
</tr>
<tr>
<td>insect-associated alphaflexivirus1</td>
<td>MN203143</td>
<td></td>
</tr>
<tr>
<td>insect-associated alphaflexivirus 2</td>
<td>MN203144</td>
<td></td>
</tr>
<tr>
<td>insect-associated alphaflexivirus 3</td>
<td>MN203145</td>
<td></td>
</tr>
</tbody>
</table>

Virus names and virus abbreviations are not official ICTV designations.
**Genus: Allexivirus**

**Distinguishing features**

Allexiviruses are distinguished by mite transmission and by the presence of a large conserved ORF4 or 5 after the position where the third, and smallest, of the triple gene block (TGB) proteins, TGB3, is found in the other plant-infecting members of the family. Whereas the start codon is missing for the TGB3 ORF in most (but not all) genus members, the coding capacity is conserved and the ORF may be translated through alternative mechanisms.

**Virion**

**Morphology**

Virions are highly flexible filamentous particles, about 800 nm in length and 12 nm in diameter. They resemble potyviruses in their length, but closteroviruses in their flexibility and cross-banded substructure (Figure 1. _Alphaflexiviridae_).

**Physicochemical and physical properties**

Virions of shallot virus X sediment with an $S_{20,w}$ of about 170S in 0.1 M Tris-HCl, pH 7.5 at 20°C and have a buoyant density in CsCl of 1.33 g cm$^{-3}$.

**Nucleic acid**

Virions contain a single molecule of linear single-stranded RNA, of about 9.0 kb, with a 3′-poly(A) tract. The genomic RNA contains six large ORFs and short untranslated regions (UTR) at the 5′- and 3′-termini (Figure 2. _Alphaflexiviridae_).

**Proteins**

Virions are composed of a 25–32 kDa polypeptide as a major capsid protein (CP). A 42 kDa polypeptide is a minor component of virions.

**Carbohydrates**

None reported.

**Genome organization and replication**

The genomic RNA contains six large ORFs and short UTRs at the 5′- and 3′-termini (Kanyuka et al., 1992) (Figure 1. _Allexivirus_). The ORFs code for polypeptides of about 195, 27, 11, 42, 28 and 15 kDa, respectively from the 5′-end to the 3′-end. The 195 kDa polypeptide is the replication-associated (Rep) protein. The 26 and 11 kDa proteins are similar to the first two proteins encoded by the TGB of related plant viruses and are probably involved in cell-to-cell movement of the virus. There is a coding sequence for a third small (7–8 kDa) TGB protein but the initiation AUG-codon is lacking in most, but not all member species. The 42 kDa polypeptide (ORF4) has no significant homology with any known protein; in plants infected with an isolate of the type species, the 42 kDa protein was expressed in relatively large amounts and was shown to be involved in virion assembly. The 28 kDa polypeptide is the CP. In SDS-polyacrylamide gel electrophoresis it migrates as an apparently 32–36 kDa protein, which could be due to its high hydrophilicity. The 15 kDa protein has a zinc-binding finger motif and an ability to bind nucleic acids. The function of this polypeptide is not known.

**Biology**

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**Figure 1.** _Allexivirus_. Genome organization and translation strategy of shallot virus X showing the relative positions of the ORFs and their expression products. Mtr, methyltransferase; Hel, helicase; RdRP, RNA-directed RNA polymerase; TGB, triple gene block; CP, capsid protein; NB, nucleic acid binding protein.
Host range

The host range of allexiviruses that encode a 15 kDa RNA-binding protein is mainly restricted to *Allium* species. Some isolates from shallot, onion, garlic and sand leek have been experimentally transmitted to *Chenopodium murale*, in which they induced local lesions. Viruses lacking the RNA-binding protein infect hosts other than *Allium* including vanilla, alfalfa, groundnut and blackberry.

Transmission

Allexiviruses are thought to be mite-borne. Garlic viruses C and D have been shown to be transmitted by the eriophyd mite, *Aceria tulipae*. All are manually transmissible by sap inoculation to healthy host plants. None could be transmitted by aphids.

Geographical distribution

Allexiviruses are widely distributed and probably occur wherever their host plants are grown.

Cytopathic effects

Most allexiviruses induce no visible or only very mild symptoms, although certain isolates can cause severe damage to crops. In infected tissue, allexiviruses can induce the formation of granular inclusion bodies and small bundles of flexible particles.

Antigenicity

Allexivirus particles are immunogenic. Some members of the genus are serologically related. Specific antisera and monoclonal antibodies against virus particles as well as antisera against recombinant CPs have been used for differentiation purposes.

Derivation of names

*Allexi* from *Allium* (the genus name for the principal host, shallot) and *exi*, a phonetic version of “X”.

Species demarcation criteria

The criteria demarcating species in the genus are:

- Members of different species have less than 72% nt identity (or 80% aa identity) in their CP or Rep genes.
- Members of different species react differently with antisera.

Member species

### Exemplar isolate of the 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><strong>Alfalfa virus S</strong></td>
<td>Alfalfa virus S</td>
<td>98.3A</td>
<td>KY699669</td>
<td>NC_034622</td>
<td>Complete genome</td>
<td>AVS</td>
</tr>
<tr>
<td><strong>Arachis pintoi virus</strong></td>
<td>Arachis pintoi virus</td>
<td>Var A</td>
<td>KX039345</td>
<td>NC_032104</td>
<td>Complete genome</td>
<td>ApV</td>
</tr>
<tr>
<td><strong>Blackberry virus E</strong></td>
<td>blackberry virus E</td>
<td>BB_Eills-1</td>
<td>UN022996</td>
<td>NC_015766</td>
<td>Complete genome</td>
<td>BVE</td>
</tr>
<tr>
<td><strong>Garlic mite-borne filamentous virus</strong></td>
<td>garlic mite-borne filamentous virus</td>
<td>XJ8991</td>
<td>NC_038864</td>
<td>Partial genome</td>
<td>GarMbFV</td>
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<td><strong>Garlic virus A</strong></td>
<td>garlic virus A</td>
<td>Sumi</td>
<td>ABO10300</td>
<td>NC_003375</td>
<td>Complete genome</td>
<td>GarVA</td>
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<td><strong>Garlic virus B</strong></td>
<td>garlic virus B</td>
<td>Mesi 13</td>
<td>KM379144</td>
<td>NC_003768</td>
<td>Complete genome</td>
<td>GarVB</td>
</tr>
<tr>
<td><strong>Garlic virus C</strong></td>
<td>garlic virus C</td>
<td>Sumi</td>
<td>ABO10302</td>
<td>NC_003376</td>
<td>Complete genome</td>
<td>GarVC</td>
</tr>
<tr>
<td><strong>Garlic virus D</strong></td>
<td>garlic virus D</td>
<td>SW10</td>
<td>KF503563</td>
<td>NC_022961</td>
<td>Complete genome</td>
<td>GarVD</td>
</tr>
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<td><strong>Garlic virus E</strong></td>
<td>garlic virus E</td>
<td>YH</td>
<td>AJ282230</td>
<td>NC_004012</td>
<td>Complete genome</td>
<td>GarVE</td>
</tr>
<tr>
<td><strong>Shallot virus X</strong></td>
<td>shallot virus X</td>
<td>Korea</td>
<td>U851243</td>
<td>NC_019342</td>
<td>Complete genome</td>
<td>Gar VX</td>
</tr>
<tr>
<td><strong>Vanilla latent virus</strong></td>
<td>Vanilla latent virus</td>
<td>CRV2148ALL</td>
<td>UF150239</td>
<td>NC_035201</td>
<td>Complete genome</td>
<td>VLV</td>
</tr>
</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>allexivirus DS-2013/CZE</td>
<td>JX082826</td>
<td></td>
</tr>
<tr>
<td>Cassia mild mosaic virus</td>
<td>GU481094</td>
<td></td>
</tr>
<tr>
<td>Senna severe yellow mosaic virus</td>
<td>MN031278</td>
<td></td>
</tr>
<tr>
<td>shallot mite-borne latent virus</td>
<td>EU835196</td>
<td></td>
</tr>
</tbody>
</table>

Virus names and virus abbreviations are not official ICTV designations.
Genus: Botrexvirus

Distinguishing features

Viruses belonging to the single species in the genus infect a filamentous fungus. The virus genome lacks the triple gene block ORFs characteristic of plant-infecting members of the family (Howitt et al., 2006).

Virion

Morphology

Virions are flexuous filaments of 720 nm modal length and about 13 nm in diameter.

Physicochemical and physical properties

No information.

Nucleic acid

Virions of Botrytis virus X (BotVX) contain a single molecule of linear single-stranded RNA of 6966 nt, excluding the 3’-poly(A) tail.

Proteins

The only structural protein of BotVX is the capsid protein composed of 400 aa (43 kDa).

Carbohydrates

None reported.

Genome organization and replication

The BotVX genomic RNA contains five putative ORFs on the positive strand, a 5’-UTR of 95 nt and a 3’-UTR of 149 nt, followed by a poly(A) tail (Figure 1. Botrexvirus). ORF1 encodes the 158 kDa replication-associated (Rep) protein, ORF3 encodes the 44 kDa capsid protein (CP) and the functions of the other predicted proteins (ORF2, 30 kDa; ORF4, 14 kDa and ORF5, 14 kDa) are unknown.

Biology

BotVX was discovered infecting an isolate of the plant pathogenic fungus Botrytis cinerea. Its mode of transmission is unknown. The same fungal isolate was also infected with a virus now classified in the species Botrytis virus F (genus Mycoflexivirus, family Gammaflexiviridae).

Derivation of names

Botrex: from Botrytis virus X, the type species in the genus

Species demarcation criteria

Since there is currently only a single species in the genus, species demarcation criteria are not yet defined, but, as delineated for other genera in the family, members of distinct species may have less than 72% nt identity (or 80% aa identity) in their CP or Rep genes.

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>Botrytis virus X</td>
<td>botrytis virus X</td>
<td>Howitt</td>
<td>AY055762</td>
<td>NC_005132</td>
<td>Complete genome</td>
<td>BotVX</td>
</tr>
</tbody>
</table>

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

Distinguishing features

This genus includes a single species, *Lolium latent virus*. The genome of the single representative, *Lolium latent virus* (LoLV) has six ORFs (although the putative ORF6 is smaller than that found in members of other genera). The capsid protein is larger and the virions are longer than those of potexviruses, which they otherwise resemble. Notably two carboxy co-terminal forms of the capsid protein are found in essentially equimolar amounts in both extracts of infected plants and in purified virions (Vaira et al., 2008).

Virion

Morphology

LoLV virions are slightly flexuous filaments of 640 nm modal length and about 13 nm diameter (Figure 1. *Lolavirus*).

![Negative-contrast electron micrograph of particles of an isolate of *Lolium latent virus* stained in phosphotungstic acid. The bar represents 500 nm (Courtesy of M.M. Dienelt).](Image)

Physicochemical and physical properties

The LoLV virus forms a single band in caesium sulphate density gradients. Purified preparations show maximum absorption at 260 nm with a $A_{260/280}$ ratio of 1.1 (corrected for light scattering).

Nucleic acid

LoLV virions contain a single molecule of linear single-stranded RNA of 7560 nt, excluding the 3'-poly(A) tail (Figure 2. *Lolavirus*).

Proteins

The only structural proteins are the two capsid protein (CP) isoforms, composed of 245 and 293 aa (28 and 32 kDa, respectively).

Carbohydrates

Both forms of the capsid protein are reported to be glycosylated (Vaira et al., 2012).

Genome organization and replication

The genomic RNA comprises six ORFs on the positive-strand, a 5′-UTR of 78 nt and a 3′-UTR of 40 nt, followed by a poly(A) tail (Figure 2. *Lolavirus*). ORF1 encodes the replication-associated protein (Rep). ORF2, ORF3 and ORF4 form the triple gene block (TGB). ORF5 encodes the CP. ORF6 encodes a putative protein of unknown function that shows limited similarity with nucleic acid-binding proteins encoded by ORF6 of allexiviruses and carlaviruses.
**Biology**

Plants infected with LoLV exhibit either no symptoms or mild chlorotic flecking that coalesce to form chlorotic to necrotic streaking on the leaves. The virus is mechanically transmissible and *Rhopalosiphum padi* may be an inefficient vector (Huth et al., 1995).

**Antigenicity**

Particles are immunogenic. Rabbit antisera can have titers of 1/128 and 1/2048 in gel diffusion and EM decoration, respectively.

**Derivation of names**

*Lola*: from *Lolium latent virus*.

**Species demarcation criteria**

Since there is currently only a single species in the genus, species demarcation criteria are not yet defined, but, as delineated for other genera in the family, members of distinct species may have less than 72% nt identity (or 80% aa identity) in their CP or Rep genes.

**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>★ Lolium latent virus</td>
<td>lolium latent virus</td>
<td>US1</td>
<td>EU486641</td>
<td>NC_010434</td>
<td>Complete genome</td>
<td>LoLV</td>
</tr>
</tbody>
</table>

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

**Distinguishing features**

This genus includes two closely related species, *Citrus yellow vein clearing virus* and *Indian citrus ringspot virus*, members of which infect citrus in west Asia and are transmitted by aphids (Loconsole et al., 2012, Rustici et al., 2002). There are six ORFs in the genome and the capsid protein (CP) is the largest of any plant-infecting member of the family.

**Virion**

**Morphology**

Virions are flexuous filaments of 650 nm modal length, 13 nm in diameter, with clearly visible cross-banding (Figure 1. Mandarivirus).

![Figure 1. Mandarivirus.](image)

**Physicochemical and physical properties**

Mandariviruses form a single band in caesium sulphate density gradients. Purified preparations show maximum absorption at 260 nm with a $A_{260/280}$ ratio of 1.1 (corrected for light scattering).

**Nucleic acid**

Virions of Indian citrus ringspot virus (ICRSV) contain a single molecule of linear single-stranded RNA of 7560 nt, excluding the 3′-poly(A) tail (Figure 2. Mandarivirus).

**Proteins**

The only structural protein of ICRSV is the CP, composed of 325 aa (34 kDa).

**Carbohydrates**

None reported.

**Genome organization and replication**

The genomic RNA of ICRSV comprises six ORFs on the positive-strand, a 5′-UTR of 78 nt and a 3′-UTR of 40 nt, followed by a poly(A) tail (Figure 2. Mandarivirus). ORF1 encodes the replication-associated protein (Rep). ORF2, ORF3 and ORF4 form the triple gene block (TGB). ORF5 encodes the CP. ORF6 encodes a putative protein of unknown function that shows limited similarity with nucleic acid-binding proteins encoded by ORF6 of allexiviruses and carlaviruses.
Biology

Mandariviruses infect citrus but cause distinct symptoms on citrus and experimental hosts depending on the virus. Citrus yellow vein clearing virus (CYVCV) causes vein clearing disease and can be mechanically transmitted and by aphids (Loconsole et al., 2012). ICRSV causes a serious disease of citrus, especially Kinnow mandarin, in India, with bright yellow ringspots on mature leaves, followed by rapid decline of the tree (Rustici et al., 2002). Experimentally ICRSV can be mechanically inoculated to leaves of Chenopodium quinoa, C. amaranticolor, Glycine max, Vigna unguiculata and Phaseolus vulgaris, giving local lesions, but systemic infection only in P. vulgaris. No natural vector is known, but ICRSV is transmitted by grafting and persists in the host.

Antigenicity

Particles are immunogenic. Rabbit antisera can have titers of 1/128 and 1/2048 in gel diffusion and EM decoration, respectively.

Derivation of names

*Mandari*: from *mandarin* (*Citrus reticulata*), the host of members of the type species, *Indian citrus ringspot virus*.

Species demarcation criteria

Members of different species should have less than 72% nt identity (or 80% aa identity) between their respective CP or Rep genes, although reaction with antisera and biological properties should also be taken into account.

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>
<th>Virus Abbrev.</th>
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Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.

Related, unclassified viruses

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<th>Virus abbreviation</th>
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<td>KT896524</td>
<td>CYMV</td>
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</table>

Virus names and virus abbreviations are not official ICTV designations.
**Genus: Platypuvirus**

**Distinguishing features**

This genus includes a single species, *Donkey orchid symptomless virus*, whose members infect native Australian orchids. The virus genome is predicted to encode seven proteins of apparently disparate origins. The replication-associated protein (Rep) and capsid protein (CP) are related to viruses of the family *Alphaflexiviridae*, whereas the movement protein (MP) shares an evolutionary history with the MP of dianthoviruses. Other putative proteins are distant from any other plant virus proteins (Wylie et al., 2013, Wylie et al., 2013).

**Virion**

**Morphology**

No information.

**Physicochemical and physical properties**

No information.

**Nucleic acid**

*Donkey orchid symptomless virus* (DOSV) virions are presumed to contain a single molecule of linear single-stranded RNA of 7838 nt, excluding the 3′-poly(A) tail (Figure 1.*Platypuvirus*).

**Proteins**

The only structural protein is the CP, composed of 202 aa (22 kDa).

**Carbohydrates**

None reported.

**Genome organization and replication**

The genomic RNA is predicted to encode seven proteins of apparently disparate origins (Figure 1. *Platypuvirus*). A 69 kDa protein (ORF1) that overlaps the Rep shares low identity with MPs of tymoviruses (*Tymoviridae*). A 157 kDa Rep (ORF2) and 22 kDa capsid protein (ORF4) share 32% and 40% amino acid identity, respectively, with homologous proteins encoded by members of the family *Alphaflexiviridae*. A 44-kDa protein (ORF3) shares low identity with myosin and an autophagy protein from squirrelpox virus. A 27 kDa protein (ORF5) shares no identity with any described protein. A 14 kDa protein (ORF6) shares low sequence identity (26%) over a limited region with the envelope glycoprotein precursor of Crimea-Congo hemorrhagic fever virus (*Bunyaviridae*) which infects mammals. The putative 25 kDa movement protein (MP) (ORF7) shares limited (27%) identity with 3A-like MPs of members of the families *Tombusviridae* and *Virgaviridae*.

**Figure 1.** *Platypuvirus*. Donkey orchid symptomless virus genome organization showing the relative positions of the ORFs and their expression products. Mtr, methyltransferase; Hel, helicase; RdRP, RNA-directed RNA polymerase; CP, capsid protein.

**Biology**

Members of the only species of this genus have been found infecting native Australian orchids and can be mechanically transmitted to *Nicotiana benthamiana*.

**Derivation of names**

*Platypuvirus* from *platypus* because it appears to combine features of different virus lineages, in the same way that the platypus (*Ornithorhynchus anatinus*) combines features of different vertebrate lineages.

**Species demarcation criteria**

www.ictv.global/report/alphaflexiviridae
Since there is currently only a single species in the genus, species demarcation criteria are not currently defined, but following criteria for other genera in the family, different species should have less than 72% nt identity (or 80% aa identity) between their respective CP or Rep genes, although biological properties should also be considered.

### Member species

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<tr>
<th>Species</th>
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<th>Available sequence</th>
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<td>NC_022894</td>
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</table>

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

Distinguishing features

Potexviruses have relatively short virions (<700 nm) and their genomes have only five ORFs. Potexviruses infect herbaceous hosts and have no known vectors.

Virion

Morphology

Virions are flexuous filaments, 470–580 nm in length and 13 nm in diameter, with helical symmetry and a pitch of 3.3–3.7 nm (Figure 1. Potexvirus). A central axial canal, about 3 nm in diameter can sometimes be discerned. The number of protein subunits per turn of the primary helix is slightly less than 9.0. The RNA backbone is at a radial position of 3.3 nm (Atabekov et al., 2007).

![Figure 1. Potexvirus. Negative-contrast electron micrograph of particles of an isolate of potato virus X. The bar represents 100 nm (Courtesy of D.-E. Lesemann).](image)

Physicochemical and physical properties

The potexvirus virion Mr is about $3.5 \times 10^6$; $S_{20,w}$ is 115–130S; buoyant density in CsCl is 1.31 g cm$^{-3}$.

Nucleic acid

Virions of potexviruses contain a single linear molecule of positive-sense RNA of 5.9–7.0 kb, comprising approximately 6% by weight of the virion. The RNA is capped at the 5′-terminus with m$^7$G and has a polyadenylated tract at the 3′-terminus (Huisman et al., 1988) (Figure 2. Potexvirus).

Proteins

The only structural protein is the 21–27 kDa capsid protein (CP).

Carbohydrates

The capsid protein of some strains of the species Potato virus X are reported to be glycosylated (Baratova et al., 2004).

Genome organization and replication

The genomic RNA of potexviruses, as exemplified by potato virus X (PVX), typically has five ORFs (Figure 2. Potexvirus). ORF1, at the 5′-terminus, encodes the replication-associated protein (Rep) and ORF5, located at the 3′-terminus, is the CP gene. Between ORF1 and ORF5 is the triple gene block (TGB) of three overlapping ORFs, the products of which (25, 12 and 8 kDa) are involved in cell-to-cell movement. The 25 kDa protein contains an NTPase-helicase domain, but is not involved in RNA replication. It has been shown to have RNA silencing suppressor activity which is necessary for virus movement. The 12 and 8 kDa proteins contain large blocks of uncharged amino acids and are associated with membrane vesicles derived from the endoplasmic reticulum. The third TGB protein of Alternanthera mosaic virus (AltMV) (but not that of PVX) is targeted to the chloroplast and is required for movement from the epidermis to the mesophyll layer. The CP is also involved in cell-to-cell movement. ORFs 2 to 5 are expressed via the production (and subsequent translation) of subgenomic RNAs.
Two or three 3′-co-terminal sgRNAs can be isolated from plants infected with potexviruses (ca. 2.1, 1.2 and 1.0 kb); the double-stranded counterparts of these sgRNAs have also been detected. The medium-sized sgRNA (1.2 kb) is probably functionally bicistronic, its translation yielding the 12 and 8 kDa proteins.

Virions of PVX contain only genomic RNA, but some other potexviruses also encapsidate the sgRNA for the CP. Genomic RNA is translated as a functionally monocistronic message; only the 5′-proximal Rep gene is translated directly by ribosomes, producing the Rep protein (150–181 kDa). The 5′-UTR leader sequence of PVX RNA consists of 83 nt (excluding the cap-structure) and enhances translation.

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## Member species

### Exemplar isolate of the species

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<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number/RefSeq number</th>
<th>Available sequence</th>
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Virus names and virus abbreviations are not official ICTV designations.

## Related, unclassified viruses

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Virus names and virus abbreviations are not official ICTV designations.
**Genus: Sclerodarnavirus**

**Distinguishing features**

There is a single species in the genus, *Sclerotinia sclerotiorum debilitation-associated RNA virus* represented by *Sclerotinia sclerotiorum debilitation-associated RNA virus*, a capsid-less mycovirus. Despite the lack of capsid, phylogenetic analysis of the replication-associated protein (Rep) places it within the *Alphaflexiviridae* family (*Xie et al.*, 2006).

**Virion**

**Morphology**

None.

**Physicochemical and physical properties**

No information.

**Nucleic acid**

A single linear molecule of positive-sense RNA of 5470 nt with a polyadenylated tract at the 3′-terminus (Figure 1. *Sclerodarnavirus*).

**Proteins**

No information available.

**Carbohydrates**

Not applicable.

**Genome organization and replication**

There is a single ORF encoding a Rep protein of 193 kDa (Figure 1. *Sclerodarnavirus*).

![Figure 1. Sclerodarnavirus. Sclerotinia sclerotiorum debilitation-associated RNA virus genome organization. Mtr, methyltransferase; Hel, helicase; RdRP, RNA-directed RNA polymerase.](www.ictv.global/report/alphaflexiviridae)

**Biology**

*Sclerotinia sclerotiorum debilitation-associated RNA virus* was discovered in the plant pathogenic fungus *Sclerotinia sclerotiorum* and appears to cause debilitation (hypovirulence).

**Derivation of names**

*Sclerodarna*: from *Sclerotinia sclerotiorum debilitation-associated RNA virus*, the type species of the genus.

**Species demarcation criteria**

Since there is currently only a single species in the genus, species demarcation criteria are not yet defined, but, as delineated for other genera in the family, members of distinct species may have less than 72% nt identity (or 80% aa identity) between Rep genes.

**Member species**

★ Exemplar isolate of the 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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Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
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Resources: Alphaflexiviridae

Sequence alignments and tree files:

Figure 3. Alphaflexiviridae:
- Tree file (newick format)
- Alignment file (FASTA format)

Figure 4. Alphaflexiviridae:
- Tree file (newick format)
- Alignment file (FASTA format)
Further reading: Alphaflexiviridae

References: Alphaflexiviridae


Citation: Alphaflexiviridae

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