**Fimoviridae**

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**Summary**

Members of the family *Fimoviridae* are plant viruses with segmented, linear, single-stranded, negative-sense RNA genomes that are distantly related to orthotospoviruses (family *Tospoviridae*) and orthobunyaviruses (family *Peribunyaviridae*) (Table 1. *Fimoviridae*). The family *Fimoviridae*, order *Bunyavirales*, includes one genus (*Emaravirus*) with nine species. Fimoviruses are transmitted to plants by eriophyid mite vectors and induce similar characteristic cytopathologies in their host plants, including the presence of double membrane bounded bodies (DMBs) in the cytoplasm of the virus-infected cells.

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

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td>European mountain ash ringspot-associated virus, Hamburg (RNA1: AY563040; RNA2: AY563041; RNA3: DQ831831; RNA4: DQ831828), species European mountain ash ringspot-associated emaravirus, genus <em>Emaravirus</em>, family <em>Fimoviridae</em>, order <em>Bunyavirales</em></td>
</tr>
<tr>
<td>Virion</td>
<td>Approximately spherical and enveloped with diameter 80–100 nm</td>
</tr>
<tr>
<td>Genome</td>
<td>Four to eight segments of negative-sense ssRNA (12.3–18.5 kb in total)</td>
</tr>
<tr>
<td>Replication</td>
<td>No information</td>
</tr>
<tr>
<td>Translation</td>
<td>From capped mRNAs (produced by &quot;cap snatching&quot; from host mRNAs) which are complementary to the vRNAs</td>
</tr>
<tr>
<td>Host range</td>
<td>Cercis, fig, kiwi, maize, pigeonpea, raspberry, rose, Sorbus, wheat</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Single genus including nine species</td>
</tr>
</tbody>
</table>

**Virion**

**Morphology**

Fimoviruses have enveloped, approximately spherical virions, with a diameter of 80–100 nm (Figure 1. *Fimoviridae*), containing at least four negative-sense ssRNA segments (Elbeaino et al., 2009).
Figure 1. **Fimoviridae.** Immunosorbent electron micrograph of virions of European mountain ash ringspot-associated virus. The bar represents 100 nm (Courtesy Inga Ludenberg, University of Hamburg, Germany).

**Physicochemical and physical properties**

None reported.

**Nucleic acid**

The viral genome comprises four (European mountain ash ringspot-associated virus) to eight segments of negative-sense ssRNA (High Plains wheat mosaic virus,) comprising 12.3 to 18.5 kb in total. Genomic RNAs are not capped or polyadenylated and all contain complementary sequences (18–20 nt, depending on the segment) at their 5′- and 3′-termini. Five conserved motifs (A–E) in the amino acid sequence of the RNA-dependent RNA polymerase (RdRP) protein are similar to those in bunyavirales L segments (Elbeaino et al., 2009b).

**Proteins**

Each RNA segment of the genome encodes a single protein translated from the complementary strand as follows: RNA1 - RNA-dependent RNA polymerase (RdRP, p1, 264–269 kDa; 226.9 kDa in Actinidia chlorotic ringspot-associated virus); RNA2 - a glycoprotein precursor (GP, p2, 73–76.6 kDa) that is predicted to be cleaved into products of 21.5–25.0 and 51–52 kDa; RNA3 - the nucleocapsid protein (NP, p3, 32–35.6 kDa); RNA4 - a putative movement protein (MP, p4, ca. 40.5–43.6 kDa)

**Lipids**

Uncharacterised.

**Carbohydrates**

Uncharacterised.

**Genome organization and replication**

Fimoviruses differ from other related viruses (orthotospoviruses and orthobunyaviruses) by having a larger number of genomic RNA segments. RNA1 to RNA4 each encode a single protein (Figure 2.Fimoviridae). The function of proteins encoded by the other RNAs (RNA5 to RNA8) remain unknown (Tatineni et al., 2014). Like other negative-sense ssRNA multipartite viruses, some fimoviruses are known to use “cap snatching” to initiate transcription and facilitate translation of their mRNAs, as it was proven in the cases of RRV and FMV (Walia and Falk 2012, Laney et al., 2011).
Biology

Depending on the host plant, symptoms of fimovirus infection vary from leaf mottling, blotching, vein clearing, chlorotic ringspots, yellowing, sterility of flowers to a general mosaic. Fimoviruses are transmitted by grafting and there is evidence that many have eriophyid mite vectors (Epstein and Hill 1995, Kumar et al., 2003).

Derivation of names

Fimo: from fig mosaic

Relationships within the family

Phylogenetic trees constructed with fimovirus RdRP (Figure 3. Fimoviridae), GP or NC protein sequences display similar topologies with two (or three) main clades (Zheng et al., 2017, Elbeaino et al., 2015). The first group includes High Plains wheat mosaic virus and raspberry leaf blotch virus, while the second comprises all the others, which in turn could be subdivided into two subgroups: i) subgroup a, comprising fig mosaic virus, rose rosette virus, pigeonpea sterility mosaic virus 2 and pigeonpea sterility mosaic virus 1, and ii) subgroup b, including European mountain ash ringspot-associated virus, redbud yellow ringspot-associated virus and Actinidia chlorotic ringspot-associated virus.
Figure 3. Fimoviridae. Phylogenetic tree constructed with amino acid sequences encoded by RNA1 (RdRP), of members of the family Fimoviridae and the orthologous L segment-encoded proteins of members of the families Peribunyaviridae and Topsoviridae. An alignment was obtained using MUSCLE within MEGA6 (Tamura et al., 2013) and a maximum likelihood tree produced with 1000 bootstrap replicates. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap is shown next to the branches (when >70%). * Blackberry leaf mottle-associated virus is an unclassified virus in the family Fimoviridae. An isolate of Grapevine fanleaf virus, genus Nepovirus, family Secoviridae, was used to root the tree. This phylogenetic tree and corresponding sequence alignment are available to download from the Resources page.

Relationships with other taxa

Viruses of the family Fimoviridae (order Bunyavirales) are related to viruses in the families Tospoviridae and Peribunyaviridae in that they share (i) a multipartite negative-sense single-stranded RNA genome of four to eight segments; (ii) high sequence identity with orthologous proteins of members of the order Bunyavirales at equivalent genome positions in the first three RNAs (corresponding to L, M, and S RNA segments), i.e. RNA-dependent RNA polymerase (RdRP, RNA1), putative glycoprotein precursor (GP, RNA2) and putative nucleocapsid protein (NP, RNA3); (iii) five conserved motifs (A-E) in the amino acid sequence of their RdRP similar to those in L segment-encoded proteins of members of the order Bunyavirales; (iv) enveloped virions; (vi) stretches of nucleotides at both 5′- and 3′-termini of all RNA segments that are almost perfectly complementary to each other. These sequences are conserved in all genomic RNAs of fimoviruses, and are similar, but not identical, to those of other members of the order Bunyavirales.

Related, unclassified viruses

<table>
<thead>
<tr>
<th>Virus name</th>
<th>Accession number</th>
<th>Virus abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>blackberry leaf mottle-associated virus</td>
<td>RNA1: KY056657; RNA2: KY056658; RNA3: KY056659; RNA4: KY056660; RNA5: KY056661</td>
<td>BLMaV</td>
</tr>
</tbody>
</table>

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

Since only one genus (*Emaravirus*) is currently recognized in the family *Firmoviridae*, the family description above corresponds to the genus description. For clarity, the additional information that can be found on the genus page is also presented below.

Derivation of names

*Emara*: from *European* mountain ash ringspot-associated virus.

Species demarcation criteria

Species in the genus are demarcated based upon the amino acid sequence of relevant gene products of RNA1 (RdRP), RNA2 (GP) and RNA3 (NP) differing by more than 25%.

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>Blackberry leaf mottle associated emaravirus</td>
<td>Blackberry leaf mottle-associated virus</td>
<td>Arkansas</td>
<td>RNA1: KY056657; RNA2: KY056658; RNA3: KY056659; RNA4: KY056660; RNA5: KY056661</td>
<td>RNA1: NC_013105; RNA2: NC_013106; RNA3: NC_013108; RNA4: NC_013107</td>
<td>Complete genome</td>
<td>BLaV</td>
</tr>
<tr>
<td><em>Fig</em> mosaic emaravirus</td>
<td><em>fig</em> mosaic virus</td>
<td>Gr 10</td>
<td>RNA1: AM941711; RNA2: FM864226; RNA3: FM991054; RNA4: FM992851; RNA5: HE830826; RNA6: HE830827</td>
<td>RNA1: NC_029565; RNA2: NC_029566; RNA3: NC_029567; RNA4: NC_029568; RNA5: NC_029569; RNA6: NC_029570</td>
<td>Complete genome</td>
<td>FMV</td>
</tr>
</tbody>
</table>

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

Sequence alignments and tree files:

Figure 3. *Fimoviridae*

Alignment file (FASTA format)

Tree file (newick format)
References: Fimoviridae


Citation: Fimoviridae

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