ICTV Virus Taxonomy Profile: **Secoviridae**

Jeremy R. Thompson, 1,* Indranil Dasgupta, 2 Marc Fuchs, 3 Toru Iwanami, 4 Alexander V. Karasev, 5 Karel Petrzik, 6 Hélène Sanfaçon, 7 Ioannis Tzanetakis, 8 René van der Vlugt, 9 Thierry Wetzel, 10 Nobuyuki Yoshikawa 11 and ICTV Report Consortium

**Abstract**

Members of the family **Secoviridae** are non-enveloped viruses with mono- or bipartite (RNA-1 and RNA-2) linear positive-sense ssRNA genomes with the size of the RNAs combined ranging from 9 to 13.7 kb. They are related to picornaviruses and are classified in the order **Picornavirales**. The majority of known members infect dicotyledonous plants and many are important plant pathogens (e.g. grapevine fanleaf virus and rice tungro spherical virus). This is a summary of the current International Committee on Taxonomy of Viruses (ICTV) report on the taxonomy of the family **Secoviridae** available at www.ictv.global/report/secoviridae.

**Table 1. Characteristics of the family Secoviridae**

<table>
<thead>
<tr>
<th>Typical member:</th>
<th>cowpea mosaic virus (RNA-1: X00206; RNA-2: X00729), species Cowpea mosaic virus, genus Comovirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Non-enveloped, 25–30 nm in diameter with icosahedral symmetry</td>
</tr>
<tr>
<td>Genome</td>
<td>9.0–13.7 kb of positive-sense, mono- or bipartite RNA</td>
</tr>
<tr>
<td>Replication</td>
<td>In association with intracellular membranes derived from the endoplasmic reticulum</td>
</tr>
<tr>
<td>Translation</td>
<td>Directly from genomic RNA as large polyproteins, which are cleaved by 3C-like proteinases</td>
</tr>
<tr>
<td>Host range</td>
<td>Plants (mainly dicots), transmitted mainly by insects or nematodes. Some seed transmission demonstrated</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>In the order <strong>Picornavirales</strong>, family includes one subfamily with three genera, five additional genera and more than 70 species</td>
</tr>
</tbody>
</table>

**VIRION**

Virions are non-enveloped, 25–30 nm in diameter and exhibit icosahedral symmetry (Table 1). Many virus preparations contain empty virus particles. In the case of viruses with a bipartite genome, the two RNAs are encapsidated in separate virions (Fig. 1) [1].

**GENOME**

The genome consists of one or two molecules of linear positive-sense ssRNA that are covalently linked to a small protein (viral protein genome-linked, Vpg; 2–4 kDa) at their 5′ end and have a 3′-terminal poly(A) tract. Each RNA encodes, in the majority of the cases, a single polyprotein (Fig. 2).

**REPLICATION**

In the case of viruses with a bipartite genome, neither RNA species alone can infect plants systemically. Viral proteins are usually expressed as large polyproteins, which are cleaved by virus-encoded 3C-like proteinases. The replication block contains the domain characteristics of nucleoside triphosphate (NTP)-binding proteins (NTB or putative helicase), 3C-like proteinases (Pro) and RNA-dependent RNA polymerases (Pol) (Fig. 2). Replication occurs in association
with intracellular membranes derived from the endoplasmic reticulum.

**TAXONOMY**

**Comovirus**

Bipartite genome (subfamily *Comovirinae*). Comoviruses usually have narrow host ranges. Mosaic and mottle symptoms are characteristic. Transmission in nature is exclusively by beetles, especially members of the family Chrysomelidae. Beetles retain their ability to transmit virus for days or weeks [2].

**Fabavirus**

Bipartite genome (subfamily *Comovirinae*). Fabaviruses have wide host ranges among dicotyledonous and some families of monocotyledonous plants. Symptoms are ringspots, mottling and wilting. In nature, they are transmitted by aphids in a non-persistent manner.

**Nepovirus**

Bipartite genome (subfamily *Comovirinae*). The genus consists of >35 species that are widely distributed in temperate regions. Ringspot symptoms are characteristic. Many nepoviruses are transmitted non-persistently by longidorid nematodes. Seed and/or pollen transmission are also common. In herbaceous plants, the symptoms induced are often transient with a so-called ‘recovery’ phenomenon. The genus can be divided into subgroups (A, B, C) based on sequence and genome organization [3].

**Cheravirus**

Bipartite genome. Symptoms are usually mild or absent. Cherry rasp leaf virus is transmitted by nematodes in the field [4].

**Sadwavirus**

Bipartite genome, only one species, *Satsuma dwarf virus*, members of which have a wide host range. The natural mode of transmission is unknown [5].

**Torradovirus**

Bipartite genome. RNA-2 contains an ORF upstream and partially overlapping the large ORF. Some torradoviruses are known to be transmitted by whiteflies in a semi-persistent manner. Aphid transmission has been demonstrated for carrot torrado virus 1 [6].

**Sequivirus**

Monopartite genome. The natural host range of sequiviruses includes plants in several families. Transmission is by aphids in a semi-persistent manner. However, it is dependent on the presence of a helper virus in the genus *Waikavirus*.

**Waikavirus**

Monopartite genome. The natural host range of waikaviruses is usually restricted to plants within a few families. Field transmission is semi-persistent by aphids or leafhoppers. Some waikaviruses are helper viruses for the insect transmission of other viruses; for example, rice tungro spherical virus is the helper virus for rice tungro bacilliform virus (family *Caulimoviridae*).
RESOURCES

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Conflicts of interest
The authors declare that there are no conflicts of interest.

References

Fig. 2. Genome organization of representative members of the family Secoviridae. Each RNA is shown with ORFs represented with boxes. Circles depict VPg molecules covalently attached at the 5'-end of the RNAs. Black circles represent VPg confirmed experimentally and open circles represent putative VPgs. Poly(A) tails are represented at the 3'-end of the RNAs when present (Aₙ). Red and blue arrows above the sequences represent regions of extensive sequence identity between RNAs 1 and 2. In the latter, for torradoviruses, this identity is also characterized by conserved indels. Protein domains with conserved motifs for the putative NTP-binding protein (NTB, shown in orange), VPg (purple), protease (Pro, yellow), RNA-dependent RNA polymerase (Pol, red), movement protein (MP, green) and coat protein(s) (CP, blue) are shown. The star represents a conserved motif found in the protease cofactor (Co-Pro) protein of comoviruses and in the equivalent protein of other viruses. Proteinase cleavage sites identified experimentally or deduced by sequence comparisons are indicated by solid or dotted vertical lines, respectively. Possible ORFs in the genome of waikaviruses are shown with dotted rectangles and putative subgenomic RNAs are shown by dotted arrows below the waikavirus genome. Representatives of each nepovirus subgroup (Sg A, B, C) are also depicted.