**Polycipiviridae**

Ingrida Olendraite, Katherine Brown, Steven M. Valles, Andrew E. Firth, Yanping Chen, Diego M. A. Guérin, Yoshifumi Hashimoto, Salvador Herrero, Joachim R. de Miranda and Eugene Ryabov

Edited by Nick J. Knowles and Sead Sabanadzovic

Corresponding author: Andrew E. Firth (aef24@cam.ac.uk)

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**Summary**

*Polycipiviridae* is a family of picorna-like viruses with non-segmented, linear, positive-sense RNA genomes of approximately 10–12 kb (Table 1.*Polycipiviridae*). Unusually for viruses within the order *Picornavirales*, their genomes are polycistronic, with four (or more) consecutive 5′-proximal open reading frames (ORFs) encoding structural (and possibly other) proteins and a long 3′ ORF encoding the replication polyprotein. Members of species within the family have all been derived from arthropods, with the majority coming from ants.

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

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td>Solenopsis invicta virus 2 (MF041813), species <em>Solenopsis invicta virus 2</em>, genus <em>Sopolycivirus</em>, family <em>Polycipiviridae</em>, order <em>Picornavirales</em></td>
</tr>
<tr>
<td>Virion</td>
<td>Thought to be non-enveloped, 33 nm in diameter</td>
</tr>
<tr>
<td>Genome</td>
<td>10–12 kb of positive-sense, non-segmented RNA</td>
</tr>
<tr>
<td>Replication</td>
<td>Not studied; presumed to be similar to other <em>Picornavirales</em> members</td>
</tr>
<tr>
<td>Translation</td>
<td>Directly from genomic RNA, presumed internal ribosome entry site elements in 5′-untranslated region and intergenic region</td>
</tr>
<tr>
<td>Host range</td>
<td>Arthropoda</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Member of the order <em>Picornavirales</em>. Includes the genera <em>Chipolycivirus</em>, <em>Hupolycivirus</em> and <em>Sopolycivirus</em></td>
</tr>
</tbody>
</table>

**Virion**

**Morphology**

Icosahedral particles approximately 33 nm in diameter have been observed by electron microscopy in samples prepared from ants infected with *Solenopsis invicta* virus 2 (SINV2) but not in samples prepared from non-infected ants and these particles are assumed to represent SINV2 virions (Valles et al., 2007) (Figure 1. *Polycipiviridae*). Genomes are picorna-like and encode three jelly-roll fold capsid proteins, thus particles are assumed to be picorna-like, i.e. non-enveloped, icosahedral, pseudo-T=3 symmetry comprising 60 copies of each of the ORF1, ORF3 and ORF4 products. However, this has not yet been experimentally confirmed.
Physicochemical and physical properties

Virion physicochemical properties have not been investigated.

Nucleic acid

The genome is thought to comprise a single positive-sense RNA molecule of 10–12 kb. The genome has a 3′-poly(A) tail and is presumed to have a small viral protein genome-linked (VPg) covalently attached to the 5′-end.

Proteins

The virion protein composition has not been experimentally determined.

Lipids

None reported.

Carbohydrates

None reported.

Genome organization and replication

The genome contains four main 5′-proximal ORFs (ORFs 1–4) and one long 3′ ORF (ORF5) (Figure 2. *Polycipiviridae*). ORF1, ORF3 and ORF4 encode products with homology to picornavirus jelly-roll fold capsid proteins. ORF2 encodes a product of unknown function. ORF5 encodes superfamily III helicase, chymotrypsin-like serine protease and superfamily I RNA dependent RNA polymerase (RdRP) domains, and is presumed to encode a viral protein genome-linked (VPg) and potentially another protein between the helicase and protease, and one or two additional proteins upstream of the helicase. ORF5 is expected to be proteolytically cleaved by the viral protease but the cleavage sites have not been mapped. The genome is flanked by 5′- and 3′-untranslated regions (UTRs) and a lengthy intergenic region (IGR) between ORF4 and ORF5. The 5′-UTR and intergenic region (IGR) are presumed to contain internal ribosome entry site (IRES) elements to direct translation of ORF1 and ORF5 whereas ORFs 2–4 have been proposed to be expressed via a ribosome re-initiation mechanism. Members of the genus *Sopolycivirus* contain an additional ORF (2b) overlapping the 5′-end of ORF2; ORF2b encodes a small protein with a predicted transmembrane domain. Members of at least one species (*Formica exsecta virus 3*) contain a further additional small ORF inserted between ORF2 and ORF3. Replication has not been studied but is assumed to be similar to other members of the order *Picornavirales*.
Figure 2. *Polycipiviridae* Genome organization of *Solenopsis invicta* virus 2 (genus *Sopolycivirus*). The 5′-proximal ORFs encode jelly-roll capsid protein domains (JR, orange), a protein of unknown function (ORF2), and a small predicted transmembrane protein (2b; specific to genus *Sopolycivirus*). The 3′ ORF encodes helicase (Hel), protease (Pro), and RNA-dependent RNA polymerase (RdRP) domains. The genome is polyadenylated and believed to have a viral protein genome-linked (VPg) covalently attached to its 5′-end. Members of the genera *Hupolycivirus* and *Chipolycivirus* have similar genome organizations except that they lack the 2b ORF.

**Biology**

All current family members derive from ants or from transcriptomic studies of arthropods. Members of the type species *Solenopsis invicta* virus 2 appear to establish a chronic, asymptomatic infection in *Solenopsis invicta* ants and high virus loads have been detected in larvae, pupae, workers and queens (Hashimoto and Valles 2008a, Hashimoto and Valles 2008b). In infected ants, 96% of SINV2 genome equivalents localize to the midgut section of the alimentary canal. Further, SINV2 has been experimentally transmitted to non-infected ants via feeding suggesting food-borne transmission probably by trophallaxis (Hashimoto and Valles 2008b). Fire ant infections with SINV2 are associated with negative impacts on queen ants resulting in significant reductions in fecundity, longer claustral periods, and slower growth of newly established colonies (Manfredini et al., 2016).

**Derivation of names**

*Polyci*: derived from *poly* (several) *cistronic* *picorna-like*.

**Genus demarcation criteria**

Genera are separated based on phylogenetic clustering based on protein sequence identities (Figure 3. *Polycipiviridae*). However formal genus demarcation criteria have not yet been established.

Figure 3. *Polycipiviridae*. Mid-point rooted phylogenetic tree constructed from full-length ORF5 amino acid sequences of members of polycipivirus species and related unclassified virus sequences. Genera are annotated at left. Sequences were aligned with MUSCLE, and a Bayesian Markov chain Monte Carlo-based phylogenetic tree (ngen=1,000,000) was produced with MrBayes. Posterior probabilities are indicated at the branching points. This phylogenetic tree and corresponding sequence alignment are available to download from the Resources page.

**Relationships within the family**

Phylogenetic analysis of the ORF5 non-structural polyprotein amino acid sequences indicates that sopolyciviruses, hupolyciviruses and chipolyciviruses form distinct monophyletic groups in the family (Figure 3. *Polycipiviridae* (Olendraite et al., 2017)). Monophyly of the *Polycipiviridae* family within the order *Picornavirales* is not completely certain (Aiewsakun and Simmonds 2018), though the unusual genome organization of these viruses justifies their current taxonomic grouping.

**Relationships with other taxa**

Similar to other members of the order *Picornavirales*, polycipiviruses have polyadenylated positive-sense RNA genomes that encode three...
jelly-roll capsid proteins, a superfamily III helicase, a 3C-like chymotrypsin-related protease and a superfamily I RdRP (Olenkraite et al., 2017). Unlike other members of the order, with the exception of marnaviruses, the polycipivirus protease has serine rather than cysteine at the active site. Polycipiviruses also have a unique genome organization (Figure 2. Polycipiviridae).
**Genus: Chipolycivirus**

**Distinguishing features**

Among currently classified members of the family, chipolyciviruses are distinguished by the presence of the amino acid triplet ADD instead of GDD in motif VI of the RdRP (Olendraite et al., 2017).

**Virion**

See discussion under family description.

**Genome organisation and replication**

See discussion under family description.

**Biology**

See discussion under family description.

**Derivation of names**

Chipolyci: from the type species *Chironomus riparius virus 1* and *polycipivirus*.

**Species demarcation criteria**

Formal species demarcation criteria have not yet been established. ORF5-encoded amino acid sequence identity between isolates and strains of a species is above 90%.

**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>★ Chironomus riparius virus 1</td>
<td>Chironomus riparius virus 1</td>
<td>Amsterdam-TSA</td>
<td>KX192549</td>
<td>Complete coding genome</td>
<td>ChriV1</td>
<td></td>
</tr>
<tr>
<td>★ Hubei chipolycivirus</td>
<td>Hubei picorna-like virus 82</td>
<td>spider133992</td>
<td>KX833688</td>
<td>Complete coding genome</td>
<td>HpIV82</td>
<td></td>
</tr>
</tbody>
</table>

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

**Distinguishing features**

Members lack the 2b ORF that is present in members of the genus *Sopolycivirus* but – in contrast to members of the genus *Chipolyivirus* – have the amino acid triplet GDD in motif VI of the RdRP.

**Virion**

See discussion under family description.

**Genome organisation and replication**

See discussion under family description.

**Biology**

See discussion under family description.

**Derivation of names**

Hupolyi: from the type species *Hupei hupolyivirus*

**Species demarcation criteria**

Formal species demarcation criteria have not yet been established. ORF5-encoded amino acid sequence identity between isolates and strains of a species is above 90%.

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number (RefSeq number)</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>★ Hupei hupolyivirus</td>
<td>Hupei picornavirus 81</td>
<td>QTM27117</td>
<td>KX883940</td>
<td>NC_033152</td>
<td>Complete coding genome HplV81</td>
</tr>
</tbody>
</table>

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

Distinguishing features

Among currently classified members of the family, sopolyciviruses are distinguished by the presence of ORF2b overlapping the 5′-end of ORF2; ORF2b encodes a small protein with a predicted transmembrane domain (Olendraite et al., 2017). Most (possibly all) members of the genus appear to infect ants (family Formicidae).

Virion

See discussion under family description.

Genome organisation and replication

See discussion under family description.

Biology

See discussion under family description.

Derivation of names

Sopolyci: from the type species Solenopsis invicta virus 2 and polycipivirus.

Species demarcation criteria

Formal species demarcation criteria have not yet been established. ORF5-encoded amino acid sequence identity between isolates and strains of a species is above 90%.

Member species

<table>
<thead>
<tr>
<th>★</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>
</tr>
</thead>
<tbody>
<tr>
<td>★</td>
<td>Formica exsecta virus 3</td>
<td>Formica exsecta virus 3</td>
<td>Hanko-TSA</td>
<td>LR935078; LR935077</td>
<td>Complete coding genome</td>
<td>FexV3</td>
<td></td>
</tr>
<tr>
<td>★</td>
<td>Lasius neglectus virus 1</td>
<td>Lasius neglectus virus 1</td>
<td>Cambridge-Line</td>
<td>MF041809</td>
<td>NC_035450</td>
<td>Complete genome</td>
<td>LneV1</td>
</tr>
<tr>
<td>★</td>
<td>Lasius neglectus virus 2</td>
<td>Lasius neglectus virus 2</td>
<td>Gil sur Yvette-TSA</td>
<td>LC526777</td>
<td>Complete coding genome</td>
<td>LneV2</td>
<td></td>
</tr>
<tr>
<td>★</td>
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<td>Lasius niger virus 1</td>
<td>Cambridge-Line</td>
<td>MF041812</td>
<td>NC_035456</td>
<td>Partial genome</td>
<td>LniV1</td>
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<td>★</td>
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<td>Linepithema humile virus 2</td>
<td>Catalonia-TSA</td>
<td>LT719234</td>
<td>Complete coding genome</td>
<td>LhuV2</td>
<td></td>
</tr>
<tr>
<td>★</td>
<td>Monomorium pharaonis virus 1</td>
<td>Monomorium pharaonis virus 1</td>
<td>Copenhagen-TSA</td>
<td>LA988223</td>
<td>Complete coding genome</td>
<td>MphV1</td>
<td></td>
</tr>
<tr>
<td>★</td>
<td>Monomorium pharaonis virus 2</td>
<td>Monomorium pharaonis virus 2</td>
<td>Copenhagen-TSA</td>
<td>LA985648</td>
<td>Complete coding genome</td>
<td>MphV2</td>
<td></td>
</tr>
<tr>
<td>★</td>
<td>Myrmica scabrinodis virus 1</td>
<td>Myrmica scabrinodis virus 1</td>
<td>Cambridge-Mac</td>
<td>MF041810</td>
<td>NC_035457</td>
<td>Complete genome</td>
<td>MsV1</td>
</tr>
<tr>
<td>★</td>
<td>Shuangao insect virus 8</td>
<td>Shuangao insect virus 8</td>
<td>insectZJ96360</td>
<td>KX983910</td>
<td>NC_032978</td>
<td>Complete coding genome</td>
<td>ShiV8</td>
</tr>
<tr>
<td>★</td>
<td>Solenopsis invicta virus 2</td>
<td>Solenopsis invicta virus 2</td>
<td>Florida-Sin</td>
<td>MF041813</td>
<td>NC_039236</td>
<td>Complete coding genome</td>
<td>SINV2</td>
</tr>
<tr>
<td>★</td>
<td>Solenopsis invicta virus 4</td>
<td>Solenopsis invicta virus 4</td>
<td>Gainesville-Sin</td>
<td>MF041808</td>
<td>NC_039233</td>
<td>Complete coding genome</td>
<td>SINV4</td>
</tr>
</tbody>
</table>

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Related, unclassified viruses

<table>
<thead>
<tr>
<th>Virus name</th>
<th>Accession number</th>
<th>Virus abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linepithema humile polycipivirus 2</td>
<td>MH213248</td>
<td>LhuPeV2</td>
</tr>
</tbody>
</table>

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Authors: Polycipiviridae

Ingrida Olendraite
Department of Pathology
University of Cambridge
Cambridge CB2 1QP
UK
Tel: +44 (0)1223 762652
E-mail: io239@cam.ac.uk

Katherine Brown
Department of Pathology
University of Cambridge
Cambridge CB2 1QP
UK
Tel: +44 (0)1223 762652
E-mail: kdb84@cam.ac.uk

Steven M. Valles
United States Department of Agriculture
Agricultural Research Service
Gainesville FL 32608
USA
Tel: (352) 374-5834
E-mail: steven.valles@ars.usda.gov

Andrew E. Firth*
Department of Pathology
University of Cambridge
Cambridge CB2 1QP
UK
Tel: +44 (0)1223 762652
E-mail: aef24@cam.ac.uk

Yanping Chen
United States Department of Agriculture
Agricultural Research Service
Beltville MD 20705
USA
Tel: (301) 504-8749
E-mail: Judy.Chen@ars.usda.gov

Diego M. A. Guérin
Department of Biochemistry and Molecular Biology
University of the Basque Country (EHU)
Biophysics Institute (CSIC-UPV/EHU)
Bº Sarriena S/N, 48940 Leioa
Spain
Tel: +34 94 601 3345
E-mail: diego.guerin@ehu.eus

Yoshifumi Hashimoto
Vector Biology
BioMarin Pharmaceutical Inc.
San Rafael, CA 94901
USA
Tel: (415) 584-2867
E-mail: yoshifumi.hashimoto@bmrn.com

Salvador Herrero
Department of Genetics
Universitat de València
Burjassot
Spain
Tel: +34 96 354 3006
E-mail: sherrero@uv.es

Joachim R. de Miranda
Department of Ecology
Swedish University of Agricultural Sciences
Uppsala 750 07
Sweden
Tel: +46 72 702 5482
E-mail: joachim.de.miranda@slu.se

Eugene Ryabov
United States Department of Agriculture
Agricultural Research Service
Beltsville MD 20705
USA
Tel: (301) 504-8185
E-mail: eugene.ryabov@gmail.com

* to whom correspondence should be addressed
Resources: Polycipiviridae

Sequence alignments and tree files:

Figure 3. Polycipiviridae:

Tree file (tre format)

Alignment file, ORF5 amino acid (FASTA format)

Alignment file, nucleotide (FASTA format)
References: Polycipiviridae


Citation: Polycipiviridae

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