Summary

The family **Artoviridae** was created in 2018 for the established monospecific genus *Peropuvirus* and six new species for invertebrate viruses all discovered by high throughput sequencing (Li et al., 2015, Shi et al., 2016). A second genus, *Hexartovirus*, including two species for viruses of sea lice (Økland et al., 2019) and barnacles (Shi et al., 2016) respectively was added in 2020. Artoviruses form a family in the haploviricotine order **Mononegavirales** (Amarasinghe et al., 2019).

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

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td>Pteromalus puparum negative-strand RNA virus 1 (KX431032), species <em>Pteromalus puparum peropuvirus,</em> genus <em>Peropuvirus</em></td>
</tr>
<tr>
<td>Virion</td>
<td>Enveloped, spherical particles, 100–130 nm in diameter</td>
</tr>
<tr>
<td>Genome</td>
<td>Negative-sense, unsegmented RNA of approximately 12 kb</td>
</tr>
<tr>
<td>Replication</td>
<td>Nuclear: the RNA-directed RNA polymerase engages with the ribonucleoprotein complex at the genome's 3′-end</td>
</tr>
<tr>
<td>Translation</td>
<td>Individual, putatively polyadenylated, mRNAs are translated in the cytoplasm</td>
</tr>
<tr>
<td>Host Range</td>
<td>Barnacles, copepods, odonates, parasitoid wasps, pillworms, woodlice</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Realm Riboviria, kingdom Orthornavirinae, phylum Negarnaviricota, subphylum Haploviricinota, class Monjiviricetes, order Mononegavirales. Genus <em>Peropuvirus</em> includes 6 species and genus <em>Hexartovirus</em> includes 2 species.</td>
</tr>
</tbody>
</table>

Virion

**Morphology**

Virions of *Pteromalus puparum* negative-strand RNA virus 1 (PpNSRV-1) are enveloped and spherical with a diameter of 100–130 nm (Figure 1. *Artoviridae*). Virion morphology and structure is not available for other artoviruses, which are only known from genomic sequence data.
Spherically shaped PpNSRV-1 particles are present in follicular cells of the ovaries of infected parasitoid wasps (Figure 1. Artoviridae). Similarly, virion-like particles stacked in intracellular vesicles have been observed in cells of the digestive tract. The spherical particles of PpNSRV-1 are similar to particles produced by nyamiviruses (Wang et al., 2017, Dietzgen et al., 2017).

Physicochemical and physical properties

None reported.

Nucleic acid

Unsegmented, single-stranded RNA genome of 11–12.5 kb.

Proteins

Artoviruses encode up to 5 structural proteins. Among them are the nucleocapsid protein (N), glycoprotein (G) and RNA-directed RNA polymerase (RdRP) domain-containing large protein (L) that are identified based on sequence similarity and structural properties shared with mononegavirus homologues. The functions of the other encoded proteins are largely unknown and likely are those of matrix and polymerase cofactor proteins.

The amino acid sequence of the PpNSRV-1 L protein is 26% identical to that of Midway virus (MIDWV, Nyamiviridae). The PpNSRV-1 ORF IV protein contains 7 potential O-linked and 4 potential N-linked glycosylation sites and 29 potential phosphorylation sites, suggesting that ORF IV may encode the viral glycoprotein G. The U1 protein is predicted to have 37 potential phosphorylation sites, whereas the U2 protein has 9 potential phosphorylation sites. The U3 protein contains 37 potential O-linked glycosylation sites. Thus, U3 may encode a glycosylated matrix protein M and U1 may encode the viral nucleoprotein N. Based on the conserved genomic organization of mononegaviruses, U2 is suggested to encode a phosphoprotein (P) (Wang et al., 2017).

Lipids

None reported.

Carbohydrates

None reported.

Genome organization and replication

Artovirus single-stranded RNA genomes are up to 12.5 kb (Figure 2. Artoviridae). All known artoviruses have unsegmented genomes. The number of open reading frames (ORFs) varies. Genomes usually encode hypothetical proteins of unknown function (U1, U2 and U3), a putative glycoprotein (G) protein and a large protein (L) encoding an RNA-directed RNA polymerase domain: in the gene order 3'-U1-U2-U3-(G)-L-5'. The complete L gene sequences for all known members are known. Knowledge of artovirus replication is limited.

The PpNSRV-1 genome contains five large independently-transcribed, non-overlapping ORFs flanked by 3'-leader and 5'-trailer regions whose terminal nucleotides do not exhibit obvious complementarity. Typical conserved transcription initiation and termination motifs are identified upstream and downstream, respectively, of each putative ORF.
**Biology**

Members of the genus *Peropuvirus* infect parasitoid wasps, barnacles, pillworms, woodlice odonates, or copepods. Members of the genus *Hexartovirus* infect sea lice (copepods) or barnacles.

PpNSRV-1 was originally isolated from a laboratory parasitoid strain of a pteromalid wasp (*Pteromalus puparum* Linnaeus, 1758). PpNSRV-1 is present in various tissues and life stages of the parasitoid and is transmitted vertically through females and males. PpNSRV-1 increases adult longevity and impairs several fitness parameters of the wasp but has no influence on successful parasitism. PpNSRV-1 moderates the offspring sex ratio by decreasing female offspring numbers (Wang et al., 2017).

Lepeophtheirus salmonis negative-strand RNA virus 1 (LsNSRV-1) was detected in salmon lice (*Lepeophtheirus salmonis* Kroger, 1837) infecting farmed Atlantic salmon (*Salmo salar* Linnaeus, 1758) in Norway. LsNSRV-1 was present in various tissues of male and female salmon lice and was detected in all developmental stages. Viral RNA was detected in both the cytoplasm and nucleoli of infected cells (Økland et al., 2019).

**Derivation of names**

*Arto*: from *arthropod*

*Peropu*: from *Pteromalus puparum*, the species to which the pteromalid wasp belongs, from which the family's typical member, PpNSRV-1, was first isolated.

*Hexarto*: from the crustacean class *Hexanauplia* and *artovirus*.

*Caligid*: member of the *Caligidae* (sea lice)

**Relationships within the family**

Phylogenetic relationships between the RdRP amino acid sequences of artoviruses and members of related mononegavirus families are shown in Figure 3.*Artoviridae.*
Figure 3. Artoviridae. Phylogenetic maximum likelihood tree of members of the family Artoviridae. Artoviruses are classified in the two genera Peropuvirus and Hexartovirus based on RdRP domain amino acid sequences. Viruses of the two genera form monophyletic clades. Representative members of related mononegavirus families are included for comparison. The ML tree was produced using an LG + G + I model 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

Members of the family Artoviridae are phylogenetically most closely related to members of the families Bornaviridae, Lispiviridae, Mymonaviridae, and Nyamiviridae (Figure 3. Artoviridae).
**Genus: Hexartovirus**

**Distinguishing features**

Members of the genus *Hexartovirus* infect sea lice (copepods) or barnacles.

Lepeophtheirus salmonis negative-strand RNA virus 1 (LsNSRV-1) was detected in salmon lice infecting farmed Atlantic salmon in Norway. LsNSRV-1 was present in various tissues of male and female salmon lice and was detected in all developmental stages. Viral RNA is detected in both the cytoplasm and nucleoli of infected cells (Økland et al., 2019).

**Virion**

See discussion under family description.

**Genome organization and replication**

See discussion under family description.

**Biology**

See discussion under family description.

**Species demarcation criteria**

No species demarcation criteria have been established beyond virus phylogeny and hosts. Viruses classified in the two *Hexartovirus* species differ by 71% in L amino acid sequence, although sequence divergence is not currently used as a formal species demarcation criterion.

**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>★ Barnacle hexartovirus</td>
<td>Běihǎi barnacle virus 8</td>
<td>8</td>
<td>KX884410</td>
<td>NC_032430</td>
<td>Complete coding genome</td>
<td>BhBV-8</td>
</tr>
<tr>
<td>★ Caligid hexartovirus</td>
<td>Lepeophtheirus salmonis negative stranded RNA virus 1</td>
<td>LS24</td>
<td>MG489864</td>
<td>Complete genome</td>
<td>LsNSRV-1</td>
<td></td>
</tr>
</tbody>
</table>

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

**Distinguishing features**

Members of the genus *Peropuvirus* infect parasitoid wasps, barnacles, pillworms, woodlice, odonates, or copepods.

*Pteromalus puparum* negative-strand RNA virus 1 (PpNSRV-1) was originally isolated from a laboratory parasitoid strain of a pteromalid wasp. The virus is present in various tissues and life stages of the parasitoid and is transmitted vertically through females and males. PpNSRV-1 increases adult longevity and impairs several fitness parameters of the wasp but has no influence on successful parasitism. PpNSRV1 moderates the offspring sex ratio by decreasing female offspring numbers (Wang et al., 2017).

**Virion**

See discussion under family description.

**Genome organization and replication**

See discussion under family description.

**Biology**

See discussion under family description.

**Species demarcation criteria**

No species demarcation criteria have been established beyond virus phylogeny and hosts. Members of different *Peropuvirus* species differ by 52–75% in L amino acid sequence, although sequence divergence is not currently used as a formal species demarcation criterion.

**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>
</tr>
</thead>
<tbody>
<tr>
<td>★ Beihai peropuvirus</td>
<td>Beihai rhabdovirus 1</td>
<td>BHTSS15729</td>
<td>KX884412</td>
<td>NC_032555</td>
<td>Complete coding genome</td>
<td>BhRLV-1</td>
<td></td>
</tr>
<tr>
<td>★ Hunan peropuvirus</td>
<td>Hunan rhabdovirus 6</td>
<td>CJTM24798</td>
<td>KX884421</td>
<td>partial genome</td>
<td>HnRLV-6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>★ Odonate peropuvirus</td>
<td>Odonate rhabdovirus 8</td>
<td>CJTM19395</td>
<td>KX884420</td>
<td>partial genome</td>
<td>HbRLV-8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>★ Pillworm peropuvirus</td>
<td>Pillworm rhabdovirus 5</td>
<td>WHSFIII19440</td>
<td>KX884444</td>
<td>partial genome</td>
<td>HbRLV-5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>★ Pteromalus puparum peropuvirus</td>
<td>Pteromalus puparum negative-strand RNA virus 1</td>
<td>T1</td>
<td>KX431032</td>
<td>NC_036269</td>
<td>Complete genome</td>
<td>PpNSRV-1</td>
<td></td>
</tr>
<tr>
<td>★ Woodlouse peropuvirus</td>
<td>Woodlouse rhabdovirus 2</td>
<td>BHTSS7258</td>
<td>KX884413</td>
<td>NC_032558</td>
<td>Complete coding genome</td>
<td>BhRLV-2</td>
<td></td>
</tr>
</tbody>
</table>

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www.ictv.global/report/artoviridae
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Resources: Artoviridae

Sequence alignments and tree files:

Figure 3. Artoviridae

Alignment file (FASTA format)

Tree file (newick format)
References: Artoviridae


Citation: Artoviridae

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