**Guttaviridae**

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**Summary**

The *Guttaviridae* is a family of enveloped viruses infecting hyperthermophilic archaea (Table 1. *Guttaviridae*). The virions are ovoid or droplet-shaped, with a diameter of 55–80 nm and a length of 75–130 nm. The genome is a circular dsDNA molecule of around 14–20 kbp. The family includes two genera, *Alphaguttavirus* and *Betaguttavirus*, each with a single species.

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

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td><em>Aeropyrum pernix ovoid virus 1</em> (HE580237), species <em>Aeropyrum pernix ovoid virus 1</em>, genus <em>Betaguttavirus</em></td>
</tr>
<tr>
<td>Virion</td>
<td>Enveloped virions of ovoid shape, with a diameter of 55–80 nm and a length of 75–130 nm.</td>
</tr>
<tr>
<td>Genome</td>
<td>Circular dsDNA of ~14–20 kbp</td>
</tr>
<tr>
<td>Replication</td>
<td>Genome is likely to be replicated by the host replisome</td>
</tr>
<tr>
<td>Translation</td>
<td>Not known</td>
</tr>
<tr>
<td>Host range</td>
<td>Hyperthermophilic archaea, phylum Crenarchaeota</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Two genera: <em>Alphaguttavirus</em> and <em>Betaguttavirus</em></td>
</tr>
</tbody>
</table>

**Virion**

**Morphology**

The virions of members of the *Guttaviridae* have an ovoid shape, measuring 55 x 75 nm (for *Aeropyrum pernix ovoid virus 1* (APOV1), *Betaguttavirus*) to 80 x 130 nm (for *Sulfolobus newzealandicus* droplet-shaped virus (SNVD), *Alphaguttavirus*), when analysed by cryo-electron microscopy (Arnold et al., 2000, Mochizuki et al., 2011). The virion surface is covered by globular subunits, which are ~3.5 nm in width. In negative-contrast electron micrographs, the virions are slightly pleomorphic, most displaying a droplet-like shape. Virions of SNVD are decorated with dense filaments attached to the pointed end of the virion; such appendages were not observed in the virions of APOV1 (Figure 1. *Guttaviridae*). The droplet-shaped morphology is unprecedented among viruses of bacteria and eukaryotes, and represents a group of archaea-specific virion morphotypes (Prangishvili et al., 2017).
Physicochemical and physical properties

Virion densities have not been determined because virions are unstable in CsCl and lyse.

Nucleic acid

Covalently closed circular dsDNA between 14–20 kbp.

Proteins

SNDV virions have one major capsid protein of ~17.5 kDa (Arnold et al., 2000), whereas those of APOV1 include one major capsid protein of ~10.5 kDa and at least 2 minor capsid proteins (Mochizuki, 2012).

Lipids

Guttaviruses appear to be enveloped but the exact lipid composition is not known.

Carbohydrates

Not known.

Genome organization and replication

There is no sequence information for SNDV. The dsDNA genome of APOV1 is 13,769 bp (56.5% GC) and contains 21 ORFs that could encode proteins of more than 56 amino acids, including an integrase of the tyrosine recombinase superfamily, a DnaA-like ATPase, a glycosidase and several DNA-binding proteins containing the helix-turn-helix motifs (Figure 2. Guttaviridae). In most cases, the ORFs are preceded by recognizable putative ribosome binding sites. The majority of putative genes (14) are located on one strand of the DNA. Of the seven putative genes on the opposite strand, five are clustered together (Figure 2. Guttaviridae). Two of the putative genes show sequence similarity to genes of members of the Fuselloviridae encoding an integrase and a DnaA-like protein, whereas three other genes, including the one for glycosidase, are most closely related to those encoded by hyperthermophilic crenarchaea. APOV1 does not carry a gene for a DNA polymerase, suggesting that its genome is replicated by the host replisome. The DnaA-like ATPase of APOV1 is distantly related to the bacterial DNA replication initiator DnaA and, thus, might be involved in the initiation of the APOV1 genome replication. However, experimental evidence to support this prediction is missing.
Figure 2. **Guttaviridae**. Genome map of *Aeropyrum pernix* ovoid virus 1. Functionally annotated open reading frames are highlighted with different colours. The names of the genes include the information on the length and function (when available) of the encoded proteins. Abbreviations: (w)HTH, (winged) helix-turn-helix DNA-binding proteins; MCP, major capsid protein.

**Biology**

APOV1 resides in the genome of *Aeropyrum pernix* as a provirus integrated into the *tRNA<sup>Leu</sup>* gene (Mochizuki et al., 2011). The attachment site on the viral genome (*attP*) is located within the integrase gene. Consequently, upon integration of the APOV1 genome into the host chromosome, the integrase gene is partitioned, as has been also described for fuselloviruses. Excision of the proviral APOV1 genome from the host chromosome, followed by genome replication and virion production, is induced under suboptimal growth conditions, namely, reduced aeration (*A. pernix* is an obligate aerobe). Similarly, SNDV resides within the host cell in a carrier state as an episomal provirus, which is spontaneously induced at the early stationary growth phase. SNDV virion release is associated with host cell lysis (Arnold et al., 2000).

**Derivation of names**

*Gutta* from Latin *gutta*, "drop".

**Genus demarcation criteria**

In the absence of the SNDV genome sequence, the *Alphaguttavirus* and *Betaguttavirus* genera are distinguished by differences in the detailed morphology of SNDV and APOV1 virions.
Relationships within the family

As only the APOV1 genome sequence is available, there is no analysis of phylogenetic relationships in the family.

Relationships with other taxa

The bipartite gene-sharing network analysis of the archaeal virosphere showed that APOV1 forms a common module with fuselloviruses, indicating that the two groups of hyperthermophilic archaeal viruses might be evolutionarily related (Krupovic et al., 2018, Iranzo et al., 2016). Fuselloviruses and APOV1 share genes for an integrase of the tyrosine recombinase superfamily and a DnaA-like ATPase.
**Genus: Alphaguttavirus**

**Distinguishing features**

The sole member of this genus has been lost from collections. Therefore, the only distinguishing features are the morphological details given below.

**Virion**

**Morphology**

The virions of Sulfolobus newzealandicus droplet-shaped virus (SNDV) are characterised by a "beard" of dense filaments at the pointed end of the particle (Figure 1. Guttaviridae).

**Physicochemical and physical properties**

See discussion under family description.

**Nucleic acid**

The genomic DNA of SNDV cannot be cut by many restriction endonucleases but can be cut by the *dam*-methylation dependent restriction endonuclease *DpnI*, indicating that it is extensively methylated by a *dam*-like methylase at the N(6) position of the adenine residue in GATC sequences (Arnold et al., 2000).

**Proteins**

SNDV virions have one major capsid protein of ~17.5 kDa.

**Lipids**

See discussion under family description.

**Carbohydrates**

See discussion under family description.

**Genome organization and replication**

See discussion under family description.

**Biology**

SNDV was found in a carrier state in a Sulfolobus strain isolated from a solataric field sample in Steaming Hill, New Zealand. Virus production starts early in the stationary phase.

**Species demarcation criteria**

Not applicable

**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>★ Sulfolobus newzealandicus droplet-shaped virus</td>
<td>Sulfolobus newzealandicus droplet-shaped virus</td>
<td></td>
<td></td>
<td></td>
<td>No entry in Genbank</td>
<td>SnDV</td>
</tr>
</tbody>
</table>

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

**Distinguishing features**

Aeropyrum pernix ovoid virus 1 (APOV1) is distinguished from Sulfolobus newzealandicus droplet-shaped virus (SNDV) on the basis of morphological details, namely the lack of filaments at one end of the virion, and a larger genomic DNA.

**Virion**

**Morphology**

See discussion under family description.

**Physicochemical and physical properties**

See discussion under family description.

**Nucleic acid**

See discussion under family description.

**Proteins**

APOV1 virions have one major capsid protein of ~10.5 kDa and at least 2 minor capsid proteins (Mochizuki 2012).

**Lipids**

See discussion under family description.

**Genome organization and replication**

See discussion under family description.

**Biology**

Aeropyrum pernix ovoid virus 1 was isolated from *Aeropyrum pernix* strain K1, which was discovered in a coastal solfataric vent at Kodakara-Jima Island, Japan. The virus is temperate and lysogenizes its host by integrating into the chromosome by recombining with the 3′-distal region of the tRNA-Leu gene (Mochizuki et al., 2011).

**Species demarcation criteria**

Not applicable

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Accession number</th>
<th>IRefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Aeropyrum pernix ovoid virus</em></td>
<td><em>Aeropyrum pernix ovoid virus</em></td>
<td>HE580237</td>
<td>-</td>
<td>Complete genome</td>
<td>ApOV1</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>Aeropyrum pernix ovoid virus 2*</td>
<td>-</td>
<td>APOV2</td>
</tr>
</tbody>
</table>

Virus names and virus abbreviations are not official ICTV designations.

* described in (Mochizuki 2012)
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Resources: Guttaviridae

Sequence alignments and tree files:

Due to the absence of genome sequence data for the two species currently in Guttaviridae, there is no alignment or tree file at the moment.
References: Guttaviridae


Citation: Guttaviridae

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