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ICTV Virus Taxonomy Profile: *Guttaviridae*

David Prangishvili,^{1,*} Tomohiro Mochizuki,² Mart Krupovic^{1,*} and ICTV Report Consortium

Abstract

Guttaviridae is a family of enveloped viruses infecting hyperthermophilic archaea. 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 droplet-shaped morphology is unprecedented among viruses of bacteria and eukaryotes and represents a group of archaea-specific virion morphotypes. The family includes two genera, *Alphaguttavirus* and *Betaguttavirus*, each with a single species. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of *Guttaviridae*, which is available at www.ictv.global/report/guttaviridae.

Table 1. Characteristics of the family *Guttaviridae*

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

VIRIONS

Virions of *Sulfolobus newzealandicus* droplet-shaped virus (SNDV), the prototypical member of the genus *Alphaguttavirus*, are approximately 80×130 nm in size and display multiple fibres at the pointed end of the virion [1]. SNDV virions contain a major capsid protein of 17.5 kDa and at least two minor capsid proteins of 13.5 and 13 kDa, respectively [1]. Virions of *Aeropyrum pernix ovoid virus 1* (APOV1), the sole representative of the genus *Betaguttavirus*, appear ovoid in cryo-electron micrographs, with dimensions of 55×75 nm (Table 1, Fig. 1) [2], i.e. 1.5 times smaller than those of SNDV. In negative-contrast electron micrographs, APOV1 virions are slightly pleomorphic (Fig. 1). APOV1 virions contain a major capsid protein of 10.5 kDa and two minor capsid proteins [3]. The droplet-shaped morphology is unprecedented among viruses of bacteria and eukaryotes and represents a group of archaea-specific virion morphotypes [4].

GENOME

The genome of guttaviruses consists of a circular dsDNA molecule. The SNDV genome is ~20 kbp and is known to

be N(6)-methylated, but sequence information is not available [1]. The APOV1 genome is 13 769 bp, consistent with its smaller virion size compared to SNDV, and has a GC content of 56.5% [2]. The genome 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 glycoside hydrolase and several DNA-binding proteins containing helix-turn-helix motifs (Fig. 2).

REPLICATION

Information on the replication cycle of guttaviruses is very scarce. APOV1 resides in the genome of *Aeropyrum pernix* as a provirus integrated into the *tRNA^{Leu}* gene. 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 [2]. APOV1 does not carry a gene for a DNA polymerase, suggesting that its genome is replicated by the host replisome. Similarly, SNDV resides within the

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Keywords: *Guttaviridae*; ICTV report; taxonomy; *Aeropyrum pernix ovoid virus 1*.

Abbreviations: SNDV, *Sulfolobus newzealandicus* droplet-shaped virus; APOV1, *Aeropyrum pernix ovoid virus 1*; (w)HTH, (winged) helix-turn-helix-DNA-binding proteins; MCP, major capsid protein.

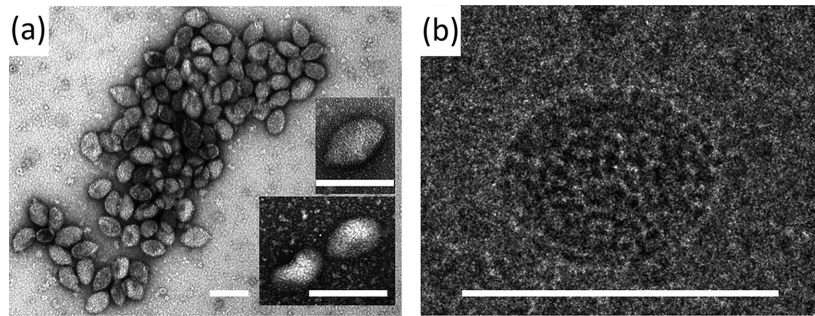


Fig. 1. Electron micrographs of virions of *Aeropyrum pernix ovoid virus 1*. Virions were negatively stained (a) or embedded in ice (b). Scale bars, 100 nm. (Reproduced with permission from [2]. Copyright © 2011, American Society for Microbiology.)

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 [1].

TAXONOMY

APOV1 and SNDV infect hosts belonging to two different orders of the phylum Crenarchaeota. APOV1 was identified as a provirus integrated within the genome of *Aeropyrum pernix* strain K1 (order Desulfurococcales), which was isolated from a coastal solfataric vent at Kodakara-Jima Island, Japan. SNDV was discovered in a carrier state in a *Sulfolobus* strain (order Sulfolobales) isolated from a solataric field sample in Steaming Hill, New Zealand. The viruses are classified in the *Guttaviridae* family on the basis of the similar

morphology and topology of their dsDNA genomes. However, the two viruses display distinguishable morphological features that justify their classification into two genera. A better understanding of *Guttaviridae* taxonomy will require the isolation of further family members. 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 [5, 6].

RESOURCES

Full ICTV Online (10th) Report
www.ictv.global/report/guttaviridae.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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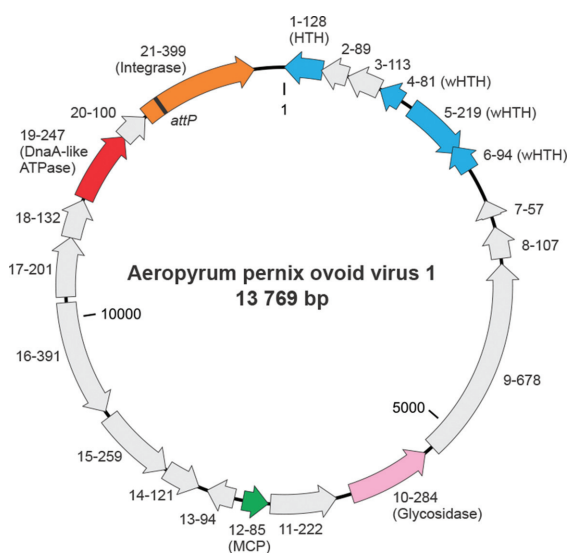


Fig. 2. Genome map of *Aeropyrum pernix ovoid virus 1*. Functionally annotated ORFs are highlighted with different colours. Gene names include information on the length and function (when available) of the encoded proteins. Abbreviations: (w)HTH, (winged) helix-turn-helix DNA-binding proteins; MCP, major capsid protein.