



ICTV Virus Taxonomy Profile: *Aoguangviridae* 2023

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Abstract

The family *Aoguangviridae* includes dsDNA viruses that have been associated with marine archaea. Currently, members of this virus family are known through metagenomics. Virions are predicted to consist of an icosahedral capsid and a helical tail, characteristic of members in the class *Caudoviricetes*. *Aoguangviruses* have some of the largest genomes among archaeal viruses and possess most of the components of the DNA replication machinery as well as auxiliary functions. The family *Aoguangviridae* includes the species *Aobingvirus yangshanense*. Many unclassified relatives of this virus group, referred to as 'magroviruses', have been discovered by metagenomics in globally distributed marine samples. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Aoguangviridae*, which is available at ictv.global/report/aoguangviridae.

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

Example	<i>Poseidoniales virus YSH_150918 (ON649702), species Aobingvirus yangshanense, genus Aobingvirus</i>
Virion	Predicted to have virions characteristic of members of the class <i>Caudoviricetes</i> , with icosahedral capsids and helical tails
Genome	Linear, dsDNA genome of 92.2 kbp
Replication	Virus encoded DNA replisome, including family B DNA polymerase
Translation	Unknown
Host range	Marine archaea
Taxonomy	Realm <i>Duplodnaviria</i> , kingdom <i>Heunggongvirae</i> , phylum <i>Uroviricota</i> , class <i>Caudoviricetes</i> , order <i>Magrovirales</i> : the family includes the genus <i>Aobingvirus</i> and the species <i>Aobingvirus yangshanense</i>

VIRION

Members of the family *Aoguangviridae* have been discovered through metagenomics and have yet to be cultured [1–4] (Table 1). However, based on the conservation of the structural module typical of bacterial and archaeal viruses of the class *Caudoviricetes* [5] and including the HK97-fold major capsid protein, capsid maturation protease, large subunit of the terminase, portal, major tail protein, baseplate, etc., virions are predicted to consist of an icosahedral capsid and a helical tail. The lack of the gene encoding a tail sheath protein suggests that the tails of *aoguangvirids* are not contractile.

GENOME

The genome of *aoguangvirids* is double-stranded DNA of 90–100 kbp, one of the largest described for archaeal viruses. The 92.2 kbp genome of virus YSH_150918 has been assembled as a circular molecule, suggesting terminal redundancy and/or circular permutation. The genome has a G+C content of 31.5% and encodes 129 predicted proteins [3]. The genes encoding functions related to genome replication and virion morphogenesis are organized into two clusters which are predicted to be transcribed in opposite directions (Fig. 1).

REPLICATION

No member of the family *Aoguangviridae* has yet been cultured and so insights into their biology can be only gleaned from

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