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ICTV Virus Taxonomy Profile: *Hypoviridae*

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Abstract

The *Hypoviridae*, comprising one genus, *Hypovirus*, is a family of capsidless viruses with positive-sense, ssRNA genomes of 9.1–12.7 kb that possess either a single large ORF or two ORFs. The ORFs appear to be translated from genomic RNA by non-canonical mechanisms, i.e. internal ribosome entry site-mediated and stop/restart translation. Hypoviruses have been detected in ascomycetous or basidiomycetous filamentous fungi, and are considered to be replicated in host Golgi-derived, lipid vesicles that contain their dsRNA as a replicative form. Some hypoviruses induce hypovirulence to host fungi, while others do not. This is a summary of the current ICTV report on the taxonomy of the *Hypoviridae*, which is available at www.ictv.global/report/hypoviridae.

Table 1. Characteristics of the family *Hypoviridae*

Typical member:	<i>Cryphonectria hypovirus 1</i> strain EP713 (M57938), species <i>Cryphonectria hypovirus 1</i> , genus <i>Hypovirus</i>
Virion	Capsidless virus unable to form rigid particles
Genome	9.1–12.7 kb of linear, positive-sense, non-segmented RNA
Replication	Replication (synthesis of complementary RNA) and transcription (synthesis of genomic RNA) occur cytoplasmically in Golgi-derived membranous vesicles
Translation	Directly from bi- or monocistronic genomic RNA containing a possible internal ribosomal entry site at the 5'-non-coding region
Host range	Fungi
Taxonomy	One genus including four species

VIRION

No true virions are associated with members of the family *Hypoviridae*. Pleomorphic vesicles 50–80 nm in diameter [1], devoid of any detectable viral structural proteins but containing replicative form dsRNA and polymerase activity [2], are the only virus-associated particles that can be isolated from infected fungal tissue (Table 1, Fig. 1).

GENOME

Hypovirus genomes range from 9.1 to 12.7 kb excluding a 3'-poly(A) tail of 20–30 nt, and possess one or two ORFs (Fig. 2) [3] flanked by relatively long 5'- and 3'-terminal non-

coding regions. Translational initiation for the first ORF on the genomic RNA is mediated by an internal ribosome entry site in the 5'-non-coding region extending to the coding domain in the case of *Cryphonectria hypovirus 1*. For hypoviruses with a two-ORF genome organization, the stop/restart translation mechanism is involved in the translation of downstream ORFs in which the pentamer, UAAUG (Fig. 2), plays a critical role [4]. Many hypoviruses have shorter-than-full-length, internally-deleted, defective interfering and defective replicative form dsRNA molecules; others have replicative forms of satellite-like RNAs [5, 6]. The host RNA silencing pathway has been reported to promote defective interfering

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Keywords: *Hypoviridae*; ICTV Report; Taxonomy.

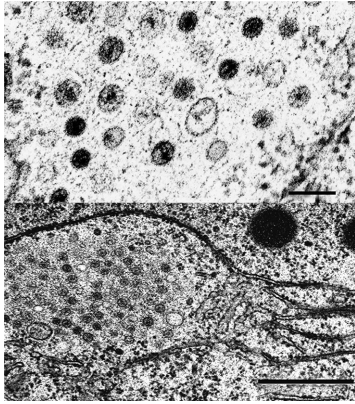


Fig. 1. Thin sections showing (top) vesicles in fungal tissue; (bottom) vesicle aggregate in fungal tissue surrounded by rough endoplasmic reticulum. Bar, 100 nm. Reproduced with permission from reference [1].

RNA production [7]. No function has been ascribed to any ancillary dsRNA.

REPLICATION

Positive- and negative-strand viral RNA synthesis is believed to occur cytoplasmically in host-derived lipid vesicles that contain linear dsRNA, regarded as the replicative form of hypoviral genomic positive-sense ssRNA. The polymerase associated with vesicles transcribes ssRNA molecules *in vitro* that correspond in size to full-length dsRNA. Approximately 80% of the polymerase products *in vitro* are of positive-sense. Except for the p50 of *Cryphonectria hypovirus 2*, hypovirus proteins are synthesized as part of a polyprotein that is autocatalytically cleaved by viral proteases such as p29 and p48 (*Cryphonectria hypovirus 1*) and p52 (*Cryphonectria hypovirus 2*). Smaller proteins encoded by the

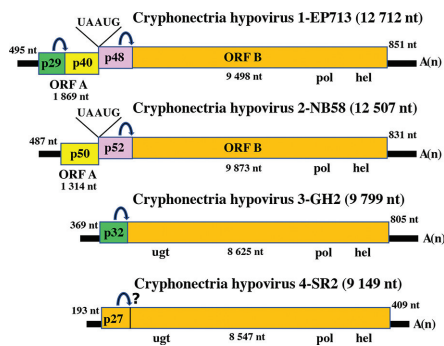


Fig. 2. Genome organization of four members of the family *Hypoviridae*. Arrows represent known or putative (*Cryphonectria hypovirus 4*) sites of autoproteolysis. The abbreviations pol, hel and ugt refer to the RNA-dependent RNA polymerase, RNA helicase and UDP-glucose/sterol glucosyltransferase domains, respectively.

3'-proximal ORF of *Cryphonectria hypovirus 1* have been identified in the vesicle-associated polymerase complex, suggesting extensive processing of the ORF B-encoded polyprotein *in vivo* by unknown viral or host proteases. *Cryphonectria hypovirus 1* p29 enhances virus replication *in cis* and *in trans* possibly by suppressing antiviral RNA silencing [7]. The p48 protein encoded by *Cryphonectria hypovirus 1* ORF B is required for initiation but not maintenance of viral RNA replication [8].

TAXONOMY

The genus *Hypovirus* includes four species: *Cryphonectria hypovirus 1*, *Cryphonectria hypovirus 2*, *Cryphonectria hypovirus 3* and *Cryphonectria hypovirus 4* [3]. Unclassified hypoviruses include *Sclerotinia sclerotiorum hypovirus 2* [9].

RESOURCES

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

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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