5-1-2018

ICTV Virus Taxonomy Profile: *Hypoviridae*

Nobuhiro Suzuki
Okayama University, Japan

Said A. Ghabrial
University of Kentucky, saghab00@uky.edu

Kook-Hyung Kim
Seoul National University, South Korea

Michael Pearson
The University of Auckland, New Zealand

Shin-Yi L. Marzano
South Dakota State University

See next page for additional authors

ICTV Virus Taxonomy Profile: *Hypoviridae*

Digital Object Identifier (DOI)
https://doi.org/10.1099/jgv.0.001055

Notes/Citation Information

Published in *Journal of General Virology*, v. 99, issue 5, p. 615-616.

Authors

Nobuhiro Suzuki, Said A. Ghabrial, Kook-Hyung Kim, Michael Pearson, Shin-Yi L. Marzano, Hajime Yaegashi, Jiatao Xie, Lihua Guo, Hideki Kondo, Igor Koloniuk, Bradley I. Hillman, and ICTV Report Consortium

JOURNAL OF GENERAL VIROLOGY

ICTV VIRUS TAXONOMY PROFILES

Suzuki *et al.*, *Journal of General Virology* 2018;99:615–616

DOI 10.1099/jgv.0.001055

MICROBIOLOGY SOCIETY

OPEN MICROBIOLOGY

ICTV Virus Taxonomy Profile: *Hypoviridae*

Nobuhiro Suzuki,[1,*] Said A. Ghabrial,[2] Kook-Hyung Kim,[3] Michael Pearson,[4] Shin-Yi L. Marzano,[5,6] Hajime Yaegashi,[7] Jiatao Xie,[8] Lihua Guo,[9] Hideki Kondo,[1] Igor Koloniuk,[10] Bradley I. Hillman[11] and ICTV Report Consortium

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:	**Cryphonectria hypovirus 1 strain EP713 (M57938), species *Cryphonectria hypovirus 1*, genus *Hypovirus***
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 membraneous 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

Received 13 March 2018; Accepted 16 March 2018

Author affiliations: [1]Institute of Plant Science and Resources, Okayama University, Kurashiki, Okayama 710-0046, Japan; [2]Plant Pathology Department, University of Kentucky, Lexington, KY 40504, USA; [3]Department of Agricultural Biotechnology and College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea; [4]School of Biological Sciences, The University of Auckland, Private Bag 92019, Auckland, New Zealand; [5]Department of Biology and Microbiology, South Dakota State University, Brookings, SD 57007, USA; [6]Department of Agronomy, Horticulture, and Plant Science, South Dakota State University, Brookings, SD 57007, USA; [7]Division of Apple Research, Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization (NARO), Morioka, Japan; [8]Plant Pathology Department, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan 430070, Hubei Province, PR China; [9]State Key Laboratory for Biology of Plant Disease and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, PR China; [10]Department of Plant Virology, Institute of Plant Molecular Biology, Biology Centre of the Czech Academy of Sciences, v.v.i., Branišovská 31, 370 05 České Budějovice, Czech Republic; [11]Department of Plant Biology and Pathology, Rutgers University, New Brunswick, NJ 08901, USA.
***Correspondence:** Nobuhiro Suzuki, nsuzuki@okayama-u.ac.jp

Keywords: *Hypoviridae*; ICTV Report; Taxonomy.

001055

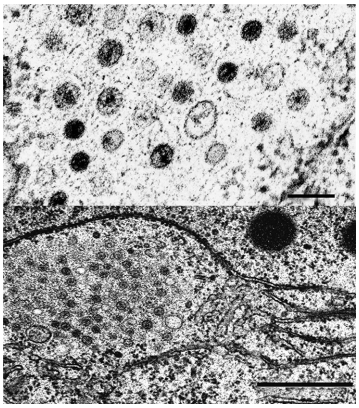

Fig. 1. Thin sections showing (top) vesicles in fungal tissue; (bottom) vesicle aggregate in fungal tissue surrounded by rough endoplasmic reticulum. Bar, 100 nm. Reproduced with permssion from reference [1].

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

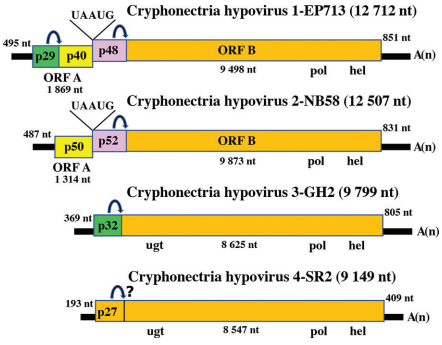

Fig. 2. Genome organization of four members of the family *Hypoviridae*. Arrows represent known or putative (Cryphonectria hypovirus 4) sites of autoproteolysis. The abbreviations pol, hel and ugt refer to the RNA-dependent RNA polymerase, RNA helicase and UDP-glucose/sterol glucosyltransferase domains,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

Funding information
Production of this summary, the online chapter and associated resources was funded by a grant from the Wellcome Trust (WT108418AIA).

Acknowledgements
Members of the ICTV Report Consortium are Elliot J. Lefkowitz, Andrew J. Davison, Stuart G. Siddell, Sead Sabanadzovic, Donald B. Smith, Richard J. Orton and Peter Simmonds.

Conflicts of interest
The authors declare that there are no conflicts of interest.

References

1. **Newhouse JR, Hoch HC, Macdonald WL.** The ultrastructure of *Endothia parasitica*. Comparison of a virulent with a hypovirulent isolate. *Can J Botany* 1983;61:389–399.
2. **Fahima T, Wu Y, Zhang L, van Alfen NK.** Identification of the putative RNA polymerase of Cryphonectria hypovirus in a solubilized replication complex. *J Virol* 1994;68:6116–6119.
3. **Hillman BI, Suzuki N.** Viruses of the chestnut blight fungus, *Cryphonectria parasitica*. *Adv Virus Res* 2004;63:423–472.
4. **Guo LH, Sun L, Chiba S, Araki H, Suzuki N.** Coupled termination/reinitiation for translation of the downstream open reading frame B of the prototypic hypovirus CHV1-EP713. *Nucleic Acids Res* 2009;37:3645–3659.
5. **Shapira R, Choi GH, Hillman BI, Nuss DL.** The contribution of defective RNAs to the complexity of viral-encoded double-stranded RNA populations present in hypovirulent strains of the chestnut blight fungus *Cryphonectria parasitica*. *EMBO J* 1991;10:741–746.
6. **Yuan W, Hillman BI.** *In vitro* translational analysis of genomic, defective, and satellite RNAs of Cryphonectria hypovirus 3-GH2. *Virology* 2001;281:117–123.
7. **Nuss DL.** Mycoviruses, RNA silencing, and viral RNA recombination. *Adv Virus Res* 2011;80:25–48.
8. **Jensen KS, Nuss DL.** Mutagenesis of the catalytic and cleavage site residues of the hypovirus papain-like proteases p29 and p48 reveals alternative processing and contributions to optimal viral RNA accumulation. *J Virol* 2014;88:11946–11954.
9. **Marzano SY, Hobbs HA, Nelson BD, Hartman GL, Eastburn DM *et al.*** Transfection of *Sclerotinia sclerotiorum* with *in vitro* transcripts of a naturally occurring interspecific recombinant of Sclerotinia sclerotiorum hypovirus 2 significantly reduces virulence of the fungus. *J Virol* 2015;89:5060–5071.