ICTV Virus Taxonomy Profile: Polycipiviridae

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Abstract

**Polycipiviridae** is a family of picorna-like viruses with non-segmented, linear, positive-sense RNA genomes of approximately 10–12 kb. Unusually for viruses within the order Picornavirales, their genomes are polycistronic, with four (or more) consecutive 5′-proximal open reading frames (ORFs) encoding structural (and possibly other) proteins and a long 3′ ORF encoding the replication polyprotein. Members of species within the family have all been detected in ants or via arthropod transcriptomic datasets. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the Polycipiviridae, which is available at [www.ictv.global/report/polycipiviridae](http://www.ictv.global/report/polycipiviridae).

Table 1. Characteristics of members of the family Polycipiviridae

| Typical member: Solenopsis invicta virus 2 (MF041813), species Solenopsis invicta virus 2, genus Sopolycivirus |
|-------------------------------------------------|
| Virion | Thought to be non-enveloped, 33 nm in diameter |
| Genome | 10–12 kb of positive-sense, non-segmented RNA |
| Replication | Not studied; presumed to be similar to other Picornavirales members |
| Translation | Directly from genomic RNA, presumed internal ribosome entry site elements in 5′-untranslated region and intergenic region |
| Host range | Arthropoda |
| Taxonomy | Member of the order Picornavirales. Includes the genera Chipolycivirus, Husopolycivirus and Sopolycivirus |

**VIRION**

Icosahedral particles approximately 33 nm in diameter have been observed by electron microscopy in samples prepared from ants infected with Solenopsis invicta virus 2, but not in samples prepared from non-infected ants [1] (Table 1) (Fig. 1). Genomes are picorna-like and appear to encode three jelly-roll fold capsid proteins; thus particles are assumed to be picorna-like, i.e. non-enveloped, with icosahedral pseudo-\(T=3\) symmetry, and comprising 60 copies of each of the ORF1, ORF3 and ORF4 products. However, this has not yet been experimentally confirmed.

**GENOME**

The positive-sense RNA genome is non-segmented and contains four main 5′-proximal ORFs (ORFs 1–4) and one long 3′ ORF (ORF5) (Fig. 2) [2]. ORF1, ORF3 and ORF4 encode proteins with homology to picornavirus jelly-roll fold capsid proteins. ORF2 encodes a product of unknown function. ORF5 encodes superfamily III helicase, chymotrypsin-like serine protease and superfamily I RNA-dependent RNA polymerase domains, and is presumed to encode a viral protein genome-linked (VPg) and potentially another protein between the helicase and protease, and one or two additional proteins upstream of the helicase. ORF5 is expected to be proteolytically cleaved by the viral protease, but the cleavage sites have not been mapped. The ORFs are flanked by 5′- and 3′-untranslated regions (UTRs) and a lengthy intergenic region between ORF4 and ORF5. The 5′-UTR and intergenic region are presumed to contain internal ribosome entry site elements to direct translation of ORF1 and ORF5, whereas ORFs 2–4 have been proposed to be expressed via a ribosome reinitiation mechanism. Similar to other members of the order Picornavirales [3], the genome has a 3′-poly(A) tail, and is presumed to have a small VPg attached at the 5′-end. Members of the genus Sopolycivirus contain an additional
high virus loads have been detected in larvae, pupae, workers and queens [4, 5]. In infected ants, 96% of Solenopsis invicta virus 2 genome equivalents localize to the midgut section of the alimentary canal, and the virus has been experimentally transmitted to non-infected ants via feeding, suggesting food-borne transmission, probably by trophallaxis [5]. Fire ant infections with Solenopsis invicta virus 2 are associated with negative impacts on queen ants, resulting in significant reductions in fecundity, longer claustral periods and slower growth of newly established colonies [6].

**TAXONOMY**

The family Polycipiviridae includes three genera: Sopolycivirus, Hupolycivirus and Chipolycivirus. Demarcation of genera is based on phylogenetic divergence. All current members were found in ants or via transcriptomic studies of arthropods. *Sopolycivirus* is currently the most species-rich genus, and nearly all members of this genus are associated with ants (family Formicidae).

**RESOURCES**

Full ICTV Report on the family Polycipiviridae: [www.ictv.global/report/polycipiviridae](http://www.ictv.global/report/polycipiviridae).

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**ORF (2b) overlapping the 5’-end of ORF2; ORF2b encodes a small protein with a predicted transmembrane domain. Members of at least one species (*Formica exsecta virus 3*) contain a further additional small ORF inserted between ORF2 and ORF3.**

**REPLICATION**

Replication has not been studied but is assumed to be similar to that of other members of the order Picornavirales.

**PATHOGENICITY**

Solenopsis invicta virus 2 appears to establish a chronic, asymptomatic infection in fire ants (*Solenopsis invicta*) and