



# ICTV Virus Taxonomy Profile: *Hadakaviridae* 2023

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## Abstract

The family *Hadakaviridae*, including the genus *Hadakavirus*, accommodates capsidless viruses with a 10- or 11-segmented positive-sense (+) RNA genome. Currently known hosts are ascomycetous filamentous fungi. Although phylogenetically related to polycovirids with a segmented double-stranded RNA genome and certain encapsidated picorna-like viruses, hadakavirids are distinct in their lack of a capsid ('hadaka' means naked in Japanese) and their consequent inability to be pelleted by conventional ultracentrifugation; they show ribonuclease susceptibility in host tissue homogenates. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Hadakaviridae*, which is available at [ictv.global/report/hadakaviridae](https://www.ictv.global/report/hadakaviridae).

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

Example:	hadaka virus 1 (LC519840–LC519850), species <i>Hadakavirus nanga</i> , genus <i>Hadakavirus</i>
Virion	No known virions (capsidless)
Genome	Multi-segmented (10 or 11) linear, positive-sense (+) RNAs comprising 14–15 kb in total; segments are 0.9–2.5 kb
Replication	Double-stranded replicative forms accumulate abundantly in infected fungal hosts. The cellular replication site remains unknown.
Translation	From non-polyadenylated monocistronic genomic RNAs
Host range	Fungi
Taxonomy	Realm <i>Riboviria</i> ; kingdom <i>Orthornavirae</i> , phylum <i>Pisuviricota</i> ; the family includes the genus <i>Hadakavirus</i> and the species <i>Hadakavirus nanga</i>

## VIRION

Hadakavirids (members of the family *Hadakaviridae*) have no true virion (Table 1). Accordingly, hadakavirids cannot be pelleted by ultracentrifugation [1] and the hadakavirid positive-sense (+) RNA genome and replicative form double-stranded (ds) RNA are accessible by and susceptible to exogenously added ribonuclease in host crude tissue homogenate under conditions in which encapsidated viral

RNA remains undigested [1, 2]. Mechanisms of hadakavirid genomic RNA protection in the host are yet to be elucidated.

## GENOME

Hadakavirids have a genome comprising 10- or 11 monocistronic (+) RNA segments (Fig. 1). The 5'-terminal three nucleotides (CGU) are conserved in all segments. The largest three genomic

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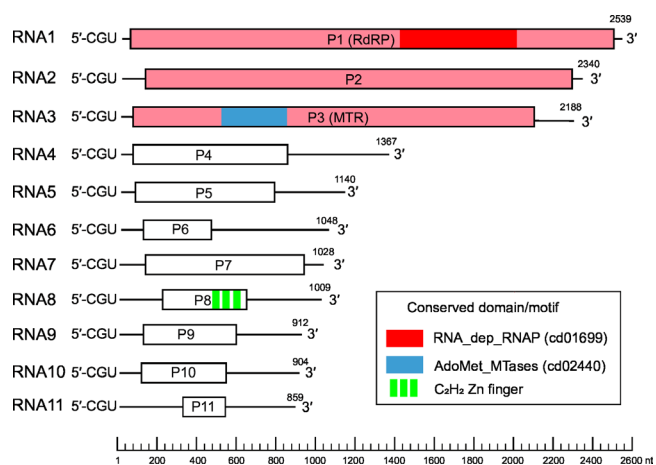
Abbreviations: (+), positive-sense; ds, double-stranded; RdRP, RNA-dependent RNA polymerase.

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**Fig. 1.** Genome organization of hadaka virus 1 isolate 7n (LC519840–50). Open reading frames are indicated by boxes. The three genes homologous between hadakavirids and polmycovirids are coloured pink: P1 (RdRP, RNA-dependent RNA polymerase), P2 (unknown function) and P3 (MTR, methyltransferase). Other coloured regions indicate conserved domains or motifs identified previously [1]

segments (RNA1–RNA3) encode proteins homologous to those of members of the family *Polmycoviridae*, namely an RNA-dependent RNA polymerase (RdRP), a hypothetical protein of unknown function and a methyltransferase [1, 3]. While the genome of hadaka virus 1 isolate 7n includes RNA8 that encodes a hypothetical protein containing a C<sub>2</sub>H<sub>2</sub>-type zinc finger motif [1], this genomic segment is missing in hadaka virus 1 isolate 1 NL [2]. The functions of virus proteins encoded by segments 2 and 4–11 are unknown.

## REPLICATION

The replication mechanism has not been investigated.

### References

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## PATHOGENICITY

No pathogenic effect on the host has been reported for isolates of hadaka virus 1 [1, 2]. However, a related, unclassified virus, *Colletotrichum fructicola* RNA virus 1, causes mild growth inhibition in a phytopathogenic fungus [4].

## TAXONOMY

Current taxonomy: [ictv.global/taxonomy](https://ictv.global/taxonomy). Hadakavirids are most closely related to members of the family *Polmycoviridae* [1, 3, 5]. In turn, the RdRPs of hadakavirids and polmycovirids show phylogenetic affinity to those of (+) RNA viruses in the phylum *Pisuviricota* (extended ‘picornavirus supergroup’), such as the members in the families *Astroviridae* and *Caliciviridae*. Capsidless hadakavirids are regarded as (+) RNA viruses, based largely on their phylogenetic affinity of their RdRP. This taxonomic placement of hadakavirids is reminiscent of that of other capsidless RNA viruses, e.g. members of the family *Hypoviridae* [6]. The catalytic core residues of hadaka/polmycov RdRPs are ‘GDNQ’, which is found in some negative-sense mononegaviruses, rather than ‘GDD’, characteristic of most (+) RNA and dsRNA viruses.

## RESOURCES

Full ICTV Report on the family *Hadakaviridae*: [ictv.global/report/hadakaviridae](https://ictv.global/report/hadakaviridae).

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### Conflicts of interest

The authors declare that there are no conflicts of interest.

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