



# ICTV Virus Taxonomy Profile: *Yadokariviridae* 2023

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## Abstract

The family *Yadokariviridae*, with the genera *Alphayadokarivirus* and *Betayadokarivirus*, includes capsidless non-segmented positive-sense (+) RNA viruses that hijack capsids from phylogenetically distant double-stranded RNA viruses. *Yadokarivirids* likely replicate inside the hijacked heterocapsids using their own RNA-directed RNA polymerase, mimicking dsRNA viruses despite their phylogenetic placement in a (+) RNA virus lineage. *Yadokarivirids* can have negative or positive impacts on their host fungi, through interactions with the capsid donor dsRNA viruses. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) report on the family *Yadokariviridae*, which is available at [ictv.global/report/yadokariviridae](https://www.ictv.global/report/yadokariviridae).

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

Example:	yado-kari virus 1 (LC006253), species <i>Alphayadokarivirus ichibani</i> , genus <i>Alphayadokarivirus</i>
Virion	<i>Trans</i> -encapsidated into non-enveloped spherical virions, 33–50 nm in diameter, encoded by phylogenetically distant dsRNA viruses
Genome	Non-segmented linear positive-sense (+) RNA of 3.6–6.3 kb
Replication	Assumed to replicate inside the heterocapsids encoded by an unrelated dsRNA virus
Translation	From a genomic RNA serving as a polyprotein-encoding monocistronic or bicistronic mRNA with or without a poly(A) tail
Host range	Fungi and possibly oomycetes
Taxonomy	Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Pisuviricota</i> , order <i>Yadokarivirales</i> ; multiple genera including >9 species.

## VIRION

*Yadokarivirids* (members of the family *Yadokariviridae*) encode no putative capsid protein (CP). Instead, *yadokarivirids* are *trans*-encapsidated by the CPs of phylogenetically distant dsRNA viruses (Table 1, Fig. 1) [1–4]. These spherical, non-enveloped heterocapsids encase the dsRNA replicative form and RNA-directed RNA polymerase (RdRP) of *yadokarivirids*. Capsid donor (partner) dsRNA viruses span at least five distinct families/genera within the order *Ghabrivirales*. Heterocapsids range from 33 to 50 nm, apparently identical to the virion size of their respective donor viruses.

Each member of a given *yadokarivirid* species only partners with a specific dsRNA virus [4].

## GENOME

*Yadokarivirids* have a non-segmented linear positive-sense (+) RNA genome with or without a poly(A) tract, most having a monocistronic genome that encodes a polyprotein containing a 2A-like self-cleaving peptide. The cleavage of the polyprotein produces mature RdRP and a relatively small protein, both

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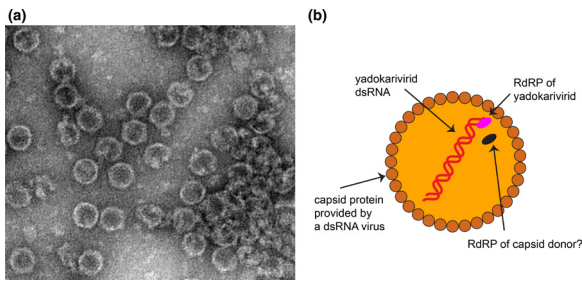
Abbreviations: (+), positive-sense; CP, capsid protein; dsRNA, double-stranded RNA; RdRP, RNA-directed RNA polymerase.

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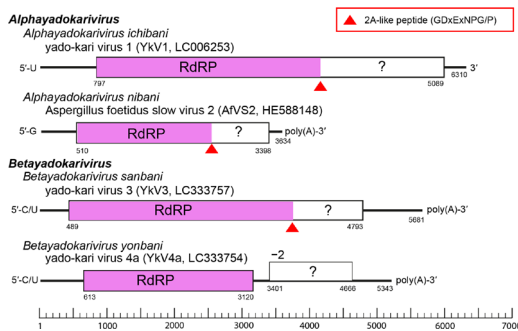
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**Fig. 1.** Virions of a yadokarivirid *trans*-encapsidated by a dsRNA virus. (a) Transmission electron micrograph of negatively-stained virions of yado-kari virus 1 and its capsid donor (yado-nushi virus 1), prepared as previously described [1]. (b) Schematic cross-section of a yadokarivirid virion. RdRP, RNA-directed RNA polymerase. Whether the RdRP of a capsid donor is co-packaged along with yadokarivirid RNA and RdRP remains unknown.



**Fig. 2.** Genome organization of four representative yadokarivirids.

essential for replication (Fig. 2) [1, 5]. Several betayadokariviruses appear to have a bicistronic genome and do not encode a 2A-like peptide (Fig. 2) [6]. Some betayadokariviruses also show heterogeneity at the 5'-terminal nucleotide of the genome (Fig. 2) [6].

## REPLICATION

Although yadokarivirids show phylogenetic affinity to (+) RNA viruses, they are hypothesized to replicate in the capsids hijacked

from dsRNA viruses, as if they were dsRNA viruses [7]. This hypothesis is based on three lines of evidence: *trans*-encapsidation of yadokarivirid replicative form dsRNA; the absolute necessity of the capsid donor dsRNA viruses for yadokarivirid replication and infection [1]; and encapsidation of yadokarivirid-encoded RdRP that is essential for replication [5]. The RdRP requirement for replication clearly distinguishes yadokarivirids from subviral RNAs such as RNA satellites or satellite viruses and deltaviruses (family *Kolmioviridae*) that do not encode their own RdRPs [8].

## PATHOGENICITY

Co-infection by the alphayadokarivirus yado-kari virus 1 and its unclassified capsid donor yado-nushi virus 1 causes a growth defect in the host phytopathogenic fungus *Rosellinia necatrix* but enhances the accumulation of the donor virus [1, 9]. In contrast, a betayadokarivirus, yado-kari virus 4a decreases the accumulation of its capsid donor dsRNA virus and rescues its host fungus *R. necatrix* from the growth defect caused by the partner dsRNA virus [4]. Another betayadokarivirus, yado-kari virus 3 has no effect on either its capsid donor or host fungus *R. necatrix* [4].

## TAXONOMY

Current taxonomy: [ictv.global/taxonomy](http://ictv.global/taxonomy). Phylogenetic analysis of RdRP amino acid sequences indicates that yadokarivirids are distantly related to members of (+) RNA virus families such as *Caliciviridae* (phylum *Pisuviricota*) [7], and so are placed in the order *Yadokarivirales*.

## RESOURCES

Full ICTV Report on the family *Yadokariviridae*: [ictv.global/report/yadokariviridae](http://ictv.global/report/yadokariviridae).

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### Conflicts of interest

The authors declare that there are no conflicts of interest.

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