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## ICTV Virus Taxonomy Profile: *Partitiviridae*

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## ICTV Virus Taxonomy Profile: *Partitiviridae*

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### Abstract

The *Partitiviridae* is a family of small, isometric, non-enveloped viruses with bisegmented double-stranded (ds) RNA genomes of 3–4.8 kbp. The two genome segments are individually encapsidated. The family has five genera, with characteristic hosts for members of each genus: either plants or fungi for genera *Alphapartitivirus* and *Betapartitivirus*, fungi for genus *Gammapartitivirus*, plants for genus *Deltapartitivirus* and protozoa for genus *Cryspovirus*. Partitiviruses are transmitted intracellularly via seeds (plants), oocysts (protozoa) or hyphal anastomosis, cell division and sporogenesis (fungi); there are no known natural vectors. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of the *Partitiviridae*, which is available at [www.ictv.global/report/partitiviridae](http://www.ictv.global/report/partitiviridae).

**Table 1.** Characteristics of the family *Partitiviridae*

<b>Typical member:</b>	<b><i>Atkinsonella hypoxylon virus</i>, 2H (RNA1, L39125; RNA2, L39126), species <i>Atkinsonella hypoxylon virus</i>, genus <i>Betapartitivirus</i></b>
Genome	3–4.8 kbp of linear bisegmented dsRNA
Virion	Isometric, non-enveloped, 25–43 nm in diameter; dsRNA1 and dsRNA2 are separately encapsidated
Replication	Cytoplasmic. Genomic RNA acts as a template for mRNA synthesis within the virus particle; transcription occurs by a semiconservative mechanism
Translation	From monocistronic positive-sense transcripts of both genomic dsRNAs
Host range	Plants, fungi and protozoa
Taxonomy	Five genera, including >40 species, and 15 species unassigned to a genus

### VIRION

Virus particles are isometric, non-enveloped, and 25–43 nm in diameter (Table 1, Fig. 1a, b). Each capsid is composed of 120 copies of a single protein arranged as 60 dimers with  $T=1$  icosahedral symmetry [1]. Dimeric surface protrusions are frequently observed on viral capsids. One or two molecules of RNA-dependent RNA polymerase (RdRP) are packaged inside each particle [2].

### REPLICATION

Each dsRNA is monocistronic. The RdRP is believed to function as both a transcriptase and a replicase and catalyzes *in vitro* end-to-end transcription of each dsRNA to produce mRNA by a semi-conservative mechanism. Virions accumulate in the cytoplasm.

### GENOME

Members of all five genera possess two essential genome segments, dsRNA1 and dsRNA2, each containing one large ORF on the positive-strand RNA molecule (Fig. 2). The smaller of the two dsRNA genome segments usually encodes the coat protein (CP) and the larger usually encodes the virion-associated RNA polymerase. The linear dsRNA segments are separately encapsidated. Additional dsRNA segments (satellite or defective) may also be present.

### TAXONOMY

#### *Alphapartitivirus*

Members of the genus *Alphapartitivirus* infect either plants, or ascomycetous or basidiomycetous fungi. The two

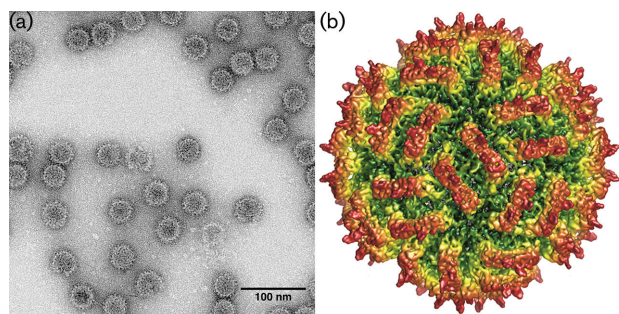
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**Keywords:** *Partitiviridae*; ICTV; taxonomy; *Alphapartitivirus*; *Betapartitivirus*; *Deltapartitivirus*; *Gammapartitivirus*; *Cryspovirus*.

**Abbreviations:** CP, coat protein; RdRP, RNA-dependent RNA polymerase.



**Fig. 1.** (a) Transmission electron micrograph of negatively-stained purified particles of *Penicillium stoloniferum* virus S, a representative member of the genus *Gammapartitivirus*. (b) Cryo-EM reconstructions of *Penicillium stoloniferum* virus S at 0.45 nm resolution, and rendered with radial colour mapping.

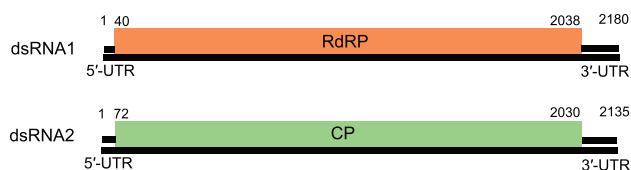
essential dsRNA genome segments are individually about 1.9–2.0 kbp (dsRNA1) and 1.7–1.9 kbp (dsRNA2), typically containing a poly(A) tract near the plus-strand 3′-terminus. There is a single major CP with predicted *Mr* of 51–57 kDa. Plant alphapartitiviruses cause persistent infections, whereas some fungal alphapartitiviruses cause host effects, such as hypovirulence or a reduced growth rate [3, 4].

### **Betapartitivirus**

Members of the genus *Betapartitivirus* infect either plants, or ascomycetous or basidiomycetous fungi. The two essential dsRNA genome segments are about 2.2–2.4 kbp (dsRNA1) and 2.1–2.4 kbp (dsRNA2), typically containing a poly(A) tract near the plus-strand 3′-terminus. There is a single major CP with predicted *Mr* of 71–77 kDa. Plant betapartitiviruses cause persistent infections [5, 6]. Some fungal betapartitiviruses cause reduced host virulence and changes in colony morphology [7].

### **Gammapartitivirus**

All known members of the genus *Gammapartitivirus* infect ascomycetous fungi. The two essential dsRNA segments are about 1.6–1.8 kbp (dsRNA1) and 1.4–1.6 kbp (dsRNA2). There is a single major CP with predicted *Mr* of 44–47 kDa. Most gammapartitiviruses seem to induce latent infections. *Aspergillus fumigatus* partitivirus 1, a related, unclassified virus, has been associated with host effects.



**Fig. 2.** *Atkinsonella hypoxylon* virus [10], an isolate of the type species of the genus *Betapartitivirus*, has a bipartite genome consisting of dsRNA1 and dsRNA2.

### **Deltapartitivirus**

All known members of the genus *Deltapartitivirus* induce persistent infections in plants [8]. They are transmitted by ovule and pollen to the seed embryo. The two essential dsRNA segments are individually 1.6–1.7 kbp (dsRNA1) and 1.4–1.6 kbp (dsRNA2). There is a single major CP with predicted *Mr* of 38–49 kDa.

### **Cryspovirus**

Members of the genus *Cryspovirus* infect apicomplexan protozoa of the genus *Cryptosporidium* [9]. The viral genome comprises two dsRNA segments, which are individually 1.5 and 1.8 kbp. There is a single major CP with predicted *Mr* of 37 kDa. Virions are disseminated within *Cryptosporidium* oocysts. Infections of the *Cryptosporidium* host cells appear to be latent.

## **RESOURCES**

Full ICTV Online (10th) Report:  
[www.ictv.global/report/partitiviridae](http://www.ictv.global/report/partitiviridae).

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### **Conflicts of interest**

The authors declare that there are no conflicts of interest.

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