ICTV Virus Taxonomy Profile: Polymycoviridae 2022

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Abstract
Members of the family Polymycoviridae are small viruses with multi-segmented and non-conventionally encapsidated double-stranded (ds) RNA genomes. Typically, polymycoviruses have four genomic segments, although some have up to eight. The genus Polymycovirus includes several species whose members infect fungi (ascomycetes and basidiomycetes), and oomycetes, altering host morphology, sporulation, growth and virulence. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family Polymycoviridae, which is available at ictv.global/report/polymycoviridae.

Table 1. Characteristics of members of the family Polymycoviridae

<table>
<thead>
<tr>
<th>Example</th>
<th>Aspergillus fumigatus tetramycovirus 1 (dsRNA 1: HG975302; dsRNA 2: HG975303; dsRNA 3: HG975304; dsRNA 4: HG975303), species Aspergillus fumigatus polymycovirus 1, genus Polymycovirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Non-conventionally encapsidated dsRNA, coated with viral protein</td>
</tr>
<tr>
<td>Genome</td>
<td>A total of 7.5–12.5 kbp of dsRNA in a multipartite genome (usually four segments, up to eight)</td>
</tr>
<tr>
<td>Replication</td>
<td>Both dsRNA and ssRNA can be isolated from infected fungal hosts. Virions accumulate in the cytoplasm</td>
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<tr>
<td>Translation</td>
<td>From positive-sense transcripts of genomic dsRNAs</td>
</tr>
<tr>
<td>Host range</td>
<td>Fungi (ascomycetes and basidiomycetes), oomycetes</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Realm Riboviria, the genus Polymycovirus includes &gt;9 species</td>
</tr>
</tbody>
</table>

VIRION
Most polymycoviruses form non-conventional virions, whereby genomic dsRNA is coated by a viral protein (Table 1) [1–3]. Only Colletotrichum camelliae filamentous virus 1 is believed to have a filamentous capsid [4], 10–20 nm in width and >1000 nm in length (Fig. 1).

GENOME
Polymycovirus genomes range from 7.5–12.5 kbp and comprise four to eight dsRNA segments. Each segment contains a single open reading frame (ORF) flanked by long non-coding regions (NCRs) with conserved termini (Fig. 2).

The ORF of dsRNA 1 encodes an RNA-directed RNA polymerase (RdRP) belonging to the protein family RdRP_1 (Pfam PF00680) and has three conserved motifs. The ORF of dsRNA 2 encodes a protein of unknown function containing a conserved N-terminus and a cysteine-rich, zinc finger-like motif. The ORF of dsRNA 3 encodes a methyl transferase, responsible for adding a capping structure to the 5'-termini of the positive-sense strands of viral dsRNAs [1, 2]. The ORF of dsRNA 4 encodes a proline–alanine–serine-rich protein (PASrp). When present, dsRNAs 5–8 encode proteins of unknown function that are non-homologous between different viruses.

REPLICATION
Polymycoviruses were the first dsRNA viruses found to be infectious not only as purified entities but also as naked dsRNA [1, 3, 4]. Replication has not been characterized in detail. Virions accumulate in the cytoplasm.
Fig. 1. Polymycovirus virions. (a) Atomic force microscopy of purified Aspergillus fumigatus tetramycovirus 1 non-conventional virions; white arrows indicate the viral protein coating the dsRNA genome. (Adapted from Ref. [1]). (b) Transmission electron microscopy of purified Colletotrichum camelliae filamentous virus 1 conventional virions. (Adapted from Ref. [4] under CC BY 4.0).

PATHOGENICITY
Polymycovirus infection has been associated with various host alterations, including changes in pigmentation [1, 2, 4, 5], sectoring [1, 2], decreased host growth [4] and host virulence [4], as well as increased sporulation [5], host growth [2, 5] and host virulence [2]. Infection has also been reported to increase sensitivity to antifungals [3] and to the bacterium Pseudomonas aeruginosa [6]. Although the molecular mechanisms underpinning the above phenotypes have not been elucidated, there is evidence that polymycoviruses modulate host carbon, nitrogen and iron metabolism [5, 7]. Finally, polymycoviruses are targeted by the host RNA silencing machinery [8].

TAXONOMY
Current taxonomy: ictv.global/taxonomy. Viruses in the family Polymycoviridae are most closely related to Hadaka virus 1 isolates, positive-sense (+) single-stranded (ss) RNA viruses in the family Hadakaviridae. Polymycovirus-encoded RdRRPs are also related to those of (+)ssRNA viruses in the families Astroviridae, Caliciviridae and Picornaviridae, and of dsRNA viruses in the family Partitiviridae in the phylum Pisciiviricota. The GDNQ motif, typically found in the RdRP of negative-sense ssRNA viruses of the order Mononegavirales, is conserved in all members of the family Polymycoviridae, instead of the GDD motif found in most dsRNA and (+) ssRNA viruses. Polymycoviruses appear to be intermediate between dsRNA and (+)ssRNA viruses, as well as between encapsidated and capsidless RNA viruses [1].

RESOURCES

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