ICTV Virus Taxonomy Profile: *Polyomaviridae*

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**Abstract**

The *Polyomaviridae* is a family of small, non-enveloped viruses with circular dsDNA genomes of approximately 5 kbp. The family includes four genera whose members have restricted host range, infecting mammals and birds. Polyomavirus genomes have also been detected recently in fish. Merkel cell polyomavirus and raccoon polyomavirus are associated with cancer in their host; other members are human and veterinary pathogens. Clinical manifestations are obvious in immunocompromised patients but not in healthy individuals. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of the *Polyomaviridae*, which is available at [www.ictv.global/report/polyomaviridae](http://www.ictv.global/report/polyomaviridae).

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

<table>
<thead>
<tr>
<th>Typical member</th>
<th>simian virus 40 strain 776 (SV40-776) (J02400), species <em>Macaca mulatta</em> polyomavirus 1, genus Betapolyomavirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Non-enveloped, 40–45 nm, icosahedral</td>
</tr>
<tr>
<td>Genome</td>
<td>Approximately 5 kbp circular dsDNA</td>
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<tr>
<td>Replication</td>
<td>Bidirectional from a unique origin of DNA replication</td>
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<td>Translation</td>
<td>Early and late transcripts, alternative splicing, alternative ORFs</td>
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<td>Host range</td>
<td>Mammals, birds and fish</td>
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<td>Taxonomy</td>
<td>Four genera including more than 70 species</td>
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</table>

**VIRION**

Virions are typically 40–45 nm in diameter and lack an envelope. The icosahedral capsid is constituted of 72 capsomers, each composed of five molecules of the major capsid protein VP1 (Table 1, Fig. 1). Minor capsid proteins are located at the internal face of the capsid [1].

**GENOME**

The circular, dsDNA genome of approximately 5 kbp is packed with cellular histones and divided into three functional domains: the early region encoding regulatory proteins, the late region encoding capsid proteins, and the non-coding control region, which contains the origin of DNA replication and the promoter/enhancer elements directing transcription of the viral genes ([1], Fig. 2).

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**Abbreviation:** LTAg, large T-antigen.
polyomavirus are so far the only members known to cause cancer in their natural host [3].

**Betapolyomavirus**
This genus includes >20 species. Members infect mammals. The well-studied human polyomaviruses BK and JC are associated with nephropathy and progressive multifocal leukencephalopathy, respectively [3].

**Gammapolyomavirus**
This genus includes <10 species. Members infect birds. Some cause severe illness and even death, but oncogenicity has not been observed [3].

**Deltapolyomavirus**
This genus includes the species *Human polyomavirus 6* and *Human polyomavirus 7*, members of which exhibit skin tropism, and *Human polyomavirus 10* and *Human polyomavirus 11*, members of which (MW polyomavirus and STL polyomavirus, respectively), are commonly detected in the gastrointestinal tract [3].

The general mode of polyomavirus diversification is co-speciation with their hosts. Recombination has shaped polyomavirus genomes and resulted in conflicting phylogenetic signals from the early and late genomic regions [4]. A distant evolutionary relationship of polyomaviruses to ssDNA viruses has been suggested on the basis of structural similarity in replicative proteins [5].

**RESOURCES**

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The authors declare that there are no conflicts of interest.

**References**