ICTV Virus Taxonomy Profile: *Circoviridae*

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**Abstract**

The family *Circoviridae* comprises viruses with small, circular, single-stranded DNA (ssDNA) genomes, including the smallest known animal viruses. Members of this family are classified into two genera, *Circovirus* and *Cyclovirus*, which are distinguished by the position of the origin of replication relative to the coding regions and the length of the intergenic regions. Within each genus, the species demarcation threshold is 80 % genome-wide nucleotide sequence identity. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of the *Circoviridae*, which is available at www.ictv.global/report/circoviridae.

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

<table>
<thead>
<tr>
<th>Typical member:</th>
<th>porcine circovirus 1 (AF071879), species Porcine circovirus 1, genus Circovirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Non-enveloped, icosahedral (T=1) symmetry, 15–25 nm diameter</td>
</tr>
<tr>
<td>Genome</td>
<td>Monopartite, circular, single-stranded DNA of 1.7–2.1 kb</td>
</tr>
<tr>
<td>Replication</td>
<td>Rolling circle replication</td>
</tr>
<tr>
<td>Translation</td>
<td>From at least two mRNAs encoding the replication-associated and capsid proteins</td>
</tr>
<tr>
<td>Host Range</td>
<td>Circovirus: mammals, birds and fish; Cyclovirus: unconfirmed for most species</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>More than 70 species in the genera <em>Circovirus</em> and <em>Cyclovirus</em></td>
</tr>
</tbody>
</table>

**VIRION**

Virions, which have only been visualized for a few members of the genus *Circovirus*, are non-enveloped and have an icosahedral \(T=1\) symmetry with a diameter of 15–25 nm [1–3] (Table 1, Fig. 1). Members of the genus *Cyclovirus* have only been described through sequence-based analyses and no structural data are available.

**GENOME**

Both genera include viruses with small, covalently closed, circular ssDNA genomes. Their genomes range in size from 1.7 to 2.1 kb and contain two major (>600 nt) open reading frames (ORFs), which encode the replication-associated (Rep) and capsid (Cp) proteins. Members of the genera *Circovirus* and *Cyclovirus* are distinguished by the location of the origin of replication (ori) relative to the coding regions, and the length of the intergenic regions (Fig. 2) [4].

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**Abbreviations:** ORF, open reading frame; Rep, replication associated protein; Cp, capsid protein; ori, origin of replication; RCR, rolling circle replication.

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Members of the genus *Circovirus* have the *ori* on the same strand as the *rep* ORF, whereas members of the genus *Cyclovirus* have the putative *ori* on the same strand as the *cp* ORF [5]. Circovirus genomes are characterized by two intergenic regions between the major ORFs; however, the intergenic region between the 3' ends of the major ORFs in cyclovirus genomes is either absent or consistently smaller [6]. In addition, introns have been identified within the ORFs of several cyclovirus genomes, while none have been observed for members of the genus *Circovirus*.

**REPLICATION**

The *ori* is characterized by a conserved nonanucleotide motif ([T/n]A(G/t)TATTAC) (Fig. 2) at the apex of a stem–loop structure located between the 5' ends of Rep- and Cp-encoding ORFs [4, 7]. In characterized members of the genus *Circovirus*, the Rep protein is thought to initiate replication through the rolling circle replication (RCR) mechanism by nicking the virion-sense strand between positions 7 and 8 of the nonanucleotide motif [8]. RCR involves the production of a dsDNA replicative form by host DNA polymerases and the generation of viral ssDNA from the replicative form template. Both circovirus and cyclovirus Rep proteins contain conserved domains that are important for RCR. Putative Rep-binding domains characterized by iterative sequences near the *ori* have been identified for members of both genera [9, 10].

**TAXONOMY**

The family *Circoviridae* includes two genera, *Circovirus* and *Cyclovirus* [4]. Members of the genus *Circovirus* have only been identified in vertebrates, whereas members of the genus *Cyclovirus* have been identified in both vertebrates and invertebrates [5]. The type species for the genus *Cyclovirus* is *Porcine circovirus 1* and the type species for the genus *Cyclovirus* is *Human-associated cyclovirus 8*. The species demarcation threshold for viruses of the family *Circoviridae* is 80% genome-wide nucleotide sequence identity.

**RESOURCES**


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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


