2017

ICTV Virus Taxonomy Profile: Circoviridae

Mya Breitbart
University of South Florida, mya@usf.edu

Eric Delwart
Blood Systems Research Institute

Karyna Rosario
University of South Florida

Joaquim Segales
UAB, Centre de Recerca en Sanitat Animal

Arvind Varsani
Arizona State University

Follow this and additional works at: https://scholarcommons.usf.edu/msc_facpub
Part of the Life Sciences Commons

Scholar Commons Citation
Breitbart, Mya; Delwart, Eric; Rosario, Karyna; Segales, Joaquim; and Varsani, Arvind, "ICTV Virus Taxonomy Profile: Circoviridae" (2017). Marine Science Faculty Publications. 682.
https://scholarcommons.usf.edu/msc_facpub/682

This Article is brought to you for free and open access by the College of Marine Science at Scholar Commons. It has been accepted for inclusion in Marine Science Faculty Publications by an authorized administrator of Scholar Commons. For more information, please contact scholarcommons@usf.edu.
ICTV Virus Taxonomy Profile: *Circoviridae*

Mya Breitbart, 1,* Eric Delwart, 2 Karyna Rosario, 1 Joaquim Segalés, 3, 4 Arvind Varsani 5 and ICTV Report Consortium

**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](http://www.ictv.global/report/circoviridae).

<table>
<thead>
<tr>
<th>Table 1. Characteristics of the family <em>Circoviridae</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member:</td>
</tr>
<tr>
<td>Virion</td>
</tr>
<tr>
<td>Genome</td>
</tr>
<tr>
<td>Replication</td>
</tr>
<tr>
<td>Translation</td>
</tr>
<tr>
<td>Host Range</td>
</tr>
<tr>
<td>Taxonomy</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].

Fig. 1. (a) 3D reconstruction of porcine circovirus 2 using cryo-electron microscopy. A structural model comprising 60 subunits ($T=1$) arranged in 12 pentameric morphological units has been proposed [1]. (b) Negative-stained transmission electron micrograph of porcine circovirus 2 (provided by Carolina Rodriguez-Cariño and Joaquim Segalés, CRESA, Spain). Scale bar=20 nm.

Received 21 June 2017; Accepted 22 June 2017

**Author affiliations:** 1 College of Marine Science, University of South Florida, 140 7th Avenue South, Saint Petersburg, FL 33701, USA; 2 Blood Systems Research Institute, San Francisco, CA 94118, USA; 3 UAB, Centre de Recerca en Sanitat Animal (CRESA, IRTA-UAB), Campus de la Universitat Autònoma de Barcelona, Facultat de Veterinària, UAB, 08193 Bellaterra, Spain; 4 Departament de Sanitat i Anatomia Animals, Facultat de Veterinària, UAB, 08193 Bellaterra, Spain; 5 The Biodesign Center for Fundamental and Applied Microbiomics, Center for Evolution and Medicine, and School of Life Sciences, Arizona State University, Tempe, AZ 85287-5001, USA.

*Correspondence:* Mya Breitbart, mya@usf.edu

**Keywords:** *Circoviridae*; *Circovirus*; *Cyclovirus*; ICTV report; taxonomy.

**Abbreviations:** ORF, open reading frame; Rep, replication associated protein; Cp, capsid protein; ori, origin of replication; RCR, rolling circle replication.
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 *Circovirus* is *Porcine circovirus 1* and the type species for the genus *Cyclovirus* is *Human-associated cylovirus 8*. The species demarcation threshold for viruses of the family *Circoviridae* is 80% genome-wide nucleotide sequence identity.

**RESOURCES**


**Funding information**

M. B. and K. R. are supported by grant DEB-1239976 from the Assembling the Tree of Life Program of the US National Science Foundation. Production of this summary, the online chapter and associated resources was funded by a grant from the Wellcome Trust (WT108418AIA).

**Acknowledgements**

The members of the ICTV Report Consortium are Elliot J. Lefkowitz, Andrew J. Davison, Stuart G. Siddell, Peter Simmonds, Michael J. Adams, Donald B. Smith, Richard J. Orton and Balázs Harrach.

**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**