**Summary**

*Corticoviridae* is a family of icosahedral, internal membrane-containing virulent viruses with highly supercoiled, double-stranded circular DNA genomes of approximately 10 kb (Table 1). Only one species, *Pseudoalteromonas virus PM2*, has been recognized. *Pseudoalteromonas* phage PM2 infects gram-negative *Pseudoalteromonas* bacteria and was isolated from seawater in 1968 ([Espejo and Canelo 1968](#), [Kivelä et al., 1999](#)). Currently, PM2 does not share significant sequence similarity to any other virus. It is the first bacterial virus in which the presence of lipids in the virion has been demonstrated. Viral lipids are acquired selectively during virion assembly from the host cytoplasmic membrane. The outer protein capsid is an icosahedron with a pseudo $T=21$ symmetry and an internal protein-rich membrane enclosing the genome ([Abrescia et al., 2008](#)).

**Table 1.** *Corticoviridae*. Characteristics of members of the family *Corticoviridae*.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td><em>Pseudoalteromonas</em> phage PM2 (AF155037), species <em>Pseudoalteromonas virus PM2</em>, genus <em>Corticovirus</em></td>
</tr>
<tr>
<td>Virion</td>
<td>Icosahedral, internal membrane-containing virions of about 57 nm with a single capsid protein P2, single spike protein P1 and 8 membrane-associated proteins P3-P10</td>
</tr>
<tr>
<td>Genome</td>
<td>10.1 kb of highly supercoiled, circular, double-stranded DNA</td>
</tr>
<tr>
<td>Replication</td>
<td>Rolling circle replication initiated by virus-encoded protein P12</td>
</tr>
<tr>
<td>Translation</td>
<td>Prokaryotic translation using viral mRNA and host ribosomes</td>
</tr>
<tr>
<td>Host Range</td>
<td>Bacteria, gram-negative <em>Pseudoalteromonas</em> strains</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>One genus containing one species</td>
</tr>
</tbody>
</table>

**Virion**

**Morphology**

Icosahedral virions consist of an internal membrane and an outer protein capsid that has a diameter of 57 nm between facets (Figure 1). The genome is enclosed by the membrane. The capsid consists of 200 major capsid protein P2 trimers that are organized on a pseudo $T=21$ lattice ([Abrescia et al., 2008](#)). Protein P2 is composed of two beta-barrels disposed normal to the capsid surface. The P2 trimers have pseudo-six-fold symmetry and the structure is stabilized by calcium ions. Spikes protrude about 8 nm from the capsid surface at the five-fold vertices. The spikes are homopentamers and formed of protein P1. P1 is composed of three beta-barrel domains arranged end to end. The distal C-terminal domains of P1 are used for receptor recognition. The N-termini of P1 form pentagonal assemblies at the vertices. The inner membrane (47 nm in diameter) contains host plasma membrane-derived phospholipids and...
virus-encoded proteins P3 to P10 (Kivelä et al., 2002). Transmembrane proteins P3 and P6 are organized into a lattice on the membrane vesicle surface, on which the outer protein capsid is assembled (Abrescia et al., 2008).

**Physicochemical and physical properties**

The mass of the virion is about 4.5×10⁷ Da and is distributed among protein (72%), lipid (14%) and nucleic acid (14%) (Camerini-Otero and Franklin 1975, Camerini-Otero et al., 1974). The buoyant density in CsCl is 1.28 g cm⁻³ and in sucrose 1.26 g cm⁻³, and the S₂₀,₀ is 293 S (Kivelä et al., 1999, Camerini-Otero and Franklin 1975). Virions are stable at pH 6–8, and are very sensitive to ether, chloroform and detergents (Espejo and Canelo 1968). The virion stability is strongly dependent on sodium and calcium ions (Kivelä et al., 2002). Virions are sensitive to freezing.

**Nucleic acid**

The genome is a highly supercoiled, circular double-stranded DNA of 10,079 bp (6.6×10⁶ Da). DNA comprises approximately 14% of the virion weight and the G+C content is 42.2%. The Pseudoalteromonas phage PM2 genome has been sequenced (Männistö et al., 1999) (AF155037).

**Proteins**

The genome has 21 putative genes, 10 of which have been shown to code for structural proteins (P1-P10), 7 of which encode non-structural proteins (P12-P18) and four of which are of unknown function. Proteins form about 72% of the virus particle weight.

**Table 2. Corticoviridae.** Pseudoalteromonas phage PM2 proteins.

<table>
<thead>
<tr>
<th>Protein²</th>
<th>Mass (kDa)</th>
<th>Location/function²</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1</td>
<td>37.5</td>
<td>Spike protein, receptor binding (S)</td>
</tr>
<tr>
<td>P2</td>
<td>30.2</td>
<td>Major capsid protein (S)</td>
</tr>
<tr>
<td>P3</td>
<td>10.8</td>
<td>Major membrane protein (S)</td>
</tr>
<tr>
<td>P4</td>
<td>4.4</td>
<td>Membrane (S)</td>
</tr>
<tr>
<td>P5</td>
<td>17.9</td>
<td>Membrane (S)</td>
</tr>
<tr>
<td>P6</td>
<td>14.3</td>
<td>Major membrane protein (S)</td>
</tr>
<tr>
<td>P7</td>
<td>3.6</td>
<td>Membrane (S)</td>
</tr>
<tr>
<td>P8</td>
<td>7.3</td>
<td>Membrane (S)</td>
</tr>
<tr>
<td>P9</td>
<td>24.7</td>
<td>Putative packaging ATPase (S)</td>
</tr>
<tr>
<td>P10</td>
<td>29.0</td>
<td>Membrane (S)</td>
</tr>
<tr>
<td>P11</td>
<td>73.4</td>
<td>Replication initiation protein (N)</td>
</tr>
<tr>
<td>P12</td>
<td>7.2</td>
<td>Transcription factor (N)</td>
</tr>
<tr>
<td>P13</td>
<td>11.0</td>
<td>Transcription factor (N)</td>
</tr>
<tr>
<td>P14</td>
<td>18.1</td>
<td>Regulative function (N)</td>
</tr>
<tr>
<td>P15</td>
<td>10.3</td>
<td>Regulative function (N)</td>
</tr>
<tr>
<td>P16</td>
<td>6.0</td>
<td>Lysis factor (N)</td>
</tr>
<tr>
<td>P17</td>
<td>5.7</td>
<td>Lysis factor (N)</td>
</tr>
</tbody>
</table>

² P is for protein; Arabic numeral corresponds to the Roman numeral of the gene.

² S is for structural protein; N is for non-structural protein.

**Lipids**
Particles are about 14% lipid by weight (Camerini-Otero and Franklin 1975). The membrane contains 34% phosphatidyl ethanolamine and 66% phosphatidyl glycerol and trace amounts of phosphatidic acid and acyl-phosphatidyl glycerol (Braunstein and Franklin 1971, Camerini-Otero and Franklin 1972, Tsukagoshi et al., 1976). The lipids are derived from the host plasma membrane, but their composition deviates from that of the host bacterium. Lipids form an internal membrane with virus-specific membrane-associated proteins.

Genome organization and replication

To infect and replicate, Pseudoalteromonas phage PM2 delivers its genome across the cell envelope of two known marine host strains: gram-negative *Pseudoalteromonas* species ER72M2 and BAL-31. Virions adsorb via the distal tips of the spike proteins to uncharacterized receptors (Abrescia et al., 2008). The internal membrane mediates the translocation of the supercoiled genome across the host cell envelopes, most probably via fusion in a process that is not fully understood. Replication of the viral genome, most probably by a rolling circle mechanism, takes place in proximity to the host cytoplasmic membrane. The largest virus protein, P12, encoded by gene XII, shares significant sequence similarity with the superfamily I group of replication initiation proteins (Männistö et al., 1999). The genome is organized in three operons (Figure 2. *Corticoviridae*). Operons OEL and OER encode early gene products: the replication initiation protein P12 and transcription regulatory proteins P13, P14, P15 and P16. Expression of the genes for structural proteins is under the control of the late promoter (OL), which is activated by the virus-encoded transcription factors P13 and P14 (Mannistö et al., 2003). The mature virions are released from the cell by lysis. Lysis factor P17 permeabilizes the cytoplasmic membrane and acts like a holin, whereas lysis factor P18 disrupt the outer membrane, and peptidoglycan is most probably disrupted by host lytic factors (Krupovic et al., 2007).

![Diagram of genome organization of Pseudoalteromonas phage PM2](https://www.ictv.global/report/corticoviridae)
Biology

Pseudoalteromonas phage PM2 is virulent and replicates in two known strains of marine host bacteria of the genus *Pseudoalteromonas*. Although the virus is virulent and the sole member of the family *Corticoviridae*, comparative genomic approaches have shown that integrated corticoviral genetic elements commonly reside within aquatic bacterial chromosomes (*Krupovic and Bamford 2007*).

Derivation of names

*Cortico:* from Latin *cortex*, “crust”, “bark”.

Relationships with other taxa

The virion of corticoviruses resembles that of other tailless icosahedral viruses with an internal membrane, such as viruses in the family *Tectiviridae*, which have a lipid bilayer underneath the isometric protein capsid. Corticoviruses and tectiviruses appear to differ in genome organization and infection mechanism, since no tectivirus-specific, tail-like membrane tube is seen upon corticovirus infection. *Pseudoalteromonas* phage PM2 major capsid protein is a trimeric protein with two beta-barrels forming hexagonal capsomers (*Abrescia et al., 2008*). The same viral jelly-roll fold has also been described at least for Salmonella virus PRD1 (family *Tectiviridae*) (*Benson et al., 1999*), the archaeal Sulfolobus turreted icosahedral virus 1 (STIV; family *Turriviridae*) (*Maaty et al., 2006*), human adenoviruses (family *Adenoviridae*, *Rux et al., 2003*), and large eukaryotic viruses Paramecium bursaria Chlorella virus 1 (family *Phycodnaviridae* *Nandhagopal et al., 2002*) and Chilo iridescent virus (family *Iridoviridae*), as well as Mimivirus-dependent virus Sputnik (family *Lavidaviridae* *Zhang et al., 2012*). In addition, bacterial and archaeal viruses in the family *Sphaerolipoviridae* most probably share the same major capsid fold (*Gil-Carton et al., 2015*, *Demina et al., 2016*).
Genus: *Corticovirus*

Since only one genus (*Corticovirus*) is currently recognized in the family *Corticoviridae*, the family description above corresponds to the genus description. For clarity, the additional information that can be found on the genus page is also presented below.

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pseudoalteromonas virus C1395B2</td>
<td>Pseudoalteromonas phage C1395B2</td>
<td>MG968648</td>
<td>MG968649</td>
<td>MG968648</td>
<td>Complete genome</td>
<td>C1395B2</td>
</tr>
<tr>
<td>Pseudoalteromonas virus PM2</td>
<td>Pseudoalteromonas phage PM2</td>
<td>AF155037</td>
<td>NC_000867</td>
<td>AF155037</td>
<td>Complete genome</td>
<td>PM2</td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
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The chapter in the Ninth ICTV Report, which served as the template for this chapter, was contributed by Oksanen, H.M and Bamford, J.K.H.
Resources: Corticoviridae

Sequence alignments and tree files:

None currently associated with this report.
Further reading: Corticoviridae


References: Corticoviridae


www.ictv.global/report/corticoviridae
Citation: Corticoviridae

A summary of this ICTV Report chapter has been published as an ICTV Virus Taxonomy Profile article in the Journal of General Virology, and should be cited when referencing this online chapter as follows:


Funding support

Support for the preparation of this ICTV Report chapter and associated Journal of General Virology taxonomy profile, was funded by a grant from the Wellcome Trust (WT108418AIA).