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ICTV VIRUS TAXONOMY PROFILE

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ICTV Virus Taxonomy Profile: *Caliciviridae*

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Abstract

The family *Caliciviridae* includes viruses with single-stranded, positive-sense RNA genomes of 7.4–8.3 kb. The most clinically important representatives are human noroviruses, which are a leading cause of acute gastroenteritis in humans. Virions are non-enveloped with icosahedral symmetry. Members of seven genera infect mammals (*Lagovirus*, *Norovirus*, *Nebovirus*, *Recovirus*, *Sapovirus*, *Valovirus* and *Vesivirus*), members of two genera infect birds (*Bavovirus* and *Nacovirus*), and members of two genera infect fish (*Minovirus* and *Salovirus*). This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Caliciviridae*, which is available at ictv.global/report/caliciviridae.

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

Typical member:	**Norwalk virus (M87661), species *Norwalk virus*, genus *Norovirus***
Virion	Non-enveloped with icosahedral symmetry, 27–40 nm in diameter
Genome	Single-stranded, positive-sense genomic RNA of 7.4–8.3 kb, with a 5′-terminal virus protein, genome-linked (VPg) and 3′-terminal poly(A)
Replication	Cytoplasmic
Translation	From genome-sized (non-structural proteins) and 3′-terminal subgenomic (structural proteins) mRNAs
Host range	Mammals (*Lagovirus*, *Norovirus*, *Nebovirus*, *Recovirus*, *Sapovirus, Valovirus* and *Vesivirus*), birds (*Bavovirus*, *Nacovirus*), fish (*Minovirus*, *Salovirus*)
Taxonomy	Realm *Riboviria*; more than ten genera

VIRION

Calicivirus virions are 27–40 nm in diameter, non-enveloped with icosahedral symmetry (Table 1). The capsid is composed of 90 dimers of the major structural protein VP1 arranged on a T=3 icosahedral lattice (Fig. 1) [1]. Caliciviruses are characterised by a capsid architecture with 32 distinct cup-shaped depressions. Generally, caliciviruses are stable in the environment and enteric caliciviruses are acid-stable.

GENOME

Caliciviruses have a single-stranded, positive-sense genomic RNA of 6.4–8.5 kb organized into either two or three major ORFs, while a further ORF4 of murine norovirus encodes virulence factor 1 (VF1). A protein [virus protein, genome-linked (VPg), 10–15 kDa] is covalently linked to the 5′-terminus of genomic RNAs, which are also polyadenylated at their 3′-termini (Fig. 2). Genus-specific conserved nucleotide motifs are found

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Abbreviations: VPg, virus protein, genome-linked.

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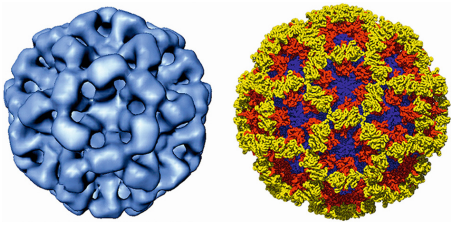

Fig. 1. The structure of the calicivirus capsid exemplified by a cryo-image reconstruction of recombinant Norwalk virus-like particles (left). X-ray structure of the Norwalk virus capsid (right) with the shell, protruding 1 and protruding 2 domains shown in blue, red and yellow, respectively. (Courtesy of B. V. Prasad.)

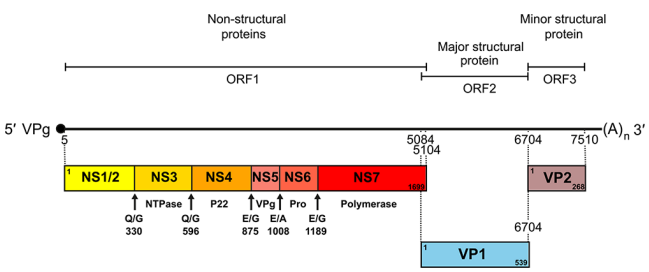

Fig. 2. Genome organization of human calicivirus MD-145 (AY032605, 7556 nt, genus *Norovirus*). Protein VPg is covalently linked to the 5′-end of genomic RNA and is depicted by a black circle. Cleavage sites in the ORF1 polyprotein are indicated by arrows; the flanking residues and amino acid coordinates are indicated, although these vary within the family. Pro: protease.

at the 5′-terminus of ORF1 and at the junction of the coding sequences for the non-structural/structural proteins.

REPLICATION

Replication of caliciviruses occurs in the cytoplasm in complexes on intracellular membranes by a VPg-mediated translation initiation process unique to the virus family and that uses genomic positive-sense RNA as the template to translate a large polyprotein that undergoes post-translational cleavage by a virus-encoded protease to form at least six mature non-structural proteins (NS1/2, NS3, NS4, NS5, NS6 and NS7) [2]. Subgenomic-sized, positive-sense RNA, co-terminal with the 3′- terminus of the genome, is the template for translation of VP1 as well as the 3′-terminal ORF product VP2 [3]. A dsRNA corresponding in size to full-length genomic RNA has been identified in feline calicivirus, murine norovirus and San Miguel sea lion virus-infected cells, indicating that replication occurs via a negative-sense intermediate. All caliciviruses require VPg; some require the function of eIF4E (feline calicivirus, porcine sapovirus), and some do not (murine norovirus).

PATHOGENICITY

Caliciviruses cause species-specific infections, with most noroviruses, sapoviruses and noboviruses restricted to the gastrointestinal tract; some lagoviruses, saloviruses and vesiviruses cause severe systemic infections in their natural hosts.

TAXONOMY

Viruses of seven genera (*Lagovirus*, *Norovirus*, *Nebovirus*, *Recovirus* [4], *Sapovirus*, *Valovirus* [5] and *Vesivirus*) infect a wide range of mammals, members of two genera infect birds (*Bavovirus* [6] and *Nacovirus* [7]) and members of two genera infect fish (*Minovirus* [8] and *Salovirus* [9]), while caliciviruses have also been detected in the greater green snake and frogs [10], highlighting the wide host range of viruses in the family. Caliciviruses are similar to picornaviruses in the presence of VPg and in sequence similarity of their RNA-directed RNA polymerase and protease proteins.

RESOURCES

Current ICTV Report on the family *Caliciviridae*: ictv.global/report/caliciviridae.

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

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