ICTV Virus Taxonomy Profile: *Geminiviridae* 2021


**Abstract**

The family *Geminiviridae* includes viruses with mono- or bipartite single-stranded, circular DNA genomes of 2.5–5.2 kb. They cause economically important diseases in most tropical and subtropical regions of the world. Geminiviruses infect dicot and monocot plants and are transmitted by insect vectors. DNA satellites are associated with some geminiviruses. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Geminiviridae* which is available at ictv.global/report/geminiviridae.

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

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<th>Example: bean golden yellow mosaic virus (DNA-A: L01635, DNA-B: L01636), species Bean golden yellow mosaic virus, genus Begomovirus</th>
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**VIRION**

Geminiviruses have a unique particle morphology of twinned (geminate) icosahedra. For maize streak virus (genus *Mastrevirus*), virions are 22×38 nm, consisting of two incomplete icosahedra (\( T=1 \)) containing 110 capsid protein (CP) subunits organized as 22 pentameric capsomers (Table 1, Fig. 1a) [1]. The structure of Ageratum yellow vein virus (genus *Begomovirus*) at 3.3 Å resolution shows that the N-terminus of CP adopts three different conformations essential for building the interface between geminate halves (Fig. 1b) [2].

**GENOME**

Viruses in most genera of the family have monopartite genomes, whereas those in the genus *Begomovirus* have mono- or bipartite genomes. The genomes of bipartite begomoviruses (Fig. 2) consist of two circular single-stranded components, DNA-A and DNA-B, each of 2.5–2.6 kb. The two components share approximately 200 bases of sequence (common region) that includes the replication origin. DNA-A encodes a capsid protein (ORF AV1, CP), a putative movement protein (ORF AV2, MP, absent in New World begomoviruses), a replication-associated protein (ORF AC1, Rep),...
**REPLICATION**

Complementary-sense DNA synthesis to produce dsDNA depends solely on host factors. Virus ssDNA synthesis is initiated by cleavage of the virion-sense strand by Rep in the 5′-TAATATTAC-3′ sequence conserved in most geminiviruses within the intergenic region (IR)/long intergenic region (LIR). Geminiviruses do not encode a DNA polymerase, relying on host factors recruited during the early stages of replication. Coding regions in both strands diverge from the IR/LIR, and transcription is bi-directional. Geminiviruses use multiple overlapping transcripts for gene expression [3, 4]. The begomovirus tomato yellow leaf curl virus replicates in the salivary glands of its insect vector via recruitment of host DNA synthesis machinery.

**TAXONOMY**

Current taxonomy: ictv.global/taxonomy. The family includes multiple genera collectively including >500 species, the most diverse genera being **Begomovirus** (>440 species) and **Mastrevirus** (>40 species). Host are dicots except for maldoviruses and mastreviruses (dicots and monocots) and eragroviruses (monocots). Vectors are whiteflies (begomoviruses), aphids (capulaviruses), treehoppers (grabloviruses, topocuruviruses), leaffoppers (becurtoviruses, curtoviruses, mastreviruses, mulcrileviruses, turncurtoviruses), or unknown (citlodaviruses, eragroviruses, maldoviruses, opunviruses, topileviruses).

**RESOURCES**


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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

**References**


**Fig. 2.** Genome organization of begomoviruses. The ORFs ([A]V1, [A]V2, [A]C1, [A]C2, [A]C3, [A]C4, BV1 and BC1) and their protein products (CP, capsid protein; MP, movement protein; Rep, replication-associated protein; TrAP, transcriptional activator protein; REn, replication enhancer protein; C4, C4 protein; NSP, nuclear shuttle protein) are shown. ORF [A]V2 is not present in New World begomoviruses. IR, intergenic region; LIR, long intergenic region; SIR, short intergenic region; CR, common region. The hairpin which includes the origin of replication is indicated in the IR/LIR.