ICTV Virus Taxonomy Profile: *Bromoviridae* 2025

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Abstract

Bromoviridae is a family of plant viruses with tripartite, positive-sense, single-stranded RNA genomes of about 8 kb in total. Genomic RNAs are packaged in separate virions that may also contain sub-genomic, defective or satellite RNAs. Virions are variable in morphology (spherical or bacilliform) and may be transmitted between hosts mechanically, via pollen, or non-persistently by insect vectors. Members of the family are responsible for major disease epidemics in fruit, vegetable and fodder crops such as tomato, cucurbits, bananas, fruit trees, common bean and alfalfa. Since the adoption of metagenomic high-throughput sequencing methodologies there has been a notable increase in detections of new species of the genus *Ilarvirus*. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Bromoviridae,* which is available at www.ictv.global/report/bromoviridae.

Virion

Virions are either spherical or quasi-spherical (Table 1, Fig. 1), having *T*=3 icosahedral symmetry and a diameter of 26–35 nm (genera *Anulavirus*, *Bromovirus*, *Cucumovirus* and *Ilarvirus*), or bacilliform (genera *Alfamovirus*, *Ilarvirus* and *Oleavirus*) with dimensions of 18–26 nm by 30–85 nm. Genomic RNAs are packaged in separate virions that may also contain subgenomic, defective or satellite RNAs [1].

Fig. 1. Cucumber mosaic virus particles. (**a**) Negative-contrast electron micrograph (courtesy of A. De Stradis, IPSP-CNR, Bari, Italy) and (**b**) reconstruction (courtesy of Dr K.L. Perry, Cornell University, Ithaca, NY, USA, Dr T. Smith, University of Texas, Galveston, Texas, USA and A. Paredes, NCTR/ORA, Arkansas USA). Bar, 50 nm.

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

Example:	**brome mosaic virus, (RNA1: X02380; RNA2: X01678; RNA3: J02042), species *Bromovirus BMV*, genus *Bromovirus***
Virion	Spherical or quasi-spherical (26–35 nm diameter) or bacilliform (18–26 nm by 30–85 nm) particles
Genome	Three segments of linear, positive-sense RNA, comprising about 8 kb in total
Replication	On cytoplasmic membranes with genomic RNAs acting as mRNAs; coat protein may be required for genome activation
Translation	Directly from genomic or sub-genomic RNA
Host range	Broad range of plants, although restricted for some virus species
Taxonomy	Realm *Riboviria*, kingdom *Orthornavirae*, phylum *Kitrinoviricota*, class *Alsuviricetes*, order *Martellivirales*; six genera, including >45 species

Genome

The genome of approximately 8 kb is split among three linear, positive-sense ssRNAs that have 5′-terminal cap structures. The 3′-termini either form tRNA-like structures that can be aminoacylated

(genera *Bromovirus* and *Cucumovirus*) or other structures that are not aminoacylated (genera *Alfamovirus*, *Anulavirus*, *Ilarvirus* and *Oleavirus*) (Fig. 2).

Fig. 2. Generalized genome organization for members of the family *Bromoviridae*. Mtr/H: methyltransferase and helicase, RdRP; RNA-directed RNA polymerse, MP, movement protein, CP, coat protein. 2b protein only in some cucumoviruses and ilarviruses, Readthrough product of CP ORF (RT) only in some ilarviuses [2].

Replication

Replication of genomic and sub-genomic RNAs occurs on cytoplasmic membranes via full-length negative-sense RNA synthesis and subsequent positive-sense RNA synthesis. Coat protein may be required for activation of replication (*Alfamovirus* and *Ilarvirus*); the ratio of cytoplasmic/nuclear coat protein accumulation modulates viral gene expression (*Alfamovirus*) [1].

Pathogenicity

Alfalfa mosaic virus (genus *Alfamovirus*) infects many herbaceous and some woody hosts inducing systemic mottling and ‘calico’ mosaic. Pelargonium zonate spot virus (genus *Anulavirus*) infects tomato plants, which display stunting, concentric chlorotic or necrotic rings and line patterns on leaves, stems and fruit [3].Members of the genus *Bromovirus* infect some *Poaceae* or *Fabaceae* and elderberry, inducing mosaic, brown streaks and reduced seed yield.Cucumber mosaic virus (genus *Cucumovirus*) exists as many strains, some supporting a 330–390 nt satellite RNA that may induce necrosis in tomato, chlorosis in tomato, tobacco and pepper or attenuate disease symptoms. Hosts include fruit crops, vegetables, ornamentals and weeds [4].Members of the genus *Ilarvirus* infect fruit trees and some herbaceous crops. Prunus necrotic ringspot virus and prune dwarf virus cause stunting and necrotic lesions on the leaves of sweet cherry, sour cherry, plum and peach trees [5].Olive latent virus 2 (genus *Oleavirus*) has been recorded in olive and in castor bean. Infections are asymptomatic in olive but produce a yellowish vein netting and mottling of the leaves of castor bean plants [6].

Taxonomy

The six genera are based on virus host range, genome content and vector. With the exception of Ilarvirus/Oleavirus, members of a genus are monophyletic by phylogenetic analysis of the RdRP. Viruses are transmitted by aphids (members of the genera *Alfamovirus* and *Cucumovirus*), thrips and/or pollen (*Anulavirus* and *Ilarvirus*), beetles (*Bromovirus*) or are unknown (*Oleavirus*).. Species demarcation criteria include natural host range, mode of transmission, particle morphology and physicochemical properties, genome structure and replication strategies, an ability to support replication of defective RNAs and satellite RNAs, and <85% amino acid identity for the whole 2a protein.

Resources

Full ICTV Report on the family *Bromoviridae*: www.ictv.global/report/bromoviridae.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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