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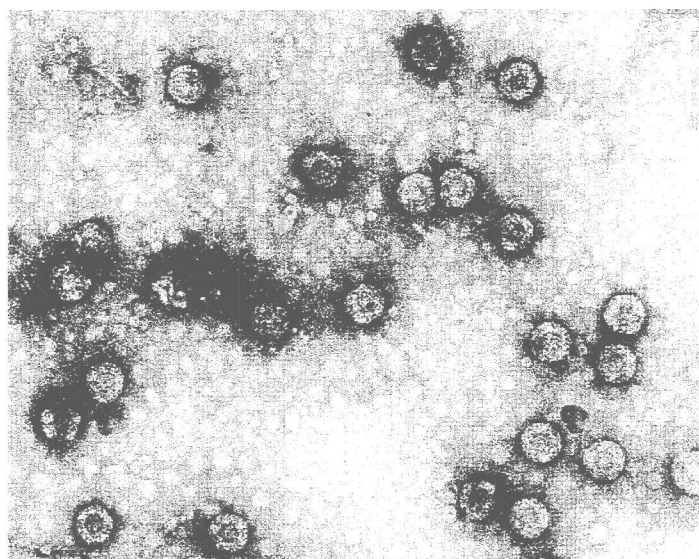
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## 15.0.1.0.001 Cauliflower mosaic virus

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### Taxonomy

*Virus Code.* 15.0.1.0.001. *Virus Accession number* 15010001.

Synonym(s): brassica virus 3, broccoli mosaic virus, cabbage mosaic virus, cabbage virus B.

Approved acronym: CaMV.

Virus infects plants.

Description is on taxonomic level of species. Virus is the type species of the genus. Virus belongs to the genus *Caulimovirus* (VC 15.0.1. ); family *Caulimoviridae* (VC 15. ).

Virus first reported in *Brassica campestris* and *B. oleracea*. From the U.S.A.  
Reference(s): Tompkins (1937).

## Properties of Virion

### Morphology

Virions not enveloped. Nucleocapsids isometric; 50 nm in diameter. Symmetry icosahedral. Nucleocapsids appear to be round. Surface capsomer arrangement not obvious.

### Physicochemical and Physical Properties

Buoyant density 1.37 g cm<sup>-3</sup> in CsCl. One sedimenting component in purified preparations. Sedimentation coefficient 208 S (Hull *et al.*, 1976). TIP: 75-80 °C. LIV: 7-15 days. DEP: log10 minus 3. Infectivity of sap not changed by treatment with diethyl ether.

### Nucleic Acid

Virions contain 16-17 % nucleic acid. Open circular (linear molecules found but not infective) double stranded DNA.

Total genome length is 8024 nt (for Cabb S; 8016 for D/H; 8031 for CM1841; 8060 for Xinjiang). Nucleotide sequence deposited at EMBL/GenBank under the following accession number CAMVG2; MCACOMGEN; CAMVG1; MCACDH. Sequence database accession code(s):

A00001 Em(40)\_vi:A00001 Gb(84)\_pat:A00001 Cauliflower mosaic virus satellite cDNA. 1/93 335bp.

D00335 Em(40)\_vi:MCAB1G6 Gb(84)\_vi:MCAB1G6 Cauliflower mosaic virus (strain Bari 1), gene VI and flanks. 3/94 1,908bp.

L09053 Em(40)\_vi:MCAMIBP. Gb(84)\_vi:MCAMIBP. Cauliflower mosaic virus major inclusion body protein (VI) gene, complete cds. 11/93 3,036bp.

M10166 Em(40)\_vi:MCAIBP Gb(84)\_vi:MCA4184P Cauliflower mosaic virus IBP. gene promoter region. 7/89 92bp

M10326 Em(40)\_vi:MCA41841 Gb(84)\_vi:MCA41841 Cauliflower mosaic virus (strain CM4-184) 5' region, segment 1. 7/89 69bp.

M10327 Em(40)\_vi:MCA41842 Gb(84)\_vi:MCA41842 Cauliflower mosaic virus (strain CM4-184) 5' region, segment 2. 7/89 135bp.

M10376 Em(40)\_vi:MCACGDH Gb(84)\_vi:MCACGDH Cauliflower mosaic virus (altered virulence isolate D/H), complete genome. 5/94 8,016bp.

M10385 Em(40)\_vi:MCA4184D Gb(84)\_vi:MCA4184D Cauliflower mosaic virus (strain CM4-184) deletion mutant DNA. 7/89 90bp.

M13776 Em(40)\_vi:MCAIS Gb(84)\_vi:MCAIS Cauliflower mosaic virus (CaMV) in vitro initiation sites. 7/89 320bp.

M14412 Em(40)\_sy:AG5MCA Gb(84)\_sy:SYNTRN5MCA Synthetic gene of Cauliflower mosaic virus promoter and Transposon Tn5 kanamycin resistant ge

M14790 Gb(84)\_vi:MCAREPREC Cauliflower mosaic virus (strain CM4-184) U5 region DNA. 5/87 2,539bp.

M16239 Em(40)\_vi:MCA4184P Gb(84)\_sy:SYN4184P1 Cauliflower mosaic virus IBP. gene promoter region with oligomer BamHI linker. 7/89 67bp

M17415 Em(40)\_vi:MCAATFA Gb(84)\_vi:MCAATFA Cauliflower mosaic virus (CaMV) BstEII/XhoI aphid transmissibility fragment DNA. 7/89 1,556bp.

M19736 Em(40)\_sy:AG35S Gb(84)\_sy:SYNMCA35S Cauliflower mosaic virus

(CaMV) 35S promoter gene under Tn10-encoded tet repressor-operator c  
M19740 Em(40)\_vi:MCACPPG2 Gb(84)\_vi:MCACPPG2 Cauliflower mosaic virus  
viable recombinant DNA, 3' flank to ORF (VIII,IV,V,V\*) region. 7/89  
M19741 Em(40)\_vi:MCACPPG1 Gb(84)\_vi:MCACPPG1 Cauliflower mosaic virus  
viable recombinant ORF VIII mRNA, 3' end; ORF V\* mRNA, complete cds;  
M23620 Em(40)\_vi:MCAMV6 Gb(84)\_vi:MCAMV6 Cauliflower mosaic virus  
(CaMV) gene six protein gene, complete cds. 12/93 1,904bp.  
M32808 Em(40)\_vi:MCAORFIX Gb(84)\_vi:MCAORFIX1 Cauliflower mosaic virus  
unidentified protein gene, partial cds. 6/92 74bp.  
M32809 Em(40)\_vi:MCAAAF1 Gb(84)\_vi:MCAAAF1 Cauliflower mosaic virus  
aphid acquisition factor 5' end. 6/92 229bp.  
M32810 Em(40)\_vi:MCAORFX2 Gb(84)\_vi:MCAORFX2 Cauliflower mosaic virus  
unidentified protein gene, 5' end. 6/92 178bp.  
M32811 Em(40)\_vi:MCAMPX Gb(84)\_vi:MCAMPX Cauliflower mosaic virus  
matrix protein (put.), partial cds. 6/92 972bp.  
M32812 Em(40)\_vi:MCACTCTP Gb(84)\_vi:MCACTCTP Cauliflower mosaic virus  
cell-to-cell transport protein, 5' end. 6/92 221bp.  
M32813 Em(40)\_vi:MCAAAFCP Gb(84)\_vi:MCAAAFCP Cauliflower mosaic virus  
aphid acquisition factor (3' end), and coat protein (5' end) genes.  
M32814 Em(40)\_vi:MCACPX Gb(84)\_vi:MCACPX Cauliflower mosaic virus coat  
protein, partial cds. 6/92 106bp  
M32815 Em(40)\_vi:MCARTRA Gb(84)\_vi:MCARTRA Cauliflower mosaic virus  
reverse transcriptase (V) gene, partial cds. 6/92 467bp.  
M37581 Em(40)\_vi:MCAORF01 Gb(84)\_vi:MCAORFIIPV Cauliflower mosaic  
virus ORF II protein gene, complete cds. 9/90 649bp.  
M37582 Em(40)\_vi:MCAORFII Gb(84)\_vi:MCAORFIICM Cauliflower mosaic  
virus ORF II protein gene, complete cds. 9/90 648bp.  
M74305 Em(40)\_sy:AGCAMVCM5 Gb(84)\_sy:SYNCAMVCM5 Synthetic  
expression vector pUC18cpPRV, constructed from cauliflower mosaic virus 35S  
gene-re  
M74306 Em(40)\_sy:AGCAMVCM3 Gb(84)\_sy:SYNCAMVCM3 Synthetic  
expression vector pUC18cpPRV constructed from cauliflower mosaic virus 35S  
gene-reg  
M90541 Em(40)\_vi:MCAMATCAP Gb(84)\_vi:MCAMATCAP Cauliflower mosaic  
virus movement protein, aphid transmission protein, DNA binding protein, c  
M90542 Em(40)\_vi:MCAMADCRI Gb(84)\_vi:MCAMADCRI Cauliflower mosaic  
virus movement protein gene, aphid transmission protein gene, DNA binding  
M90543 Em(40)\_vi:MCACOMGEN Gb(84)\_vi:MCACOMGEN Cauliflower mosaic  
virus movement protein gene, aphid transmission protein gene, DNA binding  
M94887 Em(40)\_vi:MCAORFS Gb(84)\_vi:MCAORFS Cauliflower mosaic virus  
DNA sequence, ORFs I, II, and VII. 10/92 1,692bp.  
S51055 Em(40)\_vi:S51055 Gb(84)\_vi:S51055 19S (promoter) cauliflower mosaic  
virus, Genomic, 240 nt. 11/93 240bp.  
S51061 Em(40)\_vi:S51061 Gb(84)\_vi:S51061 35S (promoter) cauliflower mosaic  
virus, Genomic, 210 nt. 11/93 210bp.  
V00140 Em(40)\_vi:CAMVG1 Gb(84)\_vi:CAMVG1 Cauliflower mosaic virus  
genome. 9/93 8,031bp.  
V00141 Em(40)\_vi:CAMVG2 Gb(84)\_vi:CAMVG2 Cauliflower mosaic virus  
genome. 9/93 8,024bp.  
X02606 Em(40)\_vi:CACM4184 Gb(84)\_vi:CACM4184 Cauliflower mosaic virus  
(CM4184) R, U5 and flanking regions. 7/86 2,539bp.  
X04879 Em(40)\_sy:ARCAMVPR Gb(84)\_sy:ARCAMVPR CaMV promoter in  
pMON273 vector (transgenic petunia) CaMV = Cauliflower Mosaic Virus 35S prom  
X14911 Em(40)\_vi:CAMVI Gb(84)\_vi:CAMVI Cauliflower mosaic virus gene VI  
for the inclusion body matrix protein. 9/93 3,131bp.  
X53860 Em(40)\_vi:CMVVIG Gb(84)\_vi:CMVVIG Cauliflower mosaic virus

(CaMV) gene VI for viroplasmin. 9/93 2,283bp.

X79465 Em(43)\_vi: Cmv dna Gb(89)n: Cmv dna Cauliflower Mosaic Virus strain B29 complete DNA sequence. 5/95 8,031bp. The largest segment 8032 nt. NCBI Taxon ID: 10641. Nucleotide sequence references: Franck *et al.* (1980); Gardner *et al.* (1981). Genome has single-stranded discontinuities at specific sites. Transcribed strand has two discontinuities. Non-transcribed strand has one discontinuity. Guanine + cytosine ratio 43 %. Poly A region absent. Non-genomic nucleic acid not found in the virions. Genomic nucleic acid isolated by Shepherd *et al.* (1970).

### Proteins

Virions contain 83-84 % protein. One structural virion protein found. Protein size 44000 Da, or 58000 Da. Method of preparation: Al Ani *et al.* (1979); Hahn and Shepherd (1980). Amino acid composition: Brunt *et al.* (1975); protein is basic because of relatively high lysine and arginine content.

### Lipids

Virions contain 0 % lipid.

### Genome Organization and Replication

Genome replicates in nuclei. Coat protein mRNA translated in the cytoplasm.

**Function of Helper and Satellite Viruses.** Virions associated with helper virus, but independent from its functions during replication.

**Cytopathology.** Virions found in all parts of the host plant; in cytoplasm. Virions found in plasmodesmata. Inclusions present in infected cells. Inclusions are unusual in shape. Electron-dense matrices. They contain virions. Other cellular changes: deeply lobed nuclei, cell wall protrusions associated with vesicles and convoluted tubules.

### Antigenic Properties

#### Serological Relationships

Virus(es) with serologically related virions: dahlia mosaic, strawberry vein-banding and carnation etched ring viruses.

### Biological Properties

#### Symptoms and Host Range

Host of virus belongs to the Domain Eucarya. Host of virus belongs to the Kingdom Plantae.

#### Natural Host Range and Symptoms

Symptoms persist.

*Arabidopsis thaliana*, *Brassica* ssp., *Raphanus* ssp. and other species of the Brassicaceae, Resedaceae - vein-clearing or banding mosaic.

**Experimental Host Range and Symptoms**

Few (<3) families susceptible. Experimentally infected plants mostly show symptoms of vein clearing, mosaic.

**Diagnostic, Propagational and Assay Host Range**

Diagnostic host: susceptible host species and symptoms

*Brassica oleracea* var. *botrytis*, *B. campestris* - vein clearing, mosaic.

*Brassica campestris* ssp. *napus* - mosaic.

Maintenance and propagation host species: *Brassica campestris* cv. Just Right.

Assay hosts (Local lesions or Whole plants) *Brassica campestris* cv. Just Right.

**Susceptible Hosts**

Experimentally infected species susceptible to virus: *Arabidopsis thaliana*, or *Brassica campestris*, or *Brassica campestris* ssp. *chinensis*, or *Brassica campestris* ssp. *napus*, or *Brassica campestris* ssp. *pekinensis*, or *Brassica campestris* ssp. *rapa*, or *Brassica oleracea*, or *Brassica oleracea* var. *botrytis*, or Brassicaceae, or *Datura stramonium*, or *Nicotiana clevelandii*, or *Raphanus*, or Resedaceae.

**Insusceptible Hosts**

Species inoculated with virus, but tested not to be susceptible: *Nicotiana bigelovii*, or *Nicotiana debneyi*, or *Nicotiana glutinosa*.

Families containing susceptible hosts: Cruciferae (9/9), or Resedaceae, or Solanaceae (2/5).

Families containing insusceptible hosts: Solanaceae (3/5).

Sources of host-range data: Tompkins (1937); Broadbent and Tinsley (1953).

**Transmission**

Transmitted by a vector. Virus transmitted by mechanical inoculation. Transmitted by an insect; *Brevicoryne brassicae*, *Myzus persicae* and at least 25 other species; Aphididae. Transmitted in a semi-persistent manner. Virus lost by the vector when it moults; does not multiply in the vector; not transmitted congenitally to the progeny of the vector.

**Geographic Distribution**

Probably distributed world-wide.

**Diagnostic and Methods**

Leaf sap contains few virions. Electron microscopy: no special treatment required but virions flatten. Method: Gardner and Shepherd (1980).

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The following references are cited in the *Sixth ICTV Report*: [rf\\_cauli.htm](#).



### Data sources and contributors.

Presented data have been collated for the plant virus database VIDEdb by R.G. Garrett, 1982. The above description has been compiled from the data presented in the *Sixth ICTV Report* by Hull R.

### Related Databases

Taxon images: [b2.gif](#)

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**Note:** The ICTV database is under development and is subject to changes and corrections. If you have questions about this project please contact us. Your comments and help will be appreciated.

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