EPPO Datasheet: *Carlavirus vignae*

Last updated: 2022-09-06

IDENTITY

Preferred name: *Carlavirus vignae*
Taxonomic position: Viruses and viroids: Riboviria: Orthornavirae: Kitrinoviricota: Alsuviricetes: Tymovirales: Betaflexiviridae
Other scientific names: *CPMMV*, *Cowpea mild mottle carlavirus*, *Cowpea mild mottle virus*
Common names: angular mosaic of beans, mild mottle of cowpea, pale chlorosis of tomato
view more common names online...
EU Categorization: Quarantine pest ((EU) 2019/2072 Annex II A)
EPPO Code: CPMMV0

Notes on taxonomy and nomenclature

Recent sequencing efforts revealed a variation in the genome of cowpea mild mottle virus (CPMMV) isolates. Furthermore, phylogenetic studies could distinguish CPMMV isolates sequences into two major groups suggesting the existence of two different viral strains (Zanardo *et al*., 2014; Zanardo & Carvalho, 2017; Yang *et al*., 2022).

Viruses causing groundnut crinkle, psophocarpus necrotic mosaic, voandzeia mosaic, and tomato pale chlorosis are serologically closely related to CPMMV and considered as CPMMV isolates (Jeyanandarajah & Brunt, 1993).

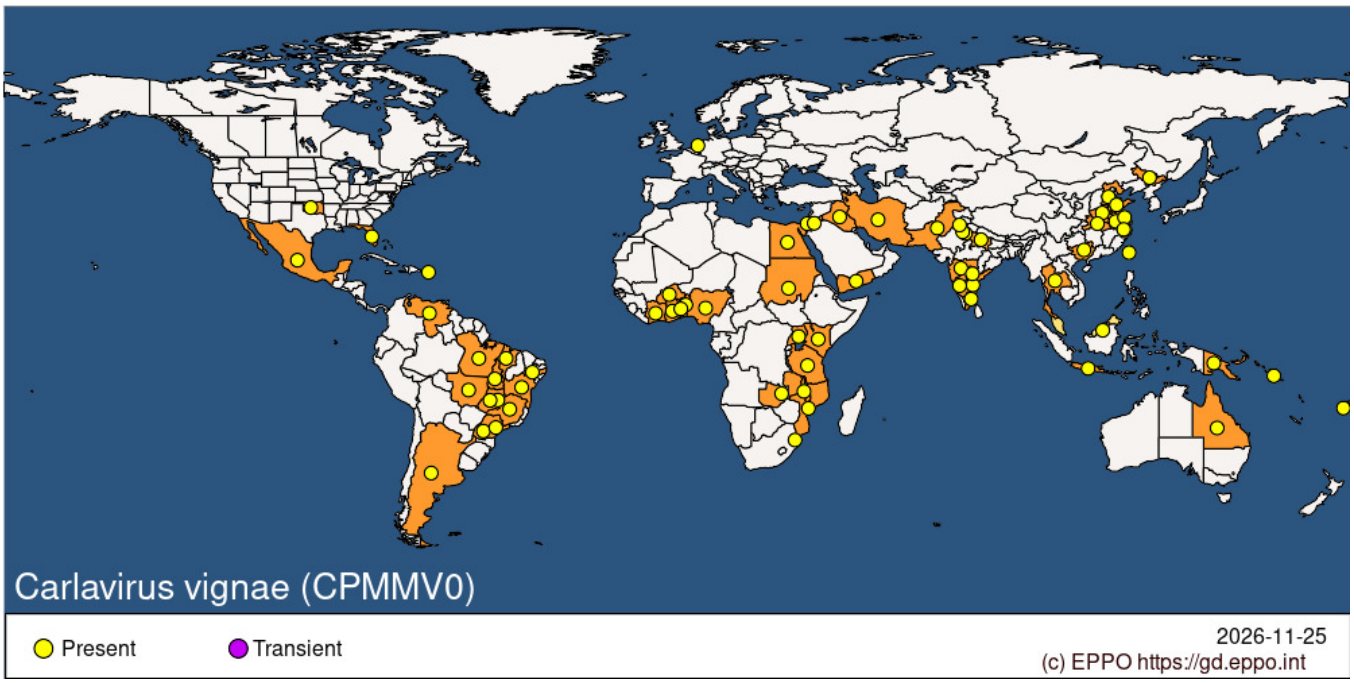
HOSTS

Natural hosts are mainly cultivated Fabaceae, including soybean (*Glycine max*), common bean (*Phaseolus vulgaris*), lima bean (*P. lunatus*), groundnut (*Arachis hypogaea*), cowpea (*Vigna unguiculata*), black gram (*V. mungo*), Bambara groundnut (*V. subterranea*), broad bean (*Vicia faba*), jack bean (*Canavalia ensiformis*), and winged bean (*Psophocarpus tetragonolobus*). CPMMV also infects, to a lesser extent, other cultivated hosts in the families Solanaceae (tomato — *Solanum lycopersicum* and aubergine — *Solanum melongena*), Caricaceae (papaya — *Carica papaya*), Lamiaceae (chia — *Salvia hispanica*), and Asparagaceae (sisal — *Agave sisalana*). The virus also occurs in various weeds (Fabaceae), including *Stylosanthes* and *Tephrosia* spp. Many more hosts can be artificially inoculated.

Host list: *Agave sisalana*, *Arachis hypogaea*, *Arachis pintoi*, *Blainvillea dichotoma*, *Calopogonium mucunoides*, *Carica papaya*, *Centrosema pubescens*, *Cleome affinis*, *Cucumis melo*, *Cucumis sativus*, *Desmodium glabrum*, *Desmodium tortuosum*, *Euphorbia heterophylla*, *Glycine max*, *Hibiscus syriacus*, *Indigofera hirsuta*, *Macroptilium atropurpureum*, *Macroptilium lathyroides*, *Macroptilium sp.*, *Mirabilis jalapa*, *Mucuna pruriens*, *Phaseolus lunatus*, *Phaseolus vulgaris*, *Pisum sativum*, *Psophocarpus tetragonolobus*, *Rhynchosia minima*, *Salvia hispanica*, *Salvia miltiorrhiza*, *Senna sp.*, *Solanum lycopersicum*, *Solanum melongena*, *Stylosanthes guianensis*, *Tephrosia purpurea*, *Tephrosia villosa*, *Vicia faba*, *Vigna angularis*, *Vigna mungo*, *Vigna radiata*, *Vigna subterranea*, *Vigna unguiculata subsp. sesquipedalis*, *Vigna unguiculata subsp. unguiculata*, *Vigna unguiculata*

GEOGRAPHICAL DISTRIBUTION

CPMMV is distributed on almost all continents, but is still absent from Europe. As CPMMV is a virus that can infect numerous host plants asymptomatically, its occurrence in different regions may be underestimated. As sequencing of virus genomes becomes more accessible, CPMMV infection has been reported more frequently.



EPPO Region: Israel, Jordan, Netherlands
Africa: Benin, Burkina Faso, Cote d'Ivoire, Egypt, Eswatini, Ghana, Kenya, Malawi, Mozambique, Nigeria, Sudan, Tanzania, United Republic of, Togo, Uganda, Zambia
Asia: China (Anhui, Guangxi, Hebei, Henan, Hubei, Jiangsu, Jilin, Shandong, Zhejiang), India (Andhra Pradesh, Delhi, Haryana, Karnataka, Maharashtra, Punjab, Tamil Nadu, Telangana, Uttar Pradesh), Indonesia (Java), Iran, Islamic Republic of, Iraq, Israel, Jordan, Malaysia, Pakistan, Taiwan, Thailand, Yemen
North America: Mexico, United States of America (Florida, Oklahoma)
Central America and Caribbean: Puerto Rico
South America: Argentina, Brazil (Bahia, Distrito Federal, Goias, Maranhao, Mato Grosso, Minas Gerais, Para, Parana, Pernambuco, Sao Paulo, Tocantins), Venezuela
Oceania: Australia (Queensland), Fiji, Papua New Guinea, Solomon Islands

BIOLOGY

Unlike carlaviruses in general, which are transmitted by aphids, CPMMV is transmitted by the whitefly *Bemisia tabaci* in a non-persistent manner (Jeyanandarajah & Brunt, 1993). The ability to transmit CPMMV is usually retained for a maximum of 20-60 min (Muniyappa & Reddy, 1983; Iwaki *et al.*, 1982). Both *B. tabaci* Middle East-Asia Minor 1 (MEAM1) and *B. tabaci* Mediterranean (MED) species transmit efficiently CPMMV isolates from Brazil (Marubayashi *et al.*, 2010; Bello *et al.*, 2019; Bello *et al.*, 2021). Whitefly populations harboring the endosymbiont *Hamiltonella* sp. are more efficient in transmitting CPMMV to beans (Bello *et al.*, 2019).

CPMMV is readily transmitted by mechanical inoculation. Seed transmission has been demonstrated in several hosts in different countries (Brunt & Keten, 1973; Iwaki *et al.*, 1982; Fauquet & Thouvenel, 1987; Yadav *et al.*, 2013), but there are also some reports of studies in which seed transmission did not occur. It seems that CPMMV seed transmission is determined by a combination of the virus isolate or strain and the host plant species (or variety). Usually, plants originating from CPMMV-infected seeds have a symptomless infection, hindering the control of the disease (Zanardo & Carvalho, 2017). Infected seeds appear to be the main source of virus inoculum in the relatively short-lived hosts of this virus in tropical countries, though weeds may also act as reservoirs.

DETECTION AND IDENTIFICATION

Symptoms

Symptoms vary, depending on the hosts, the season and the virus isolate (Naidu *et al.*, 1997). There are also several

reports of symptomless infections on many crops. On *Vigna unguiculata*, CPMMV causes diffuse chlorotic blotches on the primary leaves, systemic mottling, and leaf distortion or malformation. However, it can also cause mild symptoms, as reported on *Vigna mungo*, in Tanzania (Mink & Keswani, 1987) and typical leaf crinkle symptoms (Baranwal *et al*., 2015). On groundnuts, it causes necrotic lesions, chlorotic rings, or line patterns followed by systemic leaf chlorosis, rolling, and veinal necrosis. CPMMV is associated with stem necrosis disease on soybeans, causing stem necrosis, dwarfing, and bud blight. Other symptoms recorded on soybeans are systemic leaf chlorosis, distortion and stunting (Laguna *et al*., 2006). On *Phaseolus*, it causes vein mosaic and general leaf chlorosis, as well as mottling and mild chlorosis, followed by apical necrosis, distortion, and stunting. The response of different soybean and common bean cultivars to infection with CPMMV can result in variable symptoms. In some cultivars, CPMMV infection does not cause necrosis or distortion and may even be asymptomatic (Silva *et al.*, 2020; Mink & Keswani,1987). Furthermore, the variability of symptoms is also linked to different variants of CPMMV (Zanardo *et al.*, 2014). On tomatoes, CPMMV causes mottling and inconspicuous banding of minor veins (‘fuzzy vein’) (Brunt & Phillips, 1981). On aubergine, CPMMV induces mild leaf mosaic (Mansour *et al.*, 1998).

Morphology

CPMMV particles consist of flexuous filaments approximately 600-700 nm long and 13-15 nm wide (Brunt *et al.*, 1983; Almeida *et al.*, 2005). In leaf cells of the infected hosts, cytopathic effects include filamentous particles aggregates in sheets, bundles or brush-like inclusions (Brunt *et al*, 1983; Gaspar & Costa, 1993). CPMMV has a single-stranded positive RNA genome of about 8 200 nucleotides with a cap structure linked to the 5´end and a poly-A tail at the 3´end (Menzel *et al.*, 2010; King *et al.*, 2011; Zanardo *et al.*, 2014). The genome encodes six open reading frames (ORFs) and is typical of the viruses in the *Carlavirus* genus (Menzel *et al.*, 2010; Wei *et al.*, 2021; Zanardo *et al.*, 2014).

Detection and inspection methods

Purified preparations of CPMMV, as well as the CPMMV coat protein expressed in *Escherichia coli* system, are strongly immunogenic. The virus is detectable by serological methods such as ELISA (Mansour *et al.*, 1998; Carvalho *et al.*, 2013; Tavasoli *et al.*, 2009), immunosorbent electron microscopy — ISEM (Almeida *et al.*, 2005; Antignus & Cohen, 1987), dot-immunobinding assay — DIBA (Ali, 2017; Sutrawati *et al.*, 2021), and western blot (Carvalho *et al.*, 2013; Wei *et al.*, 2021) using antibodies from different sources. There are commercial kits available for the detection of CPMMV by ELISA.

Molecular approaches using RT-PCR are widely used to detect CPMMV in diverse hosts (Brito *et al.*, 2012; Tavasoli *et al.*, 2009; Lamas *et al.*, 2018; Zanardo *et al.*, 2014; Silva *et al.*, 2020). In addition, high throughput sequencing was also valuable in detecting CPMMV in several hosts (Alves-Freitas *et al.*, 2019; Baranwal *et al.*, 2015; Mumo *et al.*, 2020; Quintanilha-Peixoto *et al.*, 2021; Rosario, 2014; Wei *et al.*, 2021).

Indicator plants include *Arachis hypogaea*, *Cajanus cajan*, *Canavalia ensiformis*, *Glycine max*, *Vigna unguiculata*, *Nicotiana clevelandii* (systemic mottle); *Beta vulgaris*, *Chenopodium murale*, *C. quinoa* (chlorotic local lesions), however, not all CPMMV isolates infect these indicator plants.

PATHWAYS FOR MOVEMENT

CPMMV moves via its vector *Bemisia tabaci*, which can spread it between fields in infected areas. It is unlikely to be carried by host plants for planting in international trade since most CPMMV hosts are field crops which are not typically moved (a possible exception is tomato, which is however, a very minor host). The virus is seed-transmitted in some host species but, apparently, not in others (Jeyanandarajah & Brunt, 1993; Silva *et al.*, 2020; Sutrawati *et al.*, 2021). There may be some risk of movement of the virus in *B. tabaci* on other host plants (e.g. ornamentals), given the fact that the vector moves readily from one host to another. However, CPMMV is not persistent in the vector.

PEST SIGNIFICANCE

Economic impact

CPMMV was first described as widespread in Eastern Ghana on cowpeas (Brunt & Kenten, 1973). It causes a disease in soybeans and groundnuts in Kenya (Bock *et al.*, 1976), in soybeans in Côte d'Ivoire (Thouvenel *et al.*, 1982), and in groundnuts in India (Iizuka *et al*., 1984). It occurs on soybean and groundnut in many South-East Asian countries (Iwaki *et al*., 1982, 1986). In South Korea, yield losses in soybean can reach 56% (Sutrisno, 2016). However, neither Demski & Kuhn (1989) nor Reddy & Rajeshwari (1984), in their accounts of the viruses of soybean and groundnut, respectively, consider CPMMV to be of any great economic importance. On the contrary, in Brazil, a recent field study with six soybean cultivars distributed in four different growing areas showed that CPMMV infection caused a 6 to 16% yield reduction depending on the cultivar (Silva *et al.*, 2020). In Brazil, CPMMV has been recorded on *Phaseolus vulgaris*, on which it causes angular mosaic (Costa *et al*., 1983). In recent years, yield losses of about 15% to 69% have been associated with CPMMV on common beans (Souza *et al.*, 2018; Faria *et al.*, 2016). The CPMMV isolate reported on tomato in Israel seems to be only a curiosity, found on a few plants (Cohen & Antignus, 1982). In Nigeria, an 'extra mild' isolate of CPMMV has been recorded on soybeans (Anno Nyako, 1986).

Control

For soybean, beans, and cowpeas, healthy seeds should be used. As far as possible, situations of heavy whitefly infestation should be avoided. Reddy (1991), noting that the disease is rarely of any importance in groundnuts unless these are grown alongside susceptible crops of soybean or cowpea, suggests that this should be avoided. In Puerto Rico, a gene named *Rbc1* located in chromosome 18, and associated with resistance to CPMMV, was identified in the soybean genotype IA3023 (Brace, 2012). In Indonesia, another natural source of resistance to CPMMV was identified in cultivars MLG 0120 and MLG 0278 (Suryanto *et al.*, 2014). In India, a dominant gene conferring resistance to CPMMV was identified in the soybean cultivar DS-12-5, located on the linkage group H, in chromosome 12 (Cheruku *et al*., 2017). Two soybean genotypes (Daepung and Daemag-2) have been reported as a natural source of tolerance to CPMMV in South Korea (Sustrino, 2016). In Brazil, soybean and common bean cultivars with different levels of resistance or tolerance to CPMMV have been developed (Oliveira *et al*., 2018; Silva *et al*., 2022; Arias *et al*., 2015). On soybean, two distinct major genes have been reported conferring tolerance to CPMMV, one in the soybean cultivar BRS 133 and another in the cultivar BRSMT Pintado (Arias *et al*., 2015). Later, Oliveira *et al.* (2018) reported another dominant gene from the resistance source BRS133, mapped on chromosome 18 and named *Rbc2*. In addition, in Brazil, sources of natural resistance to CPMMV have been recently identified in common bean cultivars from the ‘carioca’ seed type, which were used to develop common bean lines with multiple virus resistance (CPMMV, BGMV, and BCMV) (Silva *et al.*, 2022).

Phytosanitary risk

CPMMV was included in EU A1 Quarantine pest (Annex II A) in 2019, it is a quarantine pest for other few European countries, but not included in the EPPO A1/A2 lists of pests recommended for regulation as quarantine pests. CPMMV economic importance is considered moderate, but it has increased in the last years in legumes in tropical areas outside Europe. CPMMV is transmitted non-persistently by *B. tabaci*, so there is little possibility of entry in the vector. CPMMV principally attacks tropical field crops rather than glasshouse or vegetable crops.

PHYTOSANITARY MEASURES

Because CPMMV is not transmitted persistently, the risk of introduction in the vector on other hosts is negligible. Therefore, relevant measures would be directed at the possibility of seed transmission. The use of seeds produced in areas where CPMMV is endemic should be avoided to prevent the introduction of CPMMV into new legume cultivating areas (Brown, 2020).

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Datasheet history

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