

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).

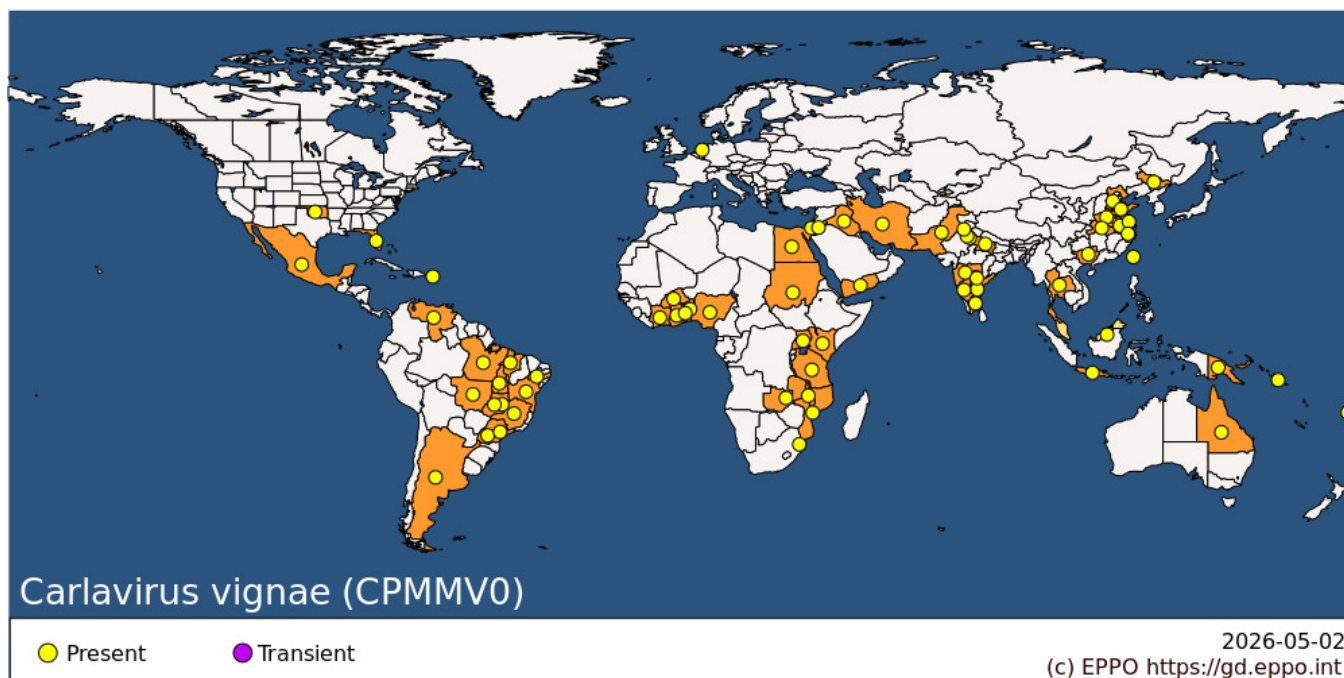
HOSTS

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*, *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 asymptotically, 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).

REFERENCES

- Ali A (2017) Rapid detection of fifteen known soybean viruses by dot-immunobinding assay. *Journal of Virological Methods* **249**, 126-129.
- Almeida AMR, Piuga FF, Marin SRR, Kitajima EW, Gaspar JO, Oliveira TG & Moraes TG (2005) Detection and

partial characterization of a carlavirus causing stem necrosis of soybean in Brazil. *Fitopatologia Brasileira* **30**, 191-194.

Alves-Freitas DMT., Pinheiro-Lima B; Faria JC, Lacorte C, Ribeiro SG & Melo FL (2019) Double-stranded RNA high-throughput sequencing reveals a new cytorhabdovirus in a bean golden mosaic virus-resistant common bean transgenic line. *Viruses* **11**, 90.

Anno Nyako FO (1986) Semipersistent transmission of an 'extra mild' isolate of cowpea mild mottle virus on soya bean by the whitefly *Bemisia tabaci* in Nigeria. *Tropical Agriculture* **63**, 193-194.

Antignus Y & Cohen S (1987) Purification and some properties of a new strain of cowpea mild mottle virus in Israel. *Annals of Applied Biology* **110**, 563-569.

Arias CAA, Almeida AMR, Mituti T, Kitajima EW, Arias CAA, Almeida AMR, Mituti T & Kitajima EW (2015) Inheritance of tolerance to cowpea mild mottle virus in soybean. *Crop Breeding and Applied Biotechnology* **15**, 132-138.

Baranwal VK, Jain P, Saritha RK, Jain RK & Gautam NK (2015) Detection and partial characterization of Cowpea mild mottle virus in mungbean and urdbean by deep sequencing and RT-PCR. *Crop Protection* **75**, 77-79.

Bello VH Watanabe LFM, Santos BR, Marubayashi JM, Yuki VA, De Marchi BR, Pavan MA & Krause-Sakate R (2019) Evidence for increased efficiency of virus transmission by populations of Mediterranean species of *Bemisia tabaci* with high *Hamiltonella* prevalence. *Phytoparasitica* **47**, 293-300.

Bello VH, Silva FB, Watanabe LFM, Vincentin E, Muller C & Bueno RCO (2021) Detection of *Bemisia tabaci* Mediterranean cryptic species on soybean in São Paulo and Paraná States (Brazil) and interaction of cowpea mild mottle virus with whiteflies. *Plant Pathology* **70**, 1508-1520.

Bock KR, Guthrie EJ, Meredith GC, Ambetsa T, Njuguna JMG & Pearson MN (1976) *Annual Report, East African Agriculture and Forestry Research Organization, Record of Research for 1974*. East African Agriculture and Forestry Research Organization, Nairobi, Kenya.

Brace R (2012) Agronomic and seed traits of soybean lines with genes for aphid resistance, inheritance and mapping of Cowpea mild mottle virus-like resistance in soybean, and fatty ester composition of low-phytate, low-saturate soybean lines. Iowa State University, Ames, Iowa, USA.

Brito M, Fernández-Rodríguez T, Garrido MJ, Mejías A, Romano M & Marys E (2012) First report of cowpea mild mottle carlavirus on yardlong bean (*Vigna unguiculata* subsp. *sesquipedalis*) in Venezuela. *Viruses* **4**, 3804-3811.

Brown JK (2020) Cowpea mild mottle virus (angular mosaic of beans). *Invasive Species Compendium*. Wallingford, UK: CABI.

Brunt AA & Kenten RH (1973) Cowpea mild mottle, a newly recognized virus infecting cowpea (*Vigna unguiculata*) in Ghana. *Annals of Applied Biology* **74**, 67-74.

Brunt AA & Phillips S (1981) 'Fuzzy vein', a disease of tomato (*Lycopersicon esculentum*) in Western Nigeria induced by cowpea mild mottle virus. *Tropical Agriculture* **58**, 177-180.

Brunt AA, Atkey PT & Woods RD (1983) Intercellular occurrence of cowpea mild mottle virus in two unrelated plant species. *Intervirology* **20**, 137-142.

Carvalho SL, Silva FN, Zanardo LG, Almeida AMR, Zerbini FM & Carvalho CM (2013) Production of polyclonal antiserum against Cowpea mild mottle virus coat protein and its application in virus detection. *Tropical Plant Pathology* **38**, 49-54.

Cheruku D, Lal SK, Talukdar A & Mandal B (2017) Inheritance and mapping of resistance against Cowpea mild mottle virus strain D1 in soybean. *Plant Breeding* **136**, 155-160.

- Cohen S & Antignus V (1982) A non-circulative whitefly-borne virus affecting tomatoes in Israel. *Phytoparasitica* **10**, 101-109.
- Costa AS, Gaspar JO & Vega J (1983) Angular mosaic of *Phaseolus vulgaris* cv. Jalo caused by a carlavirus transmitted by *Bemisia tabaci*. *Fitopatologia Brasileira* **8**, 325-337.
- Demski JW & Kuhn CW (1989) Cowpea mild mottle virus. In: *Compendium of soybean diseases* (3rd edition), pp. 60-61. American Phytopathological Society, St. Paul, USA.
- Faria J, Aragao FJL, Souza TLPO, Quintela ED, Kitajima EW & Ribeiro SG (2016) Golden mosaic of common beans in Brazil: management with a transgenic approach. APS Features. <https://www.apsnet.org/edcenter/apsnetfeatures/Pages/GoldenMosaic.aspx>
- Fauquet C & Thouvenel JC (1987) Plant Viral Diseases in the Ivory Coast. 2nd Edition. Collection Initiations - Documentations Techniques no. 46, ORSTOM, Paris, 243 pp.
- Gaspar JO & Costa AS (1993) Bean angular mosaic virus: purification and ultrastructure of infected tissues. *Fitopatologia Brasileira* **18**, 534-540.
- Iizuka N, Rajeshwari R, Reddy DVR, Goto T, Muniyappa V, Bharathan N & Ghanekar AM (1984) Natural occurrence of a strain of cowpea mild mottle virus on groundnut (*Arachis hypogaea*) in India. *Phytopathologische Zeitschrift* **109**, 245-253.
- Iwaki M, Thongmeearkom P, Prommin M, Honda Y & Hibi T (1982) Whitefly transmission and some properties of cowpea mild mottle virus on soybean in Thailand. *Plant Disease* **66**, 365-368.
- Iwaki M, Thongmeearkom P, Honda Y, Prommin M, Deema N, Hibi T, Iizuka N, Ong CA & Saleh N (1986) Cowpea mild mottle virus occurring on soybean and peanut in southeast Asian countries. *Technical Bulletin of the Tropical Agriculture Research Center* No. 21, 106-120.
- Jeyanandarajah P & Brunt AA (1993) The natural occurrence, transmission, properties and possible affinities of cowpea mild mottle virus. *Journal of Phytopathology* **137**, 148-156.
- King AMQ, Adams MJ, Carstens EB & Lefkowitz EJ (2011) *Virus taxonomy: ninth report of the International Committee on Taxonomy of Viruses*. Elsevier-Academic Press, San Diego.
- Laguna IG, Arneodo JD, Rodríguez-Pardina P & Fiorona M (2006) Cowpea mild mottle virus infecting soybean crops in northwestern Argentina. *Fitopatologia Brasileira* **31**, 317-317.
- Lamas NS, Matos VORL, Alves-Freitas DMT, Melo FL, Costa AF, Faria JC & Ribeiro SG (2017) Occurrence of cowpea mild mottle virus in common bean and associated weeds in Northeastern Brazil. *Plant Disease* **101**, 1828.
- Mansour A, Al-Musa A, Vetten HJ & Lesemann D-E (1998) Properties of a cowpea mild mottle virus (CPMMV) isolate from eggplant in Jordan and evidence for biological and serological differences between CPMMV isolates from leguminous and solanaceous hosts. *Journal of Phytopathology* **146**, 539-547.
- Marubayashi JM, Yuki VA & Wutke EB (2010) Transmission of cowpea mild mottle virus by *Bemisia tabaci* biotype B from plants of beans and soya. *Summa Phytopathologica* **36**, 158-160.
- Menzel W, Winter S & Vetten HJ (2010) Complete nucleotide sequence of the type isolate of cowpea mild mottle virus from Ghana. *Archives of Virology* **155**, 2069-2073.
- Mink GI & Keswani CL (1987) First report of cowpea mild mottle virus on bean and mung bean in Tanzania. *Plant Disease* **71**, 557.
- Mumo NN, Mamati GE, Ateka EM, Rimberia FK, Asudi GO, Boykin LM, Machuka EM, Njuguna JN, Pelle R & Stomeo F (2020) Metagenomic analysis of plant viruses associated with papaya ringspot disease in *Carica papaya* L.

in Kenya. *Frontiers Microbiology* **11**, 205.

Muniyappa V & Reddy DVR (1983) Transmission of cowpea mild mottle virus by *Bemisia tabaci* in a non-persistent manner. *Plant Disease* **67**, 391-393.

Naidu RA, Gowda S, Satyanarayana T, Boyko V, Reddy AS, Dawson WO & Reddy DV (1998) Evidence that whitefly-transmitted cowpea mild mottle virus belongs to the genus *Carlavirus*. *Archives of Virology* **143**, 769-780.

Oliveira MAR de, Carpentieri-Pípolo V, Nora TD, Vieira ESN, Prete CEC, Schuster I, Oliveira MAR de, Carpentieri-Pípolo V, Nora TD, Vieira ESN, Prete CEC & Schuster I (2018) Rbc2, a new dominant gene for resistance of soybean to Cowpea mild mottle virus: Inheritance and mapping. *Crop Breeding and Applied Biotechnology* **18**, 169-175.

Quintanilha-Peixoto G, Fonseca PLC, Raya FT, Marone MP, Bortolini DE, Mieczkowski P, Olmo RP, Carazzolle MF, Voigt CA, Soares ACF, Pereira GAG, Góes-Neto A & Aguiar ERGR (2021) The sisal virome: uncovering the viral diversity of agave varieties reveals new and organ-specific viruses. *Microorganisms* **9**, 1704.

Reddy DVR (1991) Crop profile. Groundnut viruses and virus diseases: distribution, identification and control. *Review of Plant Pathology* **70**, 665-678.

Reddy DVR & Rajeshwari R (1984) Cowpea mild mottle. In: *Compendium of peanut diseases*, p. 51. American Phytopathological Society, St. Paul, USA.

Rosario K, Capobianco H, Ng TFF, Breitbart M & Polston JE (2014) RNA viral metagenome of whiteflies leads to the discovery and characterization of a whitefly-transmitted carlavirus in North America. *PLoS ONE* **9**, e86748.

Silva F, Muller C, Bello VH, Watanabe LFM, Rossitto De Marchi B, Fusco LM, Ribeiro-Junior MR, Minozzi GB, Vivian LM, Tamai MA, Farias JR, Nogueira AM, Sartori MMP & Krause-Sakate R (2020) Effects of cowpea mild mottle virus on soybean cultivars in Brazil. *PeerJ* **8**, e9828.

Silva RS, Faria JC, Knupp AM, Aguiar MS, Pereira HS, Ferreira AL, Zaidem ALM, Pinheiro PV, Melo LC & Souza TLPO (2022) Development and selection of transgenic advanced lines of carioca seeded common bean with multiple resistance to viruses. *Euphytica* **218**, 67.

Souza TLPO, Faria JC, Aragão FJL, Peloso MJD, Faria LC, Wendland A, Aguiar MS, Quintela ED, Melo CLP, Hungria M, Vianello RP, Pereira HS & Melo LC (2018) Agronomic performance and yield stability of the RNA interference-based Bean golden mosaic virus-resistant common bean. *Crop Science* **58**, 579-591.

Suryanto A, Kuswanto K, Sitompul S & Kasno A (2014) Estimation of number and genes actions of CPMMV (cowpea mild mottle virus) disease resistance genes on soybean crop. *IOSR Journal of Agriculture and Veterinary Science* **7**, 51-56.

Sutrawati M, Hidayat SH, Suastika G, Sukarno BPW & Nurmansyah A (2021) Seed-transmission of cowpea mild mottle virus on several varieties of soybean in Indonesia. *Biodiversitas* **22**, 4182-4185.

Sutrisno S & Kuswanto H (2016) Cowpea mild mottle virus (CPMMV) infection and its effect to performance of South Korean soybean varieties. *Biodiversitas Journal of Biological Diversity* **17**, 129-133.

Tavasoli M, Shahraeen N & Ghorbani SH (2009) Serological and RT-PCR detection of cowpea mild mottle carlavirus infecting soybean. *Journal of General and Molecular Virology* **1**, 7-11.

Thouvenel JC, Monsarrat A & Fauquet C (1982) Isolation of cowpea mild mottle virus from diseased soybeans in the Ivory Coast. *Plant Disease* **66**, 336-337.

Wei Z, Mao C, Jiang C, Zhang H, Chen J & Sun Z (2021) Identification of a new genetic clade of cowpea mild mottle virus and characterization of its interaction with soybean mosaic virus in co-infected soybean. *Frontiers in Microbiology* **12**, 650773.

Yadav MK, Biswas KK, Lal SK, Baranwal VK & Jain RK (2013) A distinct strain of Cowpea mild mottle virus infecting soybean in India. *Journal of Phytopathology* **161**,739-744.

Yang S, Liu Y, Wu X, Cheng X & Wu X (2022) Synonymous codon pattern of cowpea mild mottle virus sheds light on its host adaptation and genome evolution. *Pathogens* **11**, 419.

Zanardo LG & Carvalho CM (2017) Cowpea mild mottle virus (*Carlavirus*, *Betaflexiviridae*): a review. *Tropical Plant Pathology* **42**, 417-430.

Zanardo LG, Silva FN, Bicalho AAC, Urquiza GPC, Lima ATM, Almeida AMR, Zerbini FM & Carvalho CM (2014) Molecular and biological characterization of cowpea mild mottle virus isolates infecting soybean in Brazil and evidence of recombination. *Plant Pathology* **63**, 456-465.

ACKNOWLEDGEMENTS

This datasheet was extensively revised in 2022 by Simone da Graça Ribeiro and Patricia Valle-Pinheiro. Their valuable contribution is gratefully acknowledged.

How to cite this datasheet?

EPPO (2026) *Carlavirus vignae*. EPPO datasheets on pests recommended for regulation. Available online. <https://gd.eppo.int>

Datasheet history

This datasheet was first published in 1997 in the second edition of 'Quarantine Pests for Europe', and revised in 2022. It is now maintained in an electronic format in the EPPO Global Database. The sections on 'Identity', 'Hosts', and 'Geographical distribution' are automatically updated from the database. For other sections, the date of last revision is indicated on the right.

CABI/EPPO (1997) *Quarantine Pests for Europe (2nd edition)*. CABI, Wallingford (GB).



Co-funded by the
European Union