Netherlands Food and Consumer
Product Safety Authority
*Ministry of Agriculture, Fisheries, Food
Security and Nature*

Quick scan for cotton leaf curl Gezira virus

National Plant Protection Organization, the Netherlands

Quick scan number: 2025VIR002

Quick scan date: 10 November 2025

No.	Question	Quick scan answer for cotton leaf curl Gezira virus
1.	What is the scientific name (if possible up to species level + author, also include (sub)family and order) and English/common name of the organism? *Add picture of organism/damage if available and publication allowed*.	*Begomovirus gossypigeziraense* (cotton leaf curl Gezira virus (CLCuGV)), genus *Begomovirus,* family *Geminiviridae*. Over the years the International Committee on Taxonomy of Viruses (ICTV) has updated the begomovirus taxonomy considerably resulting in a number of different viruses that are now all considered to be members of the species *Begomovirus gossypigeziraense*. These viruses include Althea rosea enation virus (ICTV, 2002), the tentative species okra enation virus (ICTV, 2002), okra leaf curl virus (ICTV, 2002; Idris et al., 2002), okra leaf curl Cameroon virus (ICTV, 2015), and hollyhock leaf crumple virus (HLCrV) (ICTV, 2015).
2.	What prompted this quick scan? *Organism detected in produce for import, export, in cultivation, nature, mentioned in publications, e.g. EPPO alert list, etc.*	Repeated findings of CLCuGV in asymptomatic plants for planting (further referred to as ‘plants’) of *Lavatera* (9 cultivars) and *Malva sylvestris* (1 cultivar) in the Netherlands or in plants originating from the Netherlands reported by other EU member states in 2022, 2023, 2024 and 2025. Note that the current preferred name of *Lavatera* is *Malva* (EPPO, 2025a). However, in the present Quick scan the name *Lavatera* is still used for plants that were labelled ‘Lavatera’.
3.	Wat is the risk assessment area?	The risk assessment area is the territory of the European Union (EU 27)

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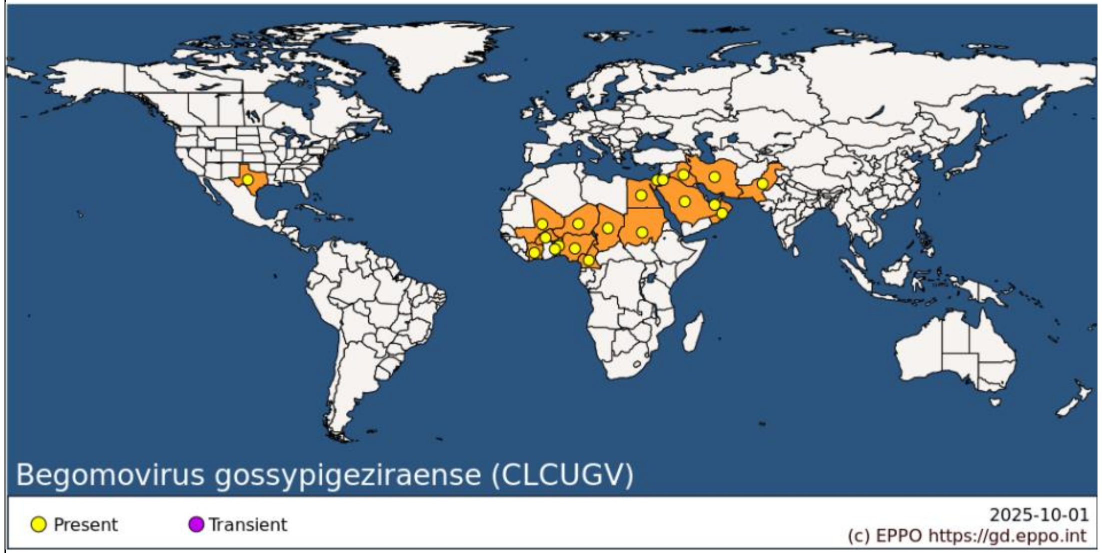
4.	What is the current area of distribution?	 2025-10-01 (c) EPPO https://gd.eppo.int According to the EPPO Global Database (see Figure above), CLCuGV is present in: - **Africa**: Benin, Burkina Faso, Cameroon, Chad, Cote d'Ivoire, Egypt, Mali, Niger, Nigeria, Sudan, Togo - **America**: United States of America (USA) - **Asia**: Iran, Iraq, Israel, Jordan, Oman, Pakistan, Saudi Arabia, United Arab Emirates. However, CLCuGV is likely more widespread then currently reported. The repeated findings of CLCuGV in asymptomatic plants of many *Lavatera* cultivars in the Netherlands but also findings in other EU member states (see below) suggest a widespread occurrence in these ornamentals in the EU. It is not known for how long CLCuGV has been present in ornamental *Lavatera* in the Netherlands (and other EU member states). Before 2022, the NPPO never tested *Lavatera* plants for CLCuGV or other viruses as they appeared healthy. The reason to test *Lavatera* plants in 2022 was the presence of yellow flecks on the leaves, which resulted in the unexpected finding of CLCuGV. However, the observed symptoms were not typical for a virus infection and likely had an abiotic cause. CLCuGV was found in plants raised from propagation material imported from Israel and Kenya (NVWA, 2022). Many plants of *Lavatera* and *Malva* have been imported from these countries for many years (Table 1). In 2022, five lots (totally 10,400 plants) originating from Israel and two lots from Kenya (totally 1,250 plants) were tested and found positive (from the tested lots none was found free from CLCuGV). From each lot 10 subsamples of five plants were tested. All subsamples tested positive except for two lots where 2 and 4 out of the 10 subsamples tested

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<tr><th>No.</th><th>Question</th><th>Quick scan answer for cotton leaf curl Gezira virus</th></tr>
<tr><td></td><td></td><td>positive. The generally high percentages of subsamples found positive indicate a high percentage of infected plants. The natural vector of CLCuGV, <i>Bemisia tabaci</i>, was not found at the nursery and most likely the plants were already infected at import. For these reasons and also because of the many cultivars in which CLCuGV has been detected in absence of symptoms (see Q2), the virus may have been introduced unnoticed many times.

After the finding in the Netherlands in 2022, Belgium reported findings in plants originating from both the Netherlands and Germany and reported that plants had been sold to French operators (EPPO, 2022). Belgium and Germany reported the pest to be eradicated but both member states also reported that plants that had already been sold to private customers were not traced back and destroyed (EPPO, 2022;2023;2025b; JKI, 2025). No information could be found on whether France applied any eradication measures.

Table 1. Number of plants for planting of <i>Lavatera</i> and <i>Malva</i> imported into the Netherlands from 2019 to 2023
<table>
<tr><th>Plant</th><th>Origin</th><th>2019</th><th>2020</th><th>2021</th><th>2022</th><th>2023</th></tr>
<tr><td><i>Lavatera</i></td><td>Israel</td><td>2.2x10^{5}</td><td>96,200</td><td>32,000</td><td>48,100</td><td>16,100</td></tr>
<tr><td></td><td>Kenya</td><td>2,100</td><td>1.7x10^{5}</td><td>1.9x10^{5}</td><td>62,400</td><td>42</td></tr>
<tr><td></td><td>United Kingdom</td><td></td><td></td><td>864</td><td>104</td><td></td></tr>
<tr><td><i>Lavatera arborea</i></td><td>Israel</td><td></td><td></td><td></td><td>4,800</td><td></td></tr>
<tr><td><i>Lavatera maritima</i></td><td>Kenya</td><td>17,364</td><td>17,364</td><td>88,296</td><td>57,800</td><td>500</td></tr>
<tr><td><i>Malva</i></td><td>Israel</td><td>50,600</td><td>39,300</td><td>4,000</td><td>9,000</td><td>10,300</td></tr>
<tr><td></td><td>Kenya</td><td></td><td>23,200</td><td>18,500</td><td>11,100</td><td>42</td></tr>
<tr><td><i>Malva sylvestris</i></td><td>Kenya</td><td></td><td>5,500</td><td>5,400</td><td>9,000</td><td>2,300</td></tr>
</table></td></tr>
<tr><td>5.</td><td>What are the host plants?</td><td>The main hosts of CLCuGV are <i>Abelmoschus esculentus</i> (okra) and <i>Gossypium</i> spp. (cotton) (Idris & Brown, 2002), both from the family <i>Malvaceae</i>. CLCuGV has also been reported in <i>Alcea rosea</i> (Idris et al., 2002), <i>Althaea</i> sp. (Salari et al., 2023), <i>Capsicum annuum (</i>Gambley et al. 2020), <i>Carica papaya</i> (Khan et al., 2012), <i>Cucumis melo</i> (Gambley et al., 2020), <i>Helianthus annuus</i> (Salari et al., 2023), <i>Malva/Lavatera</i> spp. (Bananej et al., 2021, Salari et al., 2020, Shamohammadi et al., 2023), <i>Phaseolus vulgaris</i> (Abdel-Salam & Soliman, 2025), <i>Sida alba</i> (Idris & Brown, 2002) and <i>Solanum lycopersicum</i> (Al Shihi et al., 2018).</td></tr>
<tr><td>6.</td><td>Does the organism cause any kind of plant damage in the current area of distribution and/or does the consignment demonstrate damage suspected to have been caused by this organism?
<i>Yes/no + plant species on which damage has been reported + short description of symptoms.</i>
<i>Please indicate also when the organism is otherwise harmful (e.g. predator, human/veterinary pathogen vector, etc.).</i></td><td>CLCuGV is especially known as a pathogen of cotton in which it causes various symptoms depending on the cultivar and the age of the plants (Brown, 2020):
- foliar symptoms (leaf curling, discolouration, mosaic, vein thickening),
- shortened internodes (stunting)
Estimated yield losses due to CLCuGV range up to 20% with highest yield losses in highly susceptible cultivars, and/or when infections occur early in the growing season (Brown, 2020).

In addition, high crop losses (up to 100%) have been reported in okra (Villegas et al., 2019). Symptoms in okra include yellow mosaic, bleaching, vein clearing and vein thickening of leaves (Idris et al., 2014; Villegas et al., 2019).</td></tr>
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		For several other host plants, symptoms have been described but no or limited information was found on yield losses. For *Carica papaya* (papaya), there is one disease note reporting 30-50% symptomatic plants in the surveyed fields (Khan et al., 2012). In *S. lycopersicum* (tomato), CLCuGV does not seem relevant. CLCuGV was only found in a mixed infection with other begomoviruses (Al-Shihi et al., 2018); in an experimental study CLCuGV could only be transmitted from okra to tomato by *Bemisia tabaci* already carrying tomato yellow leaf curl virus (Fouad et al., 2024). In *Capsicum* (pepper)*, Cucumis melo* (melon), and *Helianthus* (sunflower) a single symptomatic infected plant was reported; *C. melo* was co-infected with a potyvirus and only showed symptoms typical for potyviruses (Gambley et al., 2020, Salari et al., 2023). Concerning *Lavatera/Malva*: foliar symptoms have been reported in uncultivated plants of *Malva sylvestris* in Iran and *Malva parviflora* in Iraq (Bananej et al., 2021; Shahmohammadi et al., 2023). However, no (virus-like) symptoms were observed in *Lavatera/Malva* cultivars found infected in the Netherlands
7.	Assess the probability of establishment in the Netherlands (NL) (i.e. the suitability of the environment for establishment). a. In greenhouses b. Outdoors c. Otherwise (e.g. storage facilities, human environment)	The plants of *Lavatera* and *Malva sylvestris* that have been found infected are hardy perennials and CLCuGV is presumed to be present outdoors in private gardens and in greenhouses in the Netherlands and other EU member states where *Lavatera* is grown.
8.	Assess the probability of establishment in the EU (i.e. the suitability of the environment for establishment).	CLCuGV can likely establish in the EU because both host plants and natural vector (*B. tabaci*) are present in the EU. The repeated findings in different EU member states indicate that the virus is already widely present in *Lavatera/Malva* ornamentals (See also Question 7).
9.	What are the possible pathways that can contribute to spread of the organism after introduction? How rapid is the organism expected to spread (by natural dispersal and human activity)?	Begomoviruses are naturally spread by *B. tabaci* (tobacco whitefly). *Bemisia tabaci* is a species complex and CLCuGV has been reported to be transmitted by *B. tabaci* MED and MEAM1 (Abdel-Salam et al., 1998; Fouad et al., 2024). Both MED and MEAM1 are present in the EU (EFSA Panel on Plant Health, 2013). Abdel-Salam et al. (1998) carried out transmission experiments with *Bemisia argentifolii* that is currently known as *B. tabaci* MEAM1. There is uncertainty concerning the ability of *B. tabaci* to transmit CLCuGV between different host plants. Under experimental conditions, CLCGuV could not always be transmitted from one host-plant species to another. Abdel-Salam et al. (1998) showed that HLCrV could be transmitted from *A. rosea* to *A. rosea*, but poorly to okra, cotton and *M. parviflora*, and not to various other host-plant species belonging to different families, including *P. vulgaris* and *S. lycopersicum*. Idris & Brown (2002) reported that an isolate from okra could be transmitted to okra, *M. parviflora* and *A. rosea*, but not to cotton, while an isolate from cotton could be transmitted to *A. rosea* but not to okra. Fouad et al. (2024) was able to transmit an okra isolate to okra but not to *S. lycopersicum*. However, low transmission rates from *A. rosea* to *S. lycopersicum* were observed when the *B. tabaci*-population also carried TYLCV while viral titers

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		of CLCGuV in co-infected tomato plants were on average 73 times lower than of TYLCV. This is in line with the initial report of CLCuGV in *S. lycoperscium*, which also reported a co-infection with TYLCV and Chili leaf curl virus (Al Shihi et al., 2018). In addition, it is uncertain whether CLCuGV-isolates present in the *Lavatera* and *Malva sylvestris* cultivars can (still) be transmitted by *B. tabaci* because these cultivars are propagated vegetatively. The high incidence of virus infections found (see Q4) and the repeated findings in *Lavatera* suggest that this virus has been maintained and spread via vegetatively propagated host plants for some time. For a wide range of viruses evidence has been obtained that the capability of vector transmission is lost in hosts that have been vegetatively propagated for a long time (Sako, 1980, Liu et al., 2002, Whitfield et al., 2005, Pu et al., 2011), including the begomoviruses Abutilon mosaic virus, honey suckle yellow vein virus and Pseuderanthemum yellow vein virus (Bedford et al., 1994). This loss comes from a relief of selection pressure on the specific transmission trait (Elena et al., 2009, da Silva et al., 2020). There are multiple reports indicating that a few amino acid mutations in the coat protein of begomoviruses resulted in a loss of whitefly transmission (Azzam et al., 1994; Noris et al. 1998; Kheyr-Pour et al. 2000; Caciagli et al. 2009, Pan et al., 2020). In an experiment carried out by Wageningen University & Research, no evidence of CLCuGV transmission by MEAM1 from *Lavatera* to *Lavatera* nor from *Lavatera* to cotton was found. An experiment with MED is ongoing (pers. com. M. Verbeek, October 2025). In conclusion, CLCuGV can be transmitted by *B. tabaci* but it is uncertain whether the CLCuGV-isolates present in the *Lavatera/Malva* cultivars in the EU can still be transmitted by *B. tabaci* and if this is the case, whether these isolates can be transmitted to other plant species such as cotton and okra. In areas where *B. tabaci* is absent, vegetative propagation will be the only or main pathway of spread of ClCuGV.
10.	Provide an assessment of the type and amount of direct and indirect damage (e.g. lower quality, lower production, export restrictions, threat to biodiversity, etc.) likely to occur if the organism would become established in NL and the EU, respectively?	Cotton and okra are grown in southern EU member states where the vector *B. tabaci* is also present. Therefore, CLCuGV will likely have an economic impact if it were to become established in areas where these crops are grown. It is, however, uncertain whether the *Lavatera* and *Malva sylvestris* cultivars that have been found infected could act as a source of infection for cotton, okra, or other plant species (see Q9).
11.	Has the organism been detected on/in a product other than plants for planting (e.g. cut flowers, fruit, vegetables)? *If "no", go to question 13*	No
12.	If the organism has been found on/in a product other than plants for planting (e.g. cut flowers, fruit, vegetables), what is the probability of introduction (entry + establishment)?	

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	Only to be answered in case of an interception or a find.	
13.	Additional remarks	
14.	Summary and conclusions	• This Quick scan was prompted by repeated findings of CLCuGV in cultivars of *Lavatera/Malva* (*Malva* is currently the preferred name but many plants are still traded as *Lavatera*). • CLCuGV is a begomovirus and all but seven begomoviruses are regulated as Union quarantine pests. • CLCuGV is officially absent from the EU, but the virus is most likely present in ornamental plants of *Lavatera/Malva* in the EU. • Economic impact can be expected if CLCuGV were to become established in areas where susceptible host plants, especially cotton or okra, are grown and the natural vector *B. tabaci* is present. However, there is a high uncertainty whether the isolates found in the *Lavatera/Malva* cultivars can be transmitted by *B. tabaci* and if this is the case, whether these isolates can be transmitted to other plant species.
15.	References	Abdel-Salam, A. M., El-Shazly, M. A., & Thouvenel, J. C. (1998). Biological, biochemical and serological studies on hollyhock leaf crumple virus (HLCrV): a newly discovered whitefly transmitted geminivirus. *Arab J Biotechnol*, *1*(1), 41-58. Abdel-Salam, A. M., & Soliman, D. Z. (2025). A New Host Record for Cotton Leaf Curl Gezira Virus (CLCuGeV) Infecting Common Bean,(Phaseolus vulgaris) Plants in Egypt. *Egyptian Academic Journal of Biological Sciences, G. Microbiology*, *17*(1), 53-68. Al Shihi, A. A., Al Sadi, A. M., Deadman, M., Briddon, R. W., & Shahid, M. S. (2018). Identification of a distinct strain of Cotton leaf curl Gezira virus infecting tomato in Oman. *Journal of Phytopathology*, *166*(3), 199-205. Azzam, O., Frazer, J., De La Rosa, D., Beaver, J. S., Ahlquist, P., & Maxwell, D. P. (1994). Whitefly transmission and efficient ssDNA accumulation of bean golden mosaic geminivirus require functional coat protein. *Virology*, *204*(1), 289-296. Bananej, K., Shahid, M. S., & Shafiq, M. (2021). Evidence that leaf curl disease of Malva sylvestris in Iran is associated with cotton leaf curl Gezira virus and associated betasatellite. *Journal of Plant Pathology*, *103*(2), 671-672. Bedford, I. D., Briddon, R. W., Brown, J. K., Rosell, R. C., & Markham, P. G. (1994). Geminivirus transmission and biological characterisation of Bemisia tabaci (Gennadius) biotypes from different geographic regions. *Annals of applied biology*, *125*(2), 311-325. Brown J., 2020. Cotton leaf curl Gezira virus [Webpagina]. Wallingford, UK: CABI available online: https://www.cabi.org/isc/datasheet/13816 Caciagli, P., Medina Piles, V., Marian, D., Vecchiati, M., Masenga, V., Mason, G., Falcioni, T. & Noris, E. (2009). Virion stability is important for the circulative transmission of Tomato yellow leaf curl Sardinia virus by Bemisia tabaci, but virion access to salivary glands does not guarantee transmissibility. *Journal of virology*, *83*(11), 5784-5795.

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		Noris, E., Vaira, A. M., Caciagli, P., Masenga, V., Gronenborn, B., & Accotto, G. P. (1998). Amino acids in the capsid protein of tomato yellow leaf curl virus that are crucial for systemic infection, particle formation, and insect transmission. *Journal of virology*, *72*(12), 10050-10057. NVWA, 2022. Pest report cotton leaf curl Gezira virus in plants of Lavatera 2022. Netherlands Food and Consumer Product Safety Authority. Beschikbaar online: https://english.nvwa.nl/topics/pest-reporting/documents/plant/plant-health/pest-reporting/documents/pest-report-cotton-leaf-curl-gezira-virus-in-plants-of-lavatera Pan, L. L., Chi, Y., Liu, C., Fan, Y. Y., & Liu, S. S. (2020). Mutations in the coat protein of a begomovirus result in altered transmission by different species of whitefly vectors. *Virus Evolution*, *6*(1), veaa014. PFaF, 2025. Lavatera species [Web page]. Plants For a Future. Available online: https://pfaf.org/user/Plant.aspx?LatinName=Lavatera+species [Accessed: 17-10-2025] Pu, Y., Kikuchi, A., Moriyasu, Y., Tomaru, M., Jin, Y., Suga, H., Hagiwara, K., Akita, F., Shimizu, T., Netsu, O., Suzuki, N., Uehara-Ichiki, T., Sasaya, T., Wei, T., Li, Y. & Omura, T. (2011). Rice dwarf viruses with dysfunctional genomes generated in plants are filtered out in vector insects: implications for the origin of the virus. *Journal of virology*, *85*(6), 2975-2979. Sako, N. (1980). Loss of aphid transmissibility of turnip mosaic virus. *Phytopathology*, *70*(7), 647-649. Salari K, Heydarnejad J, Massumi H & Hasanvand V, 2020. First report of cotton leaf curl Gezira virus incidence and the associated betasetellite in marshmallow, okra and sunflower in Iran. Iranian Journal of Plant Pathology, 56 (4), 405-408. Salari, K., Heydarnejad, J., Massumi, H., Hasanvand, V., & Varsani, A. (2023). Incidence of cotton leaf curl Gezira virus and the associated alphasatellites and betasatellites in crops and ornamental plants in southern Iran. *Tropical Plant Pathology*, *48*(1), 62-72. Shahmohammadi, N., Dizadji, A., Al-Waeli, M., & Kvarnheden, A. (2023). First report of cotton leaf curl Gezira virus infecting Malva parviflora and in Iraq. *Australasian Plant Disease Notes*, *18*(1), 13. Whitfield, A. E., Ullman, D. E., & German, T. L. (2005). Tospovirus-thrips interactions. *Annu. Rev. Phytopathol.*, *43*(1), 459-489. Villegas, C., Ramos-Sobrinho, R., Jifon, J. L., Keith, C., Al Rwahnih, M., Sétamou, M., Brown, J. K. & Alabi, O. J. (2019). First report of cotton leaf curl Gezira virus and its associated alphasatellite and betasatellite from disease affected okra plants in the United States. *Plant Disease*, *103*(12), 3291.
16.	Follow-up measures	The NPPO of the Netherlands will give no priority to any future findings of CLCuGV in plants of *Lavatera/Malva.*