



First report of cotton leaf curl Gezira virus infecting *Malva parviflora* and in Iraq

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Abstract

In the current study, the complete genome of an isolate of cotton leaf curl Gezira virus (CLCuGeV), identified for the first time from *Malva parviflora* in Iraq, was amplified using rolling circle amplification and sequenced. The Iraqi isolate of CLCuGeV shared highest nucleotide identity at 98.2% with an Israeli isolate and clustered with isolates of the Egyptian and Cameroon strains in phylogenetic analysis.

Keywords Begomovirus · Cheeseweed · Geminivirus · Reservoir host · Weed

Weeds commonly grow along with cultivated plants and may act as reservoir hosts of various vectors and plant viruses (Varma and Malathi 2003; Hull 2014). Cotton leaf curl Gezira virus (CLCuGeV, genus *Begomovirus*, family *Geminiviridae*) is one of the begomoviruses causing cotton leaf curl disease (CLCuD), which is as a serious threat to cotton production around the world (Varma and Malathi 2003; Sattar et al. 2013). CLCuGeV was first reported from Africa in 2002 (Idris and Brown 2002) and has a circular single-stranded monopartite DNA genome of 2.7 kb (Brown et al. 2015). The natural hosts of CLCuGeV are mostly limited to wild or crop species of Malvaceae (Tahir et al. 2011; Leke et al. 2013; Bananej et al. 2021b; Salari et al. 2021). CLCuGeV in association with tomato leaf curl betasatellite is recently reported from *Malva sylvestris* plants in Iran (Bananej et al. 2021b). However, CLCuGeV has been shown to infect also papaya (Khan et al. 2012; Bananej et al. 2021a), tomato

(Al-Shihi et al. 2017), pepper and melon (Gambley et al. 2020), sunflower (Salari et al. 2021) and *Amaranthus* sp. (GenBank Accession no. MN381116; unpublished). Like other begomoviruses, CLCuGeV is transmitted by whiteflies of the *Bemisia tabaci* species complex (Ghanim 2014; Shahmohammadi et al. 2022). To date, 12 strains of CLCuGeV, including CLCuGeV-Egypt (-EG), -Niger (-NE), -Sudan (-SD), -Cameroon (-CM), -Cairo (-Ca), -Burkina Faso (-BF), -Hollyhock (-Ho), -Lysoka (-Ly), -Madagascar (-MG), -Mali (-ML), -Okra (-OK), and -Al-Batinah (-AB), have been identified (Al-Shihi et al. 2017; ICTV Online 2021), but merging of some strains according to the demarcation criterium of higher than 94% nucleotide identity for strains is proposed (Al-Shihi et al. 2017).

In 2015, nine Cheseweed mallow (*Malva parviflora*) samples showing leaf curling and yellowing were collected close to tomato fields in Dhi-Qar, Iraq, and subjected to total DNA isolation by a CTAB method (Doyle and Doyle 1987). In order to identify the begomoviruses associated with the symptoms in the collected samples, PCR was performed using the begomovirus-specific degenerate primers PAL1v1978/PAR1c496 (Rojas et al. 1993) and a fragment of 1.4 kb was amplified for four of the samples. To test the possible presence of tomato yellow leaf curl virus (TYLCV) in PCR-positive samples, a subsequent PCR was performed using a TYLCV-specific primer pair (V1 (CP) Forward/V1 (CP) Reverse), which revealed TYLCV infection of three samples (Al-Waeli et al. 2017). For the sample testing negative for TYLCV, circular viral DNA was amplified by rolling circle amplification (RCA) using a Templiphi RCA Kit

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