

LETTER TO THE EDITOR

First report of cucumber green mottle mosaic virus association with the leaf green mosaic disease of a vegetable crop, *Luffa acutangula* L.

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Cucumber green mottle mosaic virus (CGMMV), a member of the genus *Tobamovirus* is an economically significant seed transmitted pathogen infecting many cucurbit species. Crop yield losses of about 15% have been reported (1, 2). CGMMV contains a 6.4 kb (+) ssRNA genome (6). The virions are rod-shaped, approximately 300 nm in length and 18 nm in diameter (5). Ridge gourd (*Luffa acutangula* L.) is a vegetable crop commonly grown in India. It is known to get affected by several pathogens viz. virus, mycoplasma, bacteria and fungi. During the survey (March-September, 2012) of field crops, nearly 40–50% of ridge gourd plants showing the typical symptoms of *Tobamovirus* infection, i.e. systemic mosaic and mottling on leaves, blistering and deterioration of fruit pulp were observed in Rajasthan, India. Total RNA was extracted from the leaves using TRIZOL plant mini kit (Invitrogen). A single tube RT-PCR was performed using oligo-dT primer and a pair of *Tobamovirus* group-specific primers (CP(F): G(AT)CGC(GC)GA)TC(GT)GATTCGT(AT)TAAATATG and CP(R): TGGGCC(GC)CTACC(GC)G(GC)GG) binding the region of capsid protein gene under following conditions: reverse transcription at 42°C for 1 hr, initial denaturation at 94°C for 2 min, followed by 35 cycles of 94°C for 30 sec, 52°C for 1 min, 72°C for 1

min and a final extension at 72°C for 10 min. The amplified product was extracted from 1% agarose using the Gel extraction kit (Qiagen) and sequenced. MEGA 4.0 was applied for phylogenetic analysis (4).

RT-PCR from symptomatic ridge gourd samples but not from an asymptomatic sample produced an amplicon of approximately 500 bp. One sequence (isolate RKG) was deposited in NCBI GenBank Acc. No. KF702319. The nucleotide similarities with other available CGMMV CP gene sequences ranged from 85–93%. The phylogenetic tree showed that CGMMV isolates did not cluster according to their geographical origin (Fig. 1). CP gene sequence alignment of definitive *Tobamovirus* members has been shown as an appropriate tool for determination of the evolution pattern within this genus (3).

CGMMV is a very stable and easily transmissible virus. Therefore, it is essential to identify the CGMMV strains and their genetic variability for possible efficient application of detection and control strategies. To our knowledge, this is the first report on the molecular characterization of CGMMV in *Luffa acutangula* from India.

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Abbreviations: CGMMV = cucumber green mottle mosaic virus; CP = capsid protein

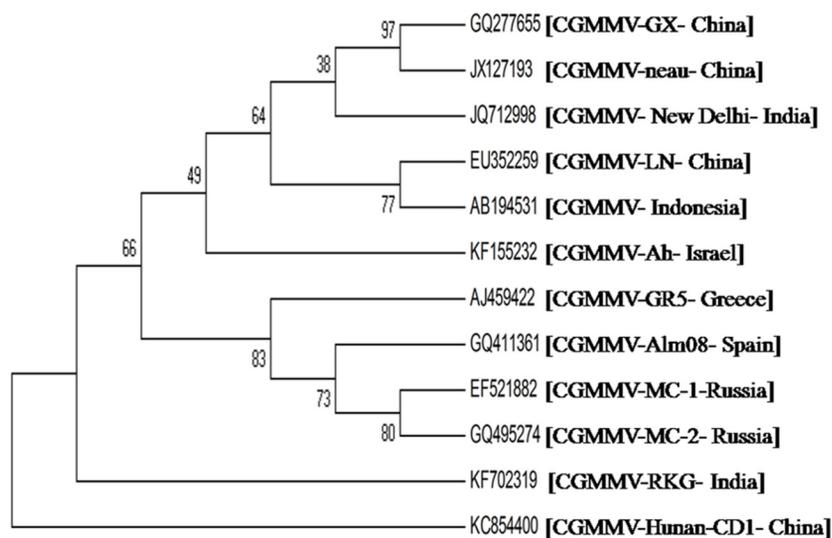


Fig. 1
Phylogenetic tree based on the CP gene nucleotide sequence of CGMMV isolates

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