

Isolation and Characterization of Cotton Infecting Begomoviruses in Alternate Hosts from Cotton Growing Regions of Pakistan

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Abstract : Castor bean (*Ricinus communis*; family Euphorbiaceae) is cultivated for the production of oil and as an ornamental plant throughout tropical regions. Leaf samples from castor bean plants with leaf curl and vein thickening were collected from areas around Okara (Pakistan) in 2011. PCR amplification using diagnostic primers showed the presence of a begomovirus and subsequently the specific pair (BurNF 5'- CCATGGTTGTGGCAGTTGATTGACAGATAC-3', BurNR 5'- CCATGGATTCACGCACAGGGGAACCC-3') was used to amplify and clone the whole genome of the virus. The complete nucleotide sequence was determined to be 2,759 nt (accession No. HE985227). Alignments showed the highest levels of nucleotide sequence identity (98.8%) with Cotton leaf curl Burewala virus (CLCuBuV; accession No. JF416947) No. JF416947). The virus in castor beans lacks on intact C2 gene, as is typical of CLCuBuV in cotton. An amplification product of ca. 1.4 kb was obtained in PCR with primers for betasatellites and the complete nucleotide sequence of a clone was determined to be 1373 nt (HE985228). The sequence showed 96.3% nucleotide sequence identity to the recombinant Cotton leaf curl Multan betasatellite (CLCuMB; JF502389). This is the first report of CLCuBuV and its betasatellite infecting castor bean, showing this plant species as an alternate host of the virus. Already many alternate host have been reported from different alternate host like tobacco, tomato, hibiscus, okra, ageratum, *Digera arvensis*, habiscus, Papaya and now in *Ricinus communis*. So, it is suggested that these alternate hosts should be avoided to grow near cotton growing regions.

Keywords : *Ricinus communis*, begomovirus, betasatellite, agriculture

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