

LETTER TO THE EDITOR

Tomato leaf curl New Delhi virus DNA A component and Cotton leaf curl Multan betasatellite can cause mild transient symptoms in cotton

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The family *Geminiviridae* comprises plant-infecting, single-stranded (ss) DNA viruses. Geminiviruses cause significant crop losses throughout tropical, sub-tropical and, increasingly, temperate regions of the world. The majority of the economically important geminiviruses belong to the genus *Begomovirus*. Begomoviruses are transmitted by a single species of whitefly *Bemisia tabaci* and infect only dicotyledonous plants. Begomoviruses native to the New World and a small number of viruses from the Old World have genomes consisting of two circular ssDNA components. On the other hand, the majority of Old World begomoviruses have genomes consisting of a single component homologous to the DNA A of the bipartite begomoviruses. However, the vast majority of monopartite begomoviruses including Cotton leaf curl Multan virus (CLCuMV) contains the additional ssDNA satellite molecule known as betasatellite. CLCuMV and its associated betasatellite (CLCuMB) are a part of the begomovirus complex that has caused losses to the cotton crops across Pakistan and northwestern India since late 1980s. First identified in the year 2000, betasatellites are a class of small circular ssDNAs approximately 1,350 nts in length. A betasatellite encodes a multifunctional protein known as β C1 that determines the viral pathogenicity. It suppresses the posttranscriptional gene silencing that raises

virus DNA levels in the diseased plants. In addition, β C1 is involved in the virus movement in plants (2).

Cotton leaf curl disease is caused by a complex consisting of one or more begomoviruses (seven species have been identified so far) associated with a single CLCuMB (1). Tomato leaf curl New Delhi virus (ToLCNDV) is a bipartite begomovirus that requires both DNA components for the systemic infection (3). It has been shown earlier that the co-inoculation of *Nicotiana tabacum* cv. Samsun with CLCuMB and either Tomato leaf curl virus, a monopartite begomovirus from Australia, or CLCuMV caused severe symptoms indistinguishable from each other. These symptoms consisted of downward curling of leaf margins, swelling, and darkening of the veins as well as formation of small enations on the veins (4, 5). Recently, it has been shown that co-inoculation of tomato plants with ToLCNDV DNA A and CLCuMB resulted in the systemic infection (6). To find out, whether ToLCNDV DNA A and CLCuMB could also cause a symptomatic infection of the cotton plants, the cotton seedlings were separately inoculated with ToLCNDV DNA A or ToLCNDV DNA A together with CLCuMB. The control plants inoculated with CLCuMV and CLCuMB developed severe symptoms at 18–21 days post infection (p.i.). Inoculation with ToLCNDV DNA A alone did not induce any symptom in the cotton plants, even 30 days p.i. In contrast, ToLCNDV DNA A and CLCuMB caused mild symptoms at 18–21 days p.i., what was recorded as the result of 3 independent experiments. The presence of ToLCNDV DNA A and CLCuMB in the inoculated plants was confirmed also by the PCR. The mild symptoms caused by ToLCNDV

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Abbreviations: CLCuMB = Cotton leaf curl Multan betasatellite; CLCuMV = Cotton leaf curl Multan virus; p.i. = post infection; ToLCNDV = Tomato leaf curl New Delhi virus

DNA A and CLCuMB in cotton plants began to diminish approx. 6 weeks p.i. and completely disappeared 8–10 weeks p.i. PCR analysis of DNA extracts from newly emerging leaves of these asymptomatic cotton plants could not detect either ToLCNDV DNA A or CLCuMB. These results indicated that although ToLCNDV DNA A and CLCuMB can cause mild symptoms in the cotton plants, they could not sustain a systemic infection beyond 10 weeks p.i. This might indicate that ToLCNDV DNA A lacked some important viral sequences/factors required for the sustained systemic infection of cotton.

A number of viruses in the genus *Begomovirus* are emergent at this time (7). Many factors are responsible for the emergent nature of begomoviruses including the genetic changes (such as random mutations, recombination, and reassortment), long-distance movement of viruses to a new agro-ecosystem, changes in the vector population dynamics, and the acquisition of novel satellites (7). Provided that weeds may act as a source of new viruses as well as reservoirs of the economically important viruses, it is possible that some weeds may harbor both ToLCNDV and CLCuMV, what lead to a component exchange. Whiteflies may transmit a mixture of begomoviruses from weeds to the cotton, but only begomoviruses capable of maintaining a sustained infection of the cotton are likely to become dominant in the crop. Consequently, in spite of the fact that ToLCNDV has

the capacity to infect cotton in the presence of CLCuMB, it has not been identified in this plant species.

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