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Journey towards the end of CLCVs -Friends from Foe

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Cotton leaf curl disease (CLCuD) is the major limitation to cotton production in Pakistan. The disease is caused by *Begomoviruses* (family *Geminiviridae*), which contains single stranded, circular DNA genome and is transmitted by a single species of whitefly (*Bemisia tabaci* Gennadius). Approximately 5-6 species of begomoviruses are infecting cotton. Cotton leaf samples showing typical begomovirus like symptoms were collected from distinct locations of Pakistan. Full length begomoviruses, alphasatellite and betasatellite were cloned from the symptomatic samples which showed high identity to Cotton leaf curl Kokhran virus (CLCuKV), Cotton leaf curl Multan Betasatellite and Cotton leaf curl Multan Alphasatellites, respectively. The partial tandem repeat constructs of begomovirus and associated components were developed which were infectious to *Nicotiana benthamiana*. An innovative approach of program cell death was used to reduce cotton infecting begomoviral infection, by targeting the viral genomes using modified cotton leaf curl betasatellite. The *Nicotiana benthamiana* transgenes showed no symptoms compared to control plants. The expression analysis of transgenes' showed high expression of *Cyt c* gene and reduced titre of CLCuKV compared to control plants. Further analyses are required to prove the concept of sustainability and durability of the technique compared to RNAi-mediated approaches to control cotton infecting begomoviruses.

Biography:

Muhammad Tahir is an Assistant Professor at Plant Biotechnology Dept. Atta-ur-Rahman School of Applied Biosciences (ASAB), National University of Sciences and Technology (NUST), Islamabad, Pakistan. He did post-doctoral research at University of Arizona, USA. His area of interest are viral diseases of Cotton, Sugarcane, Tomato and Wheat. He has published more than 40 research articles. He won competitive grants from USDA and higher Education commission of Pakistan.