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Diversity dynamics of cotton infecting *Begomovirus*, a serious threat emerged due to assorted agro-climate of Pakistan

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Pakistan is an agriculture based mono-crop economy largely dependent on cotton with 4th rank in production and 3rd in consumption globally. For last few decades cotton leaf curl disease (CLCuD) caused by a group of *Begomovirus*, is been proved to be havoc for cotton production in Pakistan with two major epidemic outbreaks after 1990s ($5 billion loss in less than five years) and still a nightmare for country as they possess great evolving potential due to diverse and changing climate and cropping practices in cotton growing zone. Globally this virus has been reported from India, and several countries of Africa after Pakistan and now from China and Philippine too threatening the Australia and America with Large infestation of *Begomovirus* vector, White fly (*Bemisia tabaci*). The targeted virus has great recombination and resistance breaking capabilities specially therefore a constant eye is required on it to predict its genetic behavior and possible recombination. In current study diversity dynamics of *Begomovirus* has been study in different wild and cultivated hosts along with cotton with coat protein marker, to evaluate the host range of virus, either are they restricted to hosts or have multiple or shared host, in same way the viruses in cotton and non-cotton regions of Pakistan are evaluated. From 25 plant samples 13 different *Begomovirus* were identified. Six different samples were with mix viral infection, 7 different wild weeds were proved to be reservoir of *Begomovirus*. 7 viruses were common in different locations 4 plants were hosting different viruses in different locations, 7 viruses were found in multiple locations and There were 13 new reports of viruses and host which were not known before. Facts revealed that in favoring multiple cropping *Begomovirus* have developed utmost important infection patterns which favor them to recombine and evolve better to overcome host resistance in short time.

Biography

Muhammad Javed Iqbal is a Ph.D Scholar at University of Punjab, Lahore, Pakistan. He is working on diversity of plant viruses especially on *Begomovirus* (A genus of ssDNA virus family, *Geminiviridae*) and on RNAi based endogenous resistance development against these viruses. He is much interested in evolving potential of these viruses in the changing climate and agro-ecological systems. This work can be helpful for a large scientific community who are fighting these pathogens for global food and agriculture security.

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