

3rd International Conference and Exhibition on Metabolomics & Systems Biology

March 24-26, 2014 Hilton San Antonio Airport, San Antonio, USA

Identification of a distinct strain of cotton leaf curl burewalavirus

Muhammad Tahir¹, Malik Nawaz Shuja¹ and Rob W Briddon²

¹National University of Sciences and Technology, Pakistan

²National Institute for Biotechnology and Genetic Engineering, Pakistan

Cotton leaf curl disease (CLCuD) is the major limitation to cotton production in Pakistan. The disease is associated with several distinct begomoviruses of which Cotton leaf curl Burewala virus(CL CuBuV) is the most widespread in Pakistan at this time. An infected cotton leaf sample (isolate C-49) showing downward leaf curl and enations was collected from areas around Layyah, a cotton growing region, in Pakistan during 2012. The complete nucleotide sequences of the components of one isolate were determined. The complete sequence of the virus was determined to be 2751bp, exhibited the arrangement of genes typical of an Old World begomovirus, and showed the highest nucleotide sequence identity (92.1%) to CLCuBuV, confirming it to belong to a distinct strain of CLCuBuV. The complete nucleotide sequence of the associated betasatellite was determined to be 1350bp and showed 98% nucleotide sequence identity to cotton leaf curl multanbetasatellite (EU384601). The partial tandem repeat constructs were produced and infectivity was shown by *Agrobacterium*-mediated inoculation to *Nicotianabenthamiana*. Since cotton is a major crop in Pakistan, the evolution of new strains of the predominant begomovirus species in the country shows that the virus is changing and may continue to affect cotton production.

gullsbs@yahoo.com