

**Research Article: PP Singhal Memorial PI Industries Award 2016 – Winner**

## Current Distribution and Severity of Leaf Curl Begomovirus Disease in Cotton Growing Areas of Northwest India

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### Abstract

Cotton leaf curl disease (CLCuD) caused by whitefly transmitted begomoviruses in association with satellite molecules is a serious constraint in cultivation of cotton (*G. hirsutum*) in Northwest (NW) India. Extensive surveys were made to study disease incidence and per cent disease index (PDI) in mostly Bt-cotton hybrids in several cotton growing areas of Haryana, Rajasthan and Punjab in NW India during the years of 2015 and 2016. The present study revealed overall CLCuD incidence of 61.0 per cent with 34.1 per cent PDI in 2015 and moderate incidence of 42.2 per cent with 17.8 per cent PDI in 2016 in Haryana; moderate of 43.9-44.1 per cent with 18.9-19.4 per cent PDI in both the years in Rajasthan, and higher of 61.1 per cent with 37.8 per cent PDI in 2015 and 42.0 per cent with 24.2 per cent PDI in 2016 in Punjab were recorded. In Haryana, the maximum incidence of 70.2 per cent with 40.2 per cent PDI in 2015 and 53.0 per cent with 29.4 per cent PDI in 2016 in Hisar; in Rajasthan, maximum of 55.2-65.2 per cent with 27.9-30.1 per cent PDI in Sri Ganganagar were observed. In Punjab maximum incidence of 70.3-72.3 per cent with 46.3-46.8 per cent PDI was recorded in Faridkot for both the years. Among all the cotton growing districts of NW India studied, only Hanumangarh district had the minimum incidence of 23.0-32.6 per cent with PDI of 8.6-12.5 per cent in both the years. Whitefly transmission and PCR test using CLCuD begomovirus specific primers determined that CLCuD in NW India is caused by whitefly transmitted CLCuD-begomoviruses. Phylogenetic analysis based on CP gene indicated that two variants of CLCuD-begomoviruses; CLCuMuV-Rajasthan and CLCuKoV-Burewala; are prevalent in NW India. The changing of the CLCuD distribution in NW India is probably attributed to cultivation of susceptible varieties, appearance of new virus strains, mixed infection with different strains and prevalence of whitefly biotype with effective transmission efficiencies.

**Key words:** Begomovirus, cotton, CLCuD, disease incidence, diagnosis, PDI, virus variants, whitefly

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