Research Article

Determination of Predominant CLCuD Begomovirus Species Infecting Cotton in Northwest India in the Current Conditions

Manisha Duhan^{1,8}, Shruti Godara², UK Bhattacharyya³, M Elangovan¹, Pradeep Kumar⁴ Rupesh Arora⁵, Man Mohan⁶, Vivek Kumar Khare⁷, Supratik Palchoudhury¹ and Kajal Kumar Biswas¹

¹Plant Virology unit, Division of Plant Pathology, ICAR-IARI, New Delhi-12; ^{1.8}Uttar Pradesh Regional office, NABARD, Lucknow-226 010; ²Genetics and Tree Improvement Division, Forest Research Institute, Dehradun, Uttarakhand- 248 006; ³ICAR-Krishi Vigyan Kendra, Goalpara, Dudhnoi, Assam, India; ⁴Agricultural Research Station, Sri Ganganagar, SKRAU-335 001; Regional Research Station, PAU, Abohar-152 116; ⁵Regional Research Station, PAU, Bhatinda-151 203; ⁶CCS Haryana Agricultural University, Hisar-125 004; ⁷Department of Plant Protection, Visva-Bharati University, West Bengal, India; Email: drkkbiswas@yahoo.co.in

Abstract

Cotton leaf curl disease (CLCuD), caused by whitefly transmitted monopartite CLCuD begomovirus associated with betasatellite and alphasatellite molecule, is a serious constrain in cultivation of cotton in Northwest (NW) India. To estimate disease incidence and per cent disease index (PDI) of CLCuD in cotton growing states Haryana, Punjab and Rajasthan of NW India, survey was made in the year 2018 and 2019. Overall disease incidence of 23.90 per cent with 15.37 PDI in 2018 and incidence of 21.17 per cent and 12.16 PDI in 2019 were recorded. Twenty nine cotton varieties and nine Bt-hybrid cottons were evaluated for resistance to CLCuD through whitefly (Bemisia tabaci) inoculation. All the varieties and hybrids were susceptible showing 66.7-100 per cent disease incidence. To identify the begomoviruses and its variants causing CLCuD in current condition, complete coat protein gene (771 nts) of 29 isolates of CLCuD begomoviruses, 13 of 2018 and 16 of 2019, collected from NW India were amplified, sequenced and analyzed. Sequence identity and phylogenetic analysis showed that the isolates of 2018 made two groups; 12 were the members of Cotton leaf curl Kokhran virus-Burewala (CLCuKoV-Bu) strain and one was the member of Cotton leaf curl Multan virus-Rajasthan (CLCuMuV-Ra) strain; whereas in 2019, two groups were formed; 13 were members of CLCuMuV-Ra and three of CLCuKoV-Bu strain indicating that CLCuKoV-Bu strain was dominant in 2018 and CLCuMuV-Ra strain in 2019. Based on sequence analysis of β C1 gene, a single betasatellite species, Cotton leaf curl Multan betasatellite (CLCuMB); and based on Rep gene, two alphasatellite species, Cotton leaf curl Multan alphasatellite (CLCuMA) and Gossypium darwinni symptomless alphasatellite (GDarSLA) associated with CLCuD-begomovirus in NW India were identified.

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

Citation: Duhan M, Godara S, Bhattacharyya UK, Elangovan M, Kumar P, Arora R, Mohan M, Khare VK, Palchoudhury S and Biswas KK. 2022. Determination of predominant CLCuD begomovirus species infecting cotton in Northwest India in the current conditions. *J Mycol Pl Pathol* 52 (1):12-24