

Diversity in alpha satellite associated with CLCuV and it's potential application

Kumari Rhaeva, Abhinav Kumar*

Department of Biotechnology, College of Engineering and Technology IILM Academy of Higher Learning,
Greater Noida, Uttar Pradesh-201306, India

*Corresponding author

ABSTRACT

Cotton (*G. hirsutum* L.) is one of the major cash crops in the Indian sub-continent region and over the year, produces over 27% of world's share, occupying the largest production area of 11.9 million hectares. It is consistently attacked by several pests and microbes, and cotton leaf curl disease (CLCuD) is become one of the major reasons for the loss. The symptoms include leaf curling, darkened veins, vein swelling and enations. For the transmission of this disease, white flies (*Bemisia tabaci*) acts as a vector, which transmit it in persistent circulative manner. A monopartite Begomoviral species Cotton leaf curl virus (CLCuV) in association with alpha satellite and beta-satellite molecules is the real cause of CLCuD. In our study, we have characterized begomo virus and its associated alpha-satellites from the diseased leaves from Rajasthan and Punjab. The satellite molecules associated with these viruses help in the development of viral gene silencing studies. Virus induced gene silencing (VIGS) is a very effective technology in which response is mediated by virus vectors containing a target gene fragment to produce double stranded RNA which then ultimately triggers RNA induced gene silencing. VIGS occurs at both transcriptional and post-transcriptional level. It is very effective and efficient for transient gene silencing. The developed VIGS vector will be tested for its efficacy.

Keywords: Cotton, whiteflies, darkened veins

