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Authors: Judith K. Brown, Muhammad Zia Ur-Rehman, Sofia Avelar, N. Chingandu, Usman Hameed, Saleem Haider, Muhammad Ilyas



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Molecular diagnostic development for two begomovirus-betasatellite complexes undergoing diversification: A case study

Judith K. Brown^{a,*}, Muhammad Zia Ur-Rehman^b, Sofia Avelar^a, N. Chingandu^a, Usman Hameed^b, Saleem Haider^b, Muhammad Ilyas^a

^aSchool of Plant Sciences, University of Arizona, Tucson, AZ 85721 USA

^bInstitute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan

***Corresponding Author:** J.K. Brown Email: jbrown@ag.arizona.edu

HIGHLIGHTS

- Outbreaks of cotton leaf curl disease in cotton crops in Asia and Africa have led to concerns that these high-risk begomoviruses will spread globally.
- Genomic surveillance of plants transported from the affected locales is needed, making the development of molecular diagnostic tests essential.
- Extensive polymorphic sites and the requirement to distinguish multiple strains and species, has confounded the design of PCR-primers for leaf curl begomoviral-betasatellite detection.
- Molecular diagnostic testing of plants destined for export from affected areas would greatly reduce the likelihood of introductions elsewhere.

ABSTRACT

At least five begomoviral species that cause leaf curl disease of cotton have emerged recently in Asia and Africa, reducing fiber quality and yield. The potential for the spread of these viruses to other cotton-vegetable growing regions throughout the world is extensive, owing to routine, global transport of alternative hosts of the leaf curl viruses, especially ornamentals. The research reported here describes the design and validation of polymerase chain reaction (PCR) primers undertaken to facilitate molecular detection of the two most-prevalent leaf curl-associated

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