Journal of
Agriculture and Biology
ISSN: 3007-1755 (Print), 3007-1763 (Online)

Research Article

Varietal Screening of Cotton (*Gossypium Hirsutum* L.) Against Cotton Leaf Curl Virus and its Association with Whitefly (*Bemisia Tabaci* L.)

Saima Naseer[1], Arbaz Hassan[2*], Muhammad Atif Shabir[3], Mehwish Naz[4], Majid Ali[5], Zia Ullah Ashraf[4], Ali Ahmed[6], Saba saeed[1], Sajawal[7], Anisa Umer[8]
[1] *Plant Pathology Research Institute, Ayub Agricultural Research Institute, Faisalabad, Pakistan.*
[2] *Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.*
[3] *Cotton Research Sub-Station Rajanpur.*
[4] *Department of Plant Pathology, University of Agriculture, Faisalabad, Pakistan.*
[5] *Department of Entomology, University of Agriculture, Faisalabad, Pakistan.*
[6] *Department of Entomology, Sindh Agriculture University, TandoJam.*
[7] *Department of plant pathology, Sindh Agriculture University, TandoJam.*
[8] *Department of Plant Breeding and Genetics, Nuclear institute for Agriculture and Biology.*

Correspondence
Arbaz Hassan
hassanarbaz40@gmail.com

Article History
Received: December 20, 2024
Accepted: March 02, 2025
Published: March 28, 2025

ABSTRACT

The disease Cotton Leaf Curl Virus (CLCuV) caused by the whitefly (*Bemisia tabaci*) is a serious threat to the production of the global economic commodity Cotton (*Gossypium hirsutum* L.), which represents an important step for fiber production of the world. The goal of this study was to determine the level of the severity of the disease and response of yield properties in ten different genotypes of cotton. As a Randomized Complete Block Design (RCBD), three treatment groups representing increasing levels of whitefly infestation were used (1, 2, and 3), as well as control. The phytochemical parameters i. e. plant height (PH), number of sympodial branches (SB), number of bolls (NOB), boll weight (BW), ginning outturn (GOT) and seed cotton yield (SCY) were recorded in the experiment along with the severity of the disease (PADI). A higher infestation of whiteflies resulted in significant increases in PDI, which resulted in significant decreases of all yield-related traits. With lower PDI values and improved yield stability in high infestation conditions, genotypes FH-333 (G1) and CKC-3 (G10) were considered the most tolerated genotypes to CLCuV. On the other hand, the mutants MNH-1016 (G8) and CIM-615 (G3) demonstrated the greatest losses in yield and PDI. While SCY was positively related to BW, GOT, SB and NOB, ANOVA and correlation analysis demonstrated a highly significant negative association between PDI and yield-related traits. Selecting CLCuV-resistant genotypes for breeding programs was suggested. The results showed that integrated pest management (IPM) techniques should be used for controlling whitefly populations and reducing the effects of disease.

Keywords: Cotton, Whitefly, Cotton Leaf Curl Virus, Yield, Genotypic Screening.

INTRODUCTION

Cotton (*Gossypium* spp.) is one of the major cash crops around the world and plays an important role in the economies of many countries. However, a number of biotic factors, some of which, the most damaging ones, are Cotton Leaf Curl Virus (CLCuV). The CLCuV is transmitted by the whitefly (*Bemisia tabaci*). It shows symptoms of leaf curling, vein thickening, enations and stunted growth of plants which adversely affect the productivity CLCuV has significant impact on morphology of cotton and causes yield loss (Sattar et al., 2013). There is need of the hour to develop resistant cotton genotypes due to increasing virulence and the spread of the virus in the Pakistan so that the yield loss can be saved from its damage

https://doi.org/10.55627/agribiol.003.01.1258

(Mansoor et al., 2006). The whitefly is a vector of CLCuV and it is very important to study its epidemiology and extent of damage in relation to population size. The larger populations of whitefly cause more damage than small populations due to less proportion of transmission of virus (Hameed et al., 2020). The response of different cultivar of cotton is different to the same population size of white fly and this provides a space to breeder and pathologists to find and select the tolerant genotypes. It is the best method to save cotton from the damage of vector and the virus (Akhtar et al., 2019). Other than that, one can only prevent the cotton to be attacked by whitefly which a hectic job and need more financial investment. The purpose of this study was to study effect of CLCuV incidence on yield and biochemical parameters of cotton and the probable relation between virus and the vector whitefly. In order to get sustainable cotton production in virus-prone areas, these findings will help to develop CLCuV-resistant cotton varieties.

The rate and severity of infection by virus is directly associated with number of whiteflies in a field. A high infestation density will significantly decrease plant vigor and yield potential (Hameed et al., 2020). The behavior of different varieties of cotton to virus is significantly different from each other so there is a space for breeders and pathologists to screen the genotypes and select resistant genotypes which lowers yield lesser on attract of virus than other varieties (Aslam et al., 2017). The integrated pest management includes biological control, chemical control, and cultural management can be proved best for combating damage caused by virus. (Akhtar et al., 2019). Controlling white fly population in the field and prevention of virus movement in the plant by using resistant cultivar is the best practice to get higher yield (Hussain et al., 2019).

For selection of resistant genotypes, it is important to gain understanding of correlations between whitefly infestation level with PDI and yield-related characteristics. Since ten cotton genotypes of different cultivars have been studied for resistant to CLCuV and for resistance to whitefly infestation in different degrees, the role of whitefly population in severity of disease and yield aspects have been investigated. The result on the influence of whitefly population on disease severity and yield characteristics in these varieties will be useful in establishing CLCuV-resistant varieties for sustainable production of cotton in virus prone areas.

MATERIALS AND METHODS

Experimental Site and Design

The experiment was carried out at Plant Pathology Research Institute, Ayub Agricultural Research Institute, Faisalabad. The two factors (Genotypes and treatments) and four treatments were used in the Factorial Randomized Complete Block Design (RCBD) i.e. Control (No whitefly infestation), T1 (5-10 per plant), T2 (20–30 per plant), T3 (>50 per plant) with three replications of each treatment. The population of white fly was maintained by rearing the white flies in cages and whiteflies were collected from previously infected fields. (Table 1).

Plant Material

Ten cotton genotypes were selected based on their previous performance under CLCuV pressure (Table 1). The seeds were obtained from Cotton Research Station Ayub Agricultural Research Institute Faisalabad. The genotypes included:

Sr#	Genotype coding	Genotype Name
1	G1	FH-333
2	G2	FH-142
3	G3	CIM-615
4	G4	CIM-616
5	G5	NIAB-1048
6	G6	NIBGE-2
7	G7	CKC-6
8	G8	MNH-1016
9	G9	FH-lalazar
10	G10	CKC-3

G1= genotype 1 G2= genotype 2 and so on

Artificial Whitefly Infestation

To ensure uniform exposure to CLCuV, artificial whitefly infestations were conducted using controlled release methods. Whiteflies were collected from virus-infected cotton fields and reared on susceptible plants in insect-proof cages. At

https://doi.org/10.55627/agribiol.003.01.1258

the three-leaf stage, whiteflies were released onto the experimental plots according to pre-described treatment plan. Infestation was maintained for four weeks to allow efficient virus transmission.

Data Recording for Infestation of Disease

CLCuV severity data were collected using a 0–5 disease rating scale (Saleem et al., 2020) and Percentage Disease index was calculated:

Scaling	Description
1	Mild vein thickening (resistant)
2	Moderate vein thickening and enations (moderately resistant)
3	Severe vein thickening, enations, and leaf curling (moderately susceptible)
4	Pronounced leaf curling, enations, and stunting (susceptible)
5	Severe curling, enations, stunting, and plant death (highly susceptible)

The Percent Disease Index (PDI) was calculated using:

$$\text{PDI}=\frac{\sum(\text{Disease rating}\times\text{Number of plants with that rating})}{(\text{Total number of plants}\times\text{Maximum disease rating})}\times 100$$

Data Recording for Yield Contributing Characters

The following yield-related traits were recorded:

Plant height (cm): Plant Height (PH) was measured at maturity from base to tip of plant using measuring tape in centimeters.

Number of sympodial branches: The sympodial branches (SB) of each selected plant were counted at maturity.

Number of bolls: The number of bolls (NOB) of each selected plant were counted at maturity

Boll weight (g): The boll weight was measured for each selected plant using electrical balance.

Ginning out turn (%): The Ginning out turn (GOT) was calculated for each selected plant after ginning using formula:

GOT%= Lint yield/Seed Cotton Yield × 100

Seed cotton yield (g): Seed cotton yield was measured for each selected plant using electrical balance in grams.

Statistical Analysis

Data were recorded and arranged in excel and analysis of variance (ANOVA) was performed using in Statistix 8.1 to determine significant differences among genotypes and treatments. Pearson correlation analysis was conducted using statistix 8.1 to assess the relationships between PDI and yield-related traits.

RESULTS AND DICUSSION

Analysis of Variance

Analysis of variance for infestation of different populations of whitefly and their impact on virus spread and yield related characters of ten genotypes of cotton is represented in the table 1.

Table 1. Analysis of variance for infestation of different populations of whitefly and their impact on virus spread and yield related characters of ten genotypes of cotton.

Sr#	Character	MSS (Genotype)	MSS (Treatment)
1	PDI	117.0**	17689.12*
2	PH	127.0*	15671.12**
3	BW	0.13*	19.65*
4	GOT	14.92*	2256.26**
5	NOB	7.31**	1105.57**
6	SB	1.44	218.38
7	SCY	242.43**	39458.81*

PDI= percentage disease index, PH=plant height, BW=boll weight, GOT=ginning out turn, NOB=number of bolls, SB=number of sympodial branches, SCY= seed cotton yield.

It can be observed that different rates of infestation of whitefly have a significantly different effect on transmission of the cotton leaf curl virus and yield related characteristic among different genotypes of cotton for all morphological and biochemical characters except sympodial branches similar results were found by Kumar et al., (2019) and they reported that there is no significant impact of CLCuV on number of sympodial branches. The transmission of CLCuV among the genotypes tested was significantly increased by the presence of whiteflies (Saleem et al., 2020). The control of whitefly can be proved to be a yield saving strategy for the farmer and get extra economic benefits (Reeve et al., 2017).

Figure 1 summarizes the mean performance of ten cotton genotypes for infestation by a variety of whitefly populations, the effects on yield-related traits and virus spread of each genotype. The high infestation rate from control to T3 is responsible for the increase of PDI values in all genotypes. Even at T3, the lowest PDI values were observed for G1, G10 and thus it can be concluded that they performed best at T3 (highest infestation rate). In addition, the genotypes with the highest PDI value at T3 were the worst. The yield and yield contributing characters deteriorated as the population of whitefly increased from control to T3. The reduction in yield was maximum in G3 and G8 while G7 and G10 still had the highest SCY at T3 which showed their tolerance to CLCuV.

In the present study, due to highest PDI of MNH-1016 (G8) and CIM-615 (G3) and weakest antioxidant defense these two genotypes were categorized as susceptible and the results verified the results of research conducted by Naveed et al., (2018) and Kumar et al., (2020) as they reported the same results. CLCuV disrupt the normal physiological processes of cotton, leading to reduced growth yield components (Hussain et al., 2022; Saleem et al., 2020).

The highest seed cotton yield (SCY) was by CKC-6 (G7) and CKC-3 (G10) even under T3, suggested that these genotypes possess stronger resistance mechanism. Similar results were found by Rahman et al., (2019) and they suggested the strong biochemical response of cotton against virus as possible reasons such results.

MNH-1016 (G8) and CIM-615 (G3) exhibited the highest reduction in SCY from control to T3, indicating that these genotypes faced the highest yield losses due to disease development. Iqbal et al., (2021) reported hormonal disturbances as possible cause of enhanced oxidative damage, and impaired carbohydrate metabolism. Hussain et al., (2022) proposed that for minimizing whitefly infestation and virus transmission in cotton crops, crop rotation, reflective mulches, and intercropping as best practices.

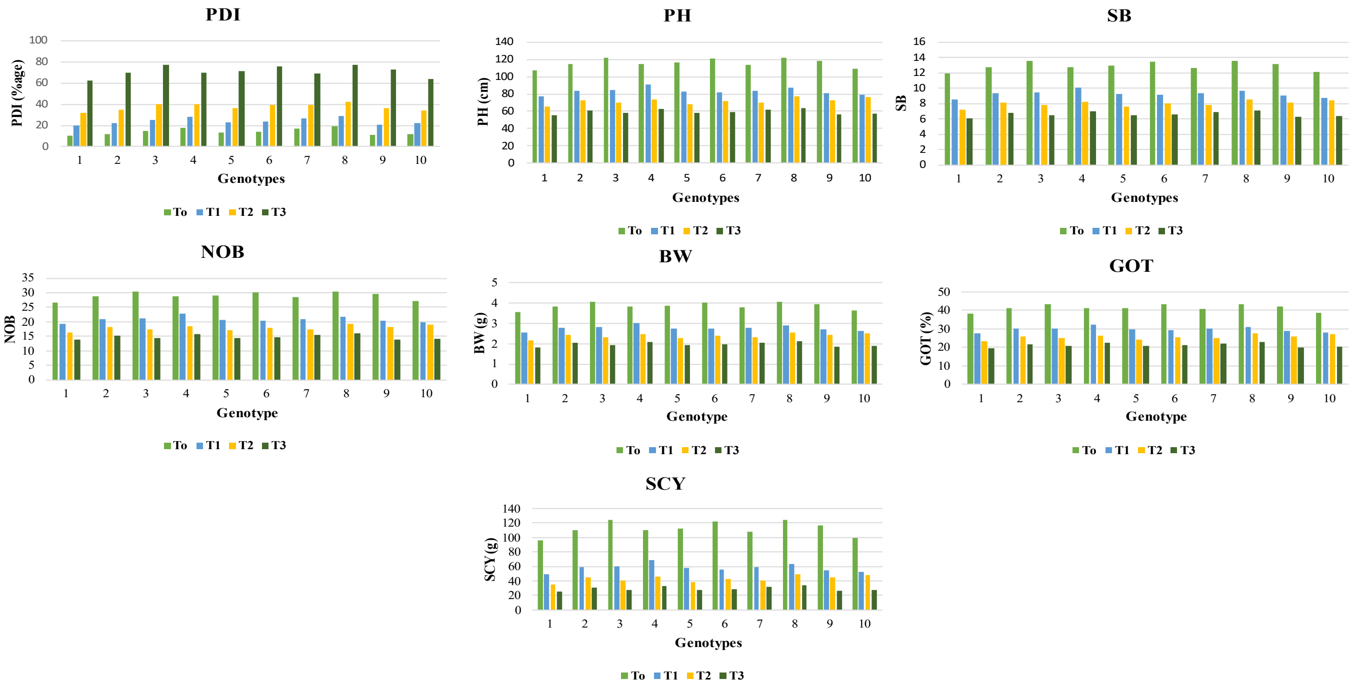

Figure 1. Infestation of different populations of whitefly and their impact on virus spread and yield related characters of ten genotypes of cotton

Correlation Analysis

Correlation analysis of infestation of various populations of whitefly and their effect on virus transmission and yield related traits of ten cotton genotypes is given in table 2. PDI and highly significant negative correlation with all the yield related traits. BW, GOT, SB, and SCY were highly significantly positively correlated. There are significant positive correlations between GOT, NOB, SB, and SCY with PH. BW, GOT, and SCY are yield attributes having highly significant negative correlation with PDI, which shows that the disease intensity greatly diminishes cotton productivity. Plant height was significantly correlated with sympodial branches (SB), number of bolls per plant NOB, GOT, and SCY in a positive manner.

Increased disease severity was attributed to low photosynthetic efficiency, nutrient deficiency, and early leaf senescence in cotton, leading ultimately to reduced seed cotton yield and lower fiber quality (Saleem et al., 2020). These traits are dependent on each other, as is supported by the extremely significant positive correlation observed between BW, GOT, SB, and SCY.

The taller cotton plants typically have more bolls and branches, which directly raises the potential yield. Kumar et al., (2020) suggested selection for higher plant height to get good yield but too much height is a negative character.

Like previous reported study by Ashfaq et al., (2021) this study suggested that we should select the genotypes having negative correlation between PDI and yield related characters. This will improve the varietal resistance against CLCuV and in turn better yield and market price.

Table 2. Correlation analysis for infestation of different populations of whitefly and their impact on virus spread and yield related characters of ten genotypes of cotton

	BW	**GOT**	**NOB**	**PDI**	**PH**	**SB**
GOT	0.76*					
NOB	0.65*	0.26				
PDI	-0.81**	-0.81	-0.76*			
PH	0.35*	0.25*	0.25*	-0.82**		
SB	0.26**	0.16**	0.16*	-0.85**	0.15*	
SCY	0.99**	0.84**	0.86**	-0.77**	0.87*	0.54*

PDI= percentage disease index, PH=plant height, BW=boll weight, GOT=ginning out turn, NOB=number of bolls, SB=number of sympodial branches, SCY= seed cotton yield

CONCLUSIONS

It is concluded that whitefly significantly increase the CLCuV infection in cotton and is a vector in transmitting the virus. The viral infection causes the oxidative damage and the biochemical response of different cotton genotypes is significantly different for all 10 cotton genotypes. The yield related parameters also affected by the viral infection which reduced yield and cause economic loss. Integrated pest management can be a good stregity to combat with whitefly and in turn viral infection.

ACKNOWLEDGEMENTS

Not applicable.

AUTHOR CONTRIBUTIONS

All the authors contributed equally to this research.

COMPETING OF INTEREST

No conflicts of interest have been disclosed by the authors.

REFERENCES

Ahmad, S., Khan, M.A., Hafeez, A., et al 2017. Impact of whitefly infestation on cotton yield and its management strategies. *Pak. J. Agric. Res.* 30(2): 235–245.

Akhtar, K.P., Haidar, M.S., Ahmad, M., et al 2019. Screening of cotton genotypes for resistance to Cotton Leaf Curl Virus disease through whitefly-mediated inoculation. *Pak. J. Agric. Res.* 32(2): 289-295.

Akhtar, K.P., Haider, S., Khan, A.I., et al 2021. Genetic variability of cotton genotypes against Cotton Leaf Curl Virus under field conditions. *J. Crop Prot.* 40(1): 89–97.

Ashfaq, M., Aslam, M., Riaz, M. 2022. Influence of plant morphological traits on whitefly (Bemisia tabaci) infestation in cotton. *Int. J. Pest Manag.* 55(3): 215–224.

Aslam, U., Ajmal, S., Khan, A.A., et al 2017. Identification of new sources of resistance against Cotton Leaf Curl Virus (CLCuV) in Gossypium hirsutum. *Euphytica.* 213(2): 57.

Hameed, S., Shahid, A.A., Asad, S., et al 2020. Molecular characterization and epidemiology of Cotton Leaf Curl Virus and its whitefly vector in Pakistan. *Virus Res.* 285: 198012.

Hussain, M., Ashfaq, M., Saleem, M.A., et al 2019. Host plant resistance and whitefly (Bemisia tabaci) management in cotton: A review. *Crop Prot.* 124: 104872.

Hussain, M., Farooq, J., Rehman, S., et al 2022. Integrated breeding approaches for the development of virus-resistant cotton genotypes. *Plant Breed. Rev.* 45(2): 112–130.

Iqbal, M.S., Javed, N., Raza, A. 2020. Resistance mechanism in cotton against whitefly and its associated virus diseases. *Plant Pathol. J.* 19(1): 12–21.

Kumar, R., Sharma, R.C., Singh, D., et al 2019. Evaluation of cotton genotypes for resistance against Cotton Leaf Curl Virus under field conditions. *Indian J. Agric. Sci.* 89(6): 1024–1030.

Kumar, R., Sharma, R.C., Singh, D., et al 2020. Evaluation of cotton genotypes for resistance against Cotton Leaf Curl Virus under field conditions. *Indian J. Agric. Sci.* 89(6): 1024–1030.

Mansoor, S., Briddon, R.W., Zafar, Y., et al 2006. Geminivirus disease complexes: An emerging threat. *Trends Plant Sci.* 11(5): 209-212.

Naveed, M., Saleem, M., Yasin, M. 2018. Morphological and biochemical defense mechanisms of cotton against whitefly. *J. Appl. Entomol.* 142(5): 457–466.

Rahman, M., Zafar, Y., Malik, T.A. 2019. Molecular markers for screening cotton genotypes resistant to Cotton Leaf Curl Virus. *Genet. Mol. Res.* 20(2): 1–12.

Saleem, M.Y., Hussain, M., Zafar, Y. 2020. Whitefly-mediated transmission of Cotton Leaf Curl Virus: Mechanisms and management. *Virol. J.* 17(1): 98–105.

Sattar, M.N., Kvarnheden, A., Saeed, M., et al 2013. Cotton Leaf Curl Disease – an emerging threat to cotton production worldwide. *J. Gen. Virol.* 94(4): 695-710.