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Performance of Different Cotton Genotypes under Different Infestation Levels of Whitefly Populations

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Cotton (Gossypium hirsutum L.) production is severely limited by biotic stresses such as whitefly (Bemisia tabaci) infestation and CLCuD. Seven cottons genotypes were evaluated under three levels of stress (Control, T1, and T2) in a factorial completely randomized design with three replications in April 2025, sown at Plant Pathology Research Institute, Ayub Agricultural Research Institute, Faisalabad, to study pests and disease dynamics, growth and yield components, as well as the relationship among important agronomic parameters. Adult whitefly densities and disease indices increased gradually from Control to T2 , while G6 was always the most susceptible and G3 the least. Growth indices followed similar trends, confirming an increase in pest and disease pressure severely compromising plant health. Similarly, plant height, bolls per plant, boll weight, and seed cotton yield decreased in whitefly treatments, with more reduction under T2. Correlation studies indicated strong negative relationships of adult whitefly populations and CLCuD incidence with growth characters, whereas bolls per plant, boll weight, and plant height were positively correlated with seed cotton yield. Seed index showed negative correlations with almost all the yield components and a positive correlation with disease incidence, revealing compensatory allocation under stress. ANOVA revealed that the causes of variation in yield-related traits were up to 80 % attributed to genetic differences, and disease expression was more affected by treatment factors. This indicated that the distribution of plant height was equally due to genetic and treatment (phenotypic plasticity) factors. These findings in general indicate that whitefly infestation, along with CLCuD have significant deterring effect on the growth and yield of cotton, as well as genotype variation for susceptibility and yield potential. These findings provide a practical foundation for cotton breeding programs by identifying stable, stress-tolerant genotypes and key selection traits that can be exploited to develop high-yielding cultivars with enhanced resistance to whitefly and CLCuD under biotic stress environments.

Keywords: Cotton, Whitefly, Leaf Curl Virus, Bemisia Tabaci, Disease Incidence, Yield

Introduction:

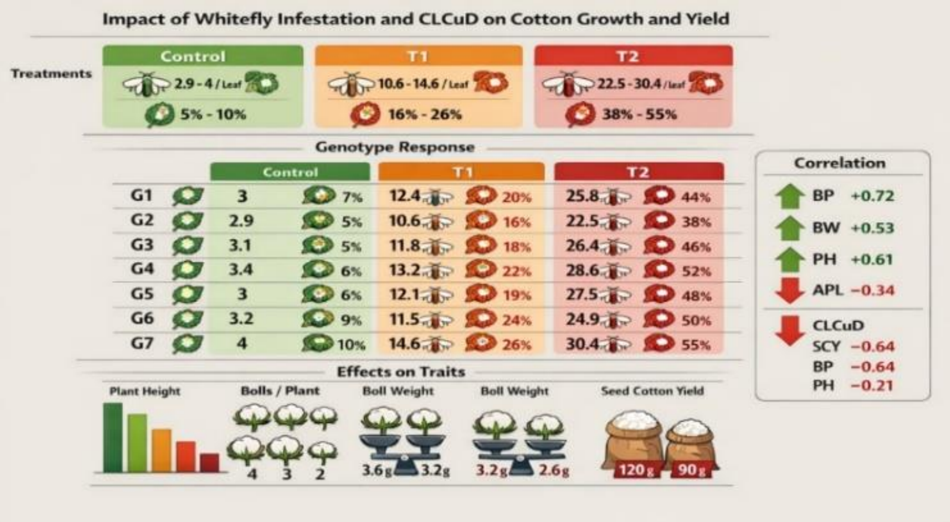
Cotton (Gossypium hirsutum L.), a leading fiber crop, is the backbone of the agricultural economy in most developing countries, including Pakistan, and it plays a vital role not only in providing employment but also in export earnings and industrial development. Though cotton is an economically important crop, its productivity is limited by various biotic stresses, including whitefly (Bemisia tabaci Genn.), which is a major devastating insect pest [1]. Damage to cotton plants by whiteflies is directly from phloem feeding and indirectly through the transmission of plant viruses, as well as by facilitating sooty mold emergence (through honeydew secretion), thereby decreasing the photosynthetic capacity and vigor of the plant [2].

The incidence of whitefly has increased during the last few years owing to changing climate variability, reckless application of insecticides, as well as resistance development against the commonly available chemicals [3][4]. This has contributed to severe infection levels, causing yield losses between 20% and more than 50% [5]. Intensive use of chemical control has enhanced the evolution of resistance and disturbed the natural enemy complex, thus intensifying the requirement for sustainable pest management approaches [6].

The novelty of this study lies in its integrated evaluation of whitefly population dynamics, CLCuD incidence, severity index, and yield-related traits across multiple stress levels (Control, T1, and T2) under field conditions. Unlike previous genotype screening studies that primarily focused on disease incidence or yield performance alone, this work simultaneously quantifies pest pressure, disease progression, and their direct physiological and agronomic consequences. Moreover, the combination of genotypes used for this study is itself novel because the genotypes are widely recommended as resistant, and at the present time, the varieties must be evaluated for their performance to ascertain whether they are performing as expected or not. So in 2025, the performance of these genotypes is itself a novel thing.

Host plant resistance is one of the most economical and environmentally friendly methods for whitefly control in cotton. Differences in morphological and biochemical traits among genotypes, such as leaf hairiness, wax content, and secondary metabolites, are key natural cues implicated in whitefly infestation and colonization [7][8]. The discovery of tolerance genotypes helps in minimizing reliance on insecticides and increasing the effectiveness of integrated pest management (IPM) programs [2].

Whitefly attack was found to significantly reduce the plant height, boll retention percentage, boll weight, and seed cotton yield [9][10]. The range of predisposition patterns is highly dependent on genotypes, and thus, it is important to perform such an evaluation on a promising genotype being attacked under various infestation levels.



	Control		T1		T2	
G1	3	7%	12.4	20%	25.8	44%
G2	2.9	5%	10.6	16%	22.5	38%
G3	3.1	5%	11.8	18%	26.4	46%
G4	3.4	6%	13.2	22%	28.6	52%
G5	3	6%	12.1	19%	27.5	48%
G6	3.2	9%	11.5	24%	24.9	50%
G7	4	10%	14.6	26%	30.4	55%

Figure 1. Graphical abstract showing the overview of the experimental layout and outcomes

Objectives:

To compare seven cotton genotypes in relation to whitefly infestation levels and

To quantify the response in terms of adult population density, severity index, and plant height, number of bolls per plant, average weight per boll, and seed cotton yield.

Materials and Methods:

Experimental Site:

The experiment was carried out in the cotton growing season on research fields of Plant Protection Research Institute (PPRI), Ayub Agricultural Research Institute (AARI), Faisalabad, Pakistan. Faisalabad is situated in the semi-arid subtropical climate of Pakistan and serves as an important cotton-growing area because of the history of repeated attacks of whitefly (Bemisia tabaci) and cotton leaf curl disease (CLCuD). The soil of the experimental area was typical alluvial loam with uniform fertility status, and standard agricultural practices recommended by AARI were used during the cropping season, except insecticides application as described elsewhere.

Plant Material:

Seven Gossypium hirsutum L. genotypes varying in insect-pest response and yield potential were chosen for the study. The selected genotypes represent commercially cultivated and advanced breeding lines commonly grown in the region, ensuring practical relevance and variability in resistance responses.

Table 1. Details of germplasm used in the experiment for checking the impact of whitefly population size on disease and growth-related parameters in cotton

Code	Name of genotype
G1	IUB-325
G2	CKC-3
G3	MNH-886
G4	IUB-313
G5	FH-938
G6	MNH-1050
G7	Hataf-3

G= genotype

Experimental Design and Treatments:

The experiment was arranged as a Factorial Completely Randomized Design (CRD) with three replications. Each experimental unit was a plot of uniform size containing one genotype to which treatments were assigned. The seeds were planted at a recommended space between hills of 75 cm with 30 cm between plants to obtain an equal plant density in each plot. Data were not collected on border plants to reduce edge effects. The parameters related to yield were obtained from such tagged plants (5 per treatment per replication).

Whitefly pressure: Three whitefly infestation levels were set up to test genotype behavior under different whitefly pressure: All genotypes received identical insecticide schedules to standardize chemical exposure, ensuring that differences in infestation levels were due to genetic responses rather than spray effects.

Low Whitefly Infestation (Protected Control):

Whitefly establishment was kept low by exclusion of whiteflies with an integrated system using a combination of physical and chemical barriers. During the early vegetative stage (up to 45 days after sowing), plots were protected with fine mesh insect-proof netting (40–50 mesh) that allowed entry of adult whitefly to be prevented. Post-net whitefly populations were kept below economic injury level (EIL) (≤5 adults/leaf) through targeted applications of neonicotinoid or insect growth regulator (IGR) chemistry based on weekly counts throughout the season. This treatment indicated very good (near the best) protection against whitefly infestation.

For observation recording, five plants per replication were randomly chosen and permanently marked for measurements of whitefly population, disease incidence and severity, growth-related parameters, full grown over time.

Moderate Whitefly Infestation (Threshold-Based Regulation):

Moderate infestation plots (Treatment 2) were maintained as unprotected and free for the natural entry of whiteflies. Applications of insecticides were delayed and minimized, and sprays were applied only when populations of whiteflies exceeded a predetermined threshold (10–15 adults per leaf). In this figure, one or two corrective sprays, during the growing season (with insecticides having short residual activity), were made to suppress population peaks without eradicating the pest. This method established continuous but intermediate levels of whitefly pressure during the crop season.

Treatment of Unprotected Stress--High Whitefly Incidence:

The high infestation treatments were not sprayed against sucking insect pests during the season, and had full exposure to whitefly populations. For improved uniformity of infestation, whitefly-infested cotton plants were regularly planted at the crop periphery during early and mid-season stages as a source of inoculum. By this means, the whitefly population pressure was maintained high (>20 adults per leaf) and continuous level, closely replicating severe field infestation.

Infestation Degree Monitoring and Validation:

Whitefly populations were examined weekly by counting adult whiteflies on the upper, middle, and lower leaves of five randomly selected plants in each plot. When statistically different population densities between treatments had been kept for at least 4 consecutive sampling dates, treatments were considered to be established for infestation levels. The average whitefly density per leaf was included as a covariate in the statistical analyses of treatment separation.

White fly infestation levels were kept within season by implementing differential pest procedures. Natural whitefly populations were used, as per the Faisalabad situation, where there was constant whitefly pressure.

Crop Husbandry:

Nursery seeds were sown at the recommended spacing, and thinning was regularly done to ensure a uniform plant population. The general cultural management practices, such as irrigation, fertilization, and weed control, were similar in all plots. No insecticides for whitefly control were used in high-infestation treatment; specific insecticides against it were applied at low and moderate levels there.

Data Collection:

Whitefly Population (Adults leaf^{-1}):

Weekly counts of whitefly (Bemisia tabaci) population were taken from 30 days after sowing up to boll maturation. Adult whiteflies were recorded early in the morning hours to reduce insect activity. Five random plants per plot were selected for data collection. One leaf from the upper, center, and lower canopy parts was collected from each plant , and the number of adult WF on the abaxial surface of the leaves was calculated by visual count. The average number of adults per leaf was figured out and referred to as adults leaf^{-1}.

Cotton Leaf Curl Disease (CLCuD) Incidence (%):

Incidence data of CLCuD were taken during its peak disease expression (i.e., between the flowering and boll formation). The number of plants and the number of visibly infected plants per plot were recorded. Disease occurrence was quantified following the equation:

$$\text{CLCuD incidence (\%)} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

The presence of leaf curling, vein thickening, enations, and stunting was used as the characteristic symptoms for recording infection in plants.

CLCuD Severity Index (0–5):

Disease severity was assessed visually on the same plants used for incidence assessment using a standard 0–5 rating scale, where:

0 = No visible symptoms
1 = Mild vein thickening, no curling
2 = Moderate vein thickening with slight leaf curling
3 = Severe leaf curling with prominent vein thickening
4 = Severe curling with enations and partial plant stunting
5 = Extreme symptoms with severe stunting and boll reduction

The disease severity index for each plot was calculated by averaging the severity scores of the assessed plants.

Plant Height (cm):

The plants were measured for height at physiological maturity. Five plants were randomly selected per plot, and height was measured from the ground surface to the growing point terminal with measuring tape. The scores for average height were announced in centimeters (cm).

Number of Bolls per Plant:

The sum of mature and harvestable bolls at maturity, from the same five plants chosen for plant height measurement, was recorded. The average number of bolls per plant was computed and noted.

Boll Weight (g):

Boll weight was calculated by harvesting 20 mature bolls per plot at random. The bolls were sun-dried, weighed with the help of an electronic balance, and the average boll weight (g) was calculated by dividing the total boll weight by the number of bolls. Results were presented in grams (g).

Seed Cotton Yield (g):

The seed cotton yield was measured in grams per plant at maturity. The sun-dried harvested seed cotton was weighed, the yield of the plot was recorded in grams, and average data were calculated for analysis.

Statistical Analysis:

The data were analyzed using the analysis of variance (ANOVA) for a completely randomized design (CRD) to test the following: genotype, population level of white fly infestation, and their interaction by Statistix 8.1. Pearson correlation was carried out to investigate relationships among whitefly population, disease incidence, and some bio-agronomic traits using Statistix 8.1. Correlograms were generated in R.

Results and Discussion:

Adults Per Leaf:

The mean adult whitefly population per leaf varied notably among the seven genotypes and across the three treatments. In the control condition, all genotypes exhibited low whitefly counts, ranging from 2.9 to 4 adults per leaf. G6 recorded the highest mean population (4 adults' leaf^{-1}), whereas G3 showed the lowest population (2.9 adults' leaf^{-1}). This indicated that under untreated conditions, the genotypes supported relatively minimal whitefly infestation, with minor variability among them.

Under T1 treatment, the adult whitefly populations increased substantially across all genotypes compared to the control. The mean populations ranged from 10.6 to 14.6 adults per leaf, with G6 again exhibiting the highest infestation (14.6 adults' leaf^{-1}) and G3 the lowest (10.6 adults' leaf^{-1}). This trend suggested that T1 conditions favored whitefly multiplication, and the genotypic differences became more pronounced under this treatment. In the T2 treatment, the adult whitefly counts further escalated, indicating a strong response of the pest to the more favorable conditions. The populations ranged from 22.5 to 30.4 adults per leaf. G6 maintained the highest mean population (30.4 adults' leaf^{-1}), followed closely by G4 (28.6 adults' leaf^{-1}), whereas G3 consistently had the lowest population (22.5 adults' leaf^{-1}). These results demonstrated that whitefly infestation intensified under T2, with some genotypes, particularly G6 and G4, being highly susceptible, while G3 remained comparatively less infested.

Disease Incidence:

The percentage disease incidence differed significantly between genotypes and treatments. In the control treatments, disease incidence (per genotype) was overall low and comprised 5–10%. The maximum number of diseases was recorded in G6 (10%) and the minimum in G3 (5%), followed by G4 (9%). The pattern suggested that disease pressure was low when not treated with PCs, and there was little genotypic variation.

All genotypes showed a significantly higher disease incidence (%) compared to the control when treated with T1. The prevalence estimates varied between 16% and 26%. Once more, the highest disease occurrence was observed in G6 (26%), which was followed by G4 (24%) and G2 (22%), whereas G3 contained the lowest incidence levels of disease (16%). This showed that T1 symptoms favored disease development and indicated that there were noticeable differences in genotypic susceptibility. The greatest incidence of disease was observed in T2 treatment, with all genotypes showing a remarkable rise in the level of infection. The prevalence of disease was between 38% and 55%. G6 demonstrated the highest incidence (55%), followed by G4 (52%), and after G2 (48%); G3 still presented the lowest incidence of them (38%). This fashion suggested that T2 generated a permissive environment of disease development, provoking strong infection in all genotypes Figure 2.

Severity Index:

The index of severity increases proportionally from Control to T2 treatments, which indicates that the attack of whitefly develops progressively throughout the sampling days. Severity values are low (0.7–1.2) for the Under Control conditions, indicative of low pest pressure and a relatively good plant stand. Significantly, the severity indices are 'moderate' (1.9–2.8) for T1 treatment, indicating some level of noticeable increase in whitefly infestation. This means that plants are no longer under only mild stress, and differences in sensitivity can be increasingly observed. The Maximum Severity (MS) under

T2 (3.6–4.7) stands extremely high , indicating heavy whitefly infestation. This steepening curve shows that high pest pressure greatly reduces plant health.

Plant Height:

A decreasing pattern in plant height was maintained between the Control and T2 treatments at all observations. In Plants grown under Control, the plants that reached their maximum height (128–140 cm) were supposed to be of optimal growth status without stress. In T1, a significant reduction in plant height (122–132 cm) was registered, suggesting that treatment began to restrict vegetative development. This decrease indicated the partial inhibition of growth by escalating stress. The least plant height was observed for T2 (110–120 cm), and the results showed that severe stress restrained the elongation of plants and dry matter production (Figure 2).

Bolls Per Plant:

The number of bolls per plant decreased gradually from Control to T2 for all genotypes. More bolls per plant (30–36) were observed Under Control conditions, indicating good growth and reproductive performance. In T1, a slight reduction in bolls per plant was also noticed (26–31) as the stress started to detrimental influence on boll formation. The lowest boll figures were detected under T2 (19–24), which was indicative of the considerable decrease in reproductive potential that occurred under severe stress (Figure 2).

Boll Weight:

Boll weight presented a progressive reduction from Control to T2 in the other observations. Higher boll weights (3.3–3.7 g) were observed under Control conditions, suggesting integrated assimilate partitioning and favorable growth conditions. In T1, a slight decrease in boll weight (3.0-3.4 g) was noticed, indicating that the stress started to restrict dry matter accumulation in bolls. Boll weights were lowest under T2 (2.5–2.9 g), and severe stress indicated a significant impact on boll development and filling (Figure 2).

Seed Cotton Yield:

Seed cotton yield significantly decreased with an increase in both irrigation and fertilization levels from Control to T2, no matter at which observation point. Productivity: Higher yields (99.0–133.2 g) were obtained under Control conditions, reflecting the best growth and productivity achieved (fig 2). In T1, a significant reduction of yield (78.0–105.4 g) indicated that moderate stress unfavorably affected boll retention and biomass accumulation.

Minimum seed cotton yield was observed in treatment T2 (47.5–69.6 g), as the most extreme level of stress caused a significant decline in yield (Figure 2).

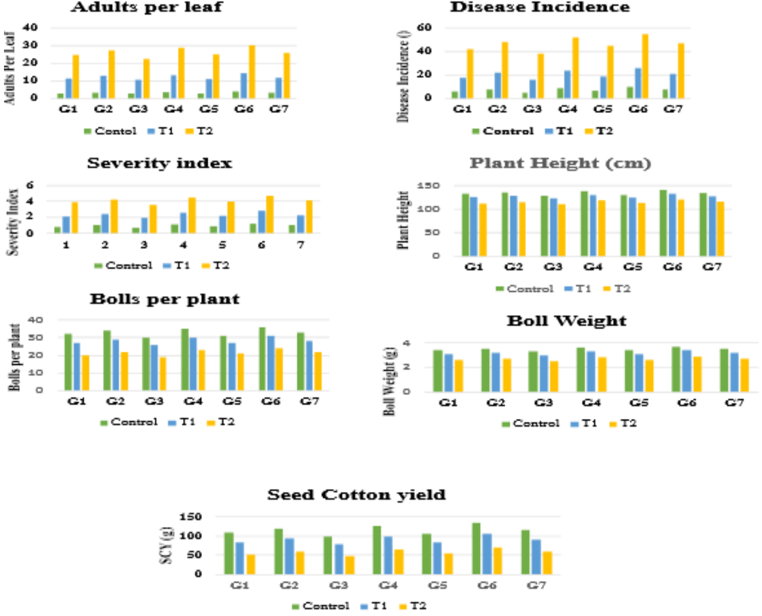


Figure 2. Graphical representation of the studied parameters in the experiment

Correlation Analysis:

Correlation study revealed statistically significant and biologically plausible relationships between the characters studied. APL exhibited strong to moderate negative correlation coefficients with BP (r = −0.88); BW (r = −0.87); PH (r = −0.85), and SCY (r = −0.34), indicating that the highest APL has a relationship with low plant vigor and productivity. The trend suggested that lift red weight, number of plants/m2, and rep handling options NPK corresponding to higher pest attack and disease per cent were suppressive growth characters and yield components.

BP had a positive high correlation with SCY (r = 0.72) and low to moderate with BW (r = 0.60) and PH (r = 0.50), which means that it is an important trait for yield potential. The negative correlation of BP to CLCuD (–0.64) indicated the disease pressure as corresponding to suppression in boll setting and therefore yield reductions. In parallel, BW had a significant positive correlation with SCY (r = 0.53), suggesting that heavier bolls significantly contributed towards ultimate yield, and a weak negative correlation with CLCuD, which indicated somewhat lesser but still damaging effect of the disease on boll development.

The negative associations of CLCuD with SCY (r = −0.64) and BP (r = −0.64), respectively, suggest the negative effect of this disease on yield per se and one of its components. For PH, the weak negative correlation (r = −0.21) suggests that disease incidence restricted somewhat vegetative growth and exerted a stronger effect on the reproductive characters. PH expressed positive SCA with SCY (r = 0.61), which showed that the taller plants gave higher yield potential, and yielded a strong negative correlation with SI (r = −0.82), suggesting a balance between vegetative and seed traits (Table 2).

Table 2. Correlation matrix of studied disease and growth parameters for whitefly infestation in cotton

	APL	BP	BW	CLCuD	PH	SI
BP	-0.88					
BW	-0.87	0.60				
CLCuD	0.01	-0.64	-0.24			
PH	-0.85	0.50	0.20	-0.21		
SI	0.50	-0.55	-0.45	0.59	-0.82	
SCY	-0.34	0.72	0.53	-0.64	0.61	-0.42

Analysis of Variance:

Analysis of variance revealed highly significant ($p < 0.01$) effects of both genotype (G) and treatment (T) on all studied traits. For bolls per plant (BP), treatment mean sum of squares (MSS = 230.90) was substantially higher than genotype (MSS = 10.49), indicating a stronger treatment influence. Adult population per leaf (APL) and CLCuD incidence also showed markedly higher MSS values for treatments (940.28 and 2773.48, respectively) compared to genotypes, demonstrating that pest pressure and disease expression were predominantly governed by treatment conditions. Plant height (PH) exhibited extremely high treatment MSS (35201.4) relative to genotype (12.4), confirming strong environmental sensitivity. Similarly, seed index (SI) and seed cotton yield (SCY) showed higher treatment MSS than genotype, though both sources of variation remained significant. Boll weight (BW) also responded significantly to both factors, with treatment effects exceeding genetic effects. The genotype × treatment interaction was highly significant for all traits, indicating that genotypes responded differently across treatments. Strong interaction effects were observed for seed cotton yield, plant height, and CLCuD incidence, followed by adult whitefly population and seed index. Moderate interactions were noted for bolls per plant, while boll weight showed comparatively lower but significant interaction.

Table 3. Analysis of variance of the studied parameters for whitefly infestation in cotton

Character	MSS (G)	MSS (T)	MSS (G xT)
BP	10.49**	230.90**	20.90**
APL	6.41**	940.28**	94.58**
BW	0.05**	1.14**	6.34**
CLCuD	39.94**	2773.48**	273.58**
PH	12.4**	35201.4**	301.43**
SI	41.429**	646.33**	66.34**
SCY	51.1**	3421.1**	341.12**

BP= bolls per plant, BW=boll weight, CLCuD= cotton leaf curl disease incidence, PH=plant height, SI=Susceptibility index, SCY=Seed cotton yield

Discussion:

The gradual rise in adult whitefly numbers from Control to T2 showed that treatment factors impacted pest multiplication. These are typical tendencies that have also been reported elsewhere, in which favorable microclimatic conditions and host preference led to increased levels of whitefly reproduction and survival [5]. The relatively higher population in G6 and G4 revealed their susceptibility, whereas the lower one in G3 denoted the least tolerance. Whitefly resistance at the genotypic level has been linked to morphological factors such as leaf pubescence, wax content, and biochemical defenses that affect insect feeding and oviposition [7].

The index of severity mirrored the pattern of whitefly population, and significantly increased from Control to T2. This supported a direct correlation between pest infestation level and damage severity, as previously observed for cotton and other crops [2]. Severe plants (T2) had longer feeding-damage, honeydew excretion, and sooty mold infestation that affects photosynthetic intensity and plant vigor [5]. The least magnitude of severity incidence in G3 further confirmed its resistance nature, which is also affirmed by a similar study, and showed that resistant genotypes suffered less damage, even at a higher intensity of pest load [8].

Plant height decreased from the Control to T2, which indicated that a heavy infestation of whitefly had caused physiological stress. Under stress, shorter plant height has been associated with hindrance in photosynthesis and nutrient movement, together with unbalancing of hormone content due to continuous extraction of sap [10]. This decrease in non-reproductive growth and its effect on reproductive success.

The number of bolls per plant and the weight of bolls were considerably decreased as infestation pressure intensified. These decreases may be due to a higher degree of boll shed, decreased assimilate supply, and alterations in source–sink relations resulting from whitefly feeding. Heavy whitefly population has been found to cause impermanent boll retention and reduced boll size, resulting in significant yield losses according to previous studies.

The highest decrease in seed cotton yield was observed from the Control to T2, indicating an increasing effect of whitefly injury on cotton productivity. The whitefly has been reported to reduce yield by 20–50%, and the loss depends on the prevalence of infestation and the susceptibility of specific genotypes. Relatively good performance of G3 under stress suggested its stable yield and possible suitability for resistance breeding.

All in all, the correlation of whitefly population with severity index and yield-related traits mainly verified that the insect pressure is a major factor determining cotton yield. The constant susceptibility of G6 and tolerance in G3 underlined the necessity to prioritize genetic resistance as a sustainable control measure. Combining biotic resistance with integrated pest management (IPM) can provide substantial reductions in pesticide use and contribute to crop resilience.

The associations reported in this study represented a combined effect of growth, yield components, and biotic stress under field conditions. The significant positive correlation of BP, BW, and PH with SCY indicated that the yield formation in cotton mainly depended on reproductive sink strength, which was favored by vigorous vegetative growth. Similar relationships have been broadly reported in literature and bolls number and weight were most significant contributors to yield variation contributing through their major contribution directly through assimilate partitioning towards economic yield [11]. Positive correlation of PH with SCY illustrated that the moderate plant height contributed to the photosynthetic organs for boll development.

Nevertheless, the relatively significant associations of APL and CLCuD with BP, PH, and SCY clearly demonstrated that the impacts on cotton yield were suppressed by insect pressure and virus disease. The high disease incidence and the lesser vector population brought about reduced effective leaf area, photosynthesis, and assimilate translocation , contributing towards less boll retention and low yield [12]. The high negative correlation of CLCuD was found with SCY in the present study, which also supports the previous findings that "CLCuD" is one of the most yield depressed factor under South Asian cotton growing conditions.

The negative association of SI with PH, BP, and SCY can suggest a compensatory response as a result of stressed conditions, limiting assimilates used to speed up seed size at the expense of seed number and over-yielding. Trade-offs between seed index and yield components have been documented in cotton as well as other crops, particularly under biotic or abiotic stress that altered carbon allocation [13]. Overall, such results can be further evidence that a combination of high-yielding components and good resistance to pest and disease pressure would be essential in order to achieve effective yield improvement under field conditions.

ANOVA indicated significant genetic and treatment effects on trait variation. MSS G was substantially greater than MSS T for BP and BW, indicating that genetic differences among genotypes played a preponderant role in variation between the two traits. This finding was in agreement with the report of various researchers working on cotton that yield component traits (boll number and boll weight) generally could be genetically more variable than the effect due to environmental or treatment, and hence it can be a reliable selection criterion in breeding programs. In all these studies, high genotypic variance for yield and its components is considered as a prerequisite for successful genetic improvements [14].

G3 can be practically utilized as a donor parent in breeding programs to introgress whitefly and CLCuD tolerance into high-yielding but susceptible cultivars through conventional or marker-assisted selection. Under farmer field conditions, G3 may also be deployed directly as a tolerant variety in endemic areas, where its stable performance can reduce pest pressure and reliance on insecticides. Integration of G3 with IPM strategies, including early monitoring and targeted sprays, will further enhance field-level disease suppression and yield stability.

On the other hand, disease expression due to genetic differences among genotypes was not more significant than that due to treatment (pathogen pressure, inoculation level, or environmental stress) factors for CLCuD, as it showed a much higher MSS T/MSS G ratio. This direction was consistent with the general knowledge of crop physiology in which the degree of disease severity and expression of stress responses were largely affected by environmental and management practices [15].[16]

Recommendations:

Genotype G3 should be prioritized in breeding programs due to its consistent tolerance to whitefly and CLCuD, while G6 may be used as a susceptible check. Selection should emphasize bolls per plant and boll weight as key yield determinants, alongside integrated pest management to limit disease spread.

Conclusions:

Whitefly infestation and CLCuD significantly reduce cotton growth and yield, with G6 being most susceptible and G3 most tolerant. Yield traits are largely genetically determined, while disease severity is treatment-dependent. Selection of genotypes combining strong yield potential and pest–disease resistance is essential for effective cotton breeding under biotic stress.

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