



### Research Article

## GENETIC DIVERSITY AMONG COTTON (*GOSSYPIMUM HIRSUTUM* L.) GERMPLASM FOR YIELD AND FIBRE TRAITS UNDER ARID CLIMATIC CONDITION

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### Abstract

Climate change has drastically affected the performance of several agricultural crops. Cotton is an important fibre crop which is severely influenced by the climate change in recent years. Presence of genetic variability among germplasm is a key source for selecting the genotypes that are more adapted to the agro-climatic conditions with respect to yield and fibre related traits. For this purpose, 180 cotton genotypes were sown under augmented design with recommended management practices. Data for the morphological, yield and fibre traits viz plant height (PH), CLCuD(%), bolls per plant, boll weight (g), yield/plant (g), GOT (%), staple length (mm), mike (ug/inch), staple strength (g/tex) were recorded and analysed. The results of variance analysis revealed that significant variability was observed among genotypes for all the traits under study. PCA biplot showed that 26% variability was observed in PC1 and 15.5% in PC2. Genotypes no. 30 was found with distant yield and fibre characteristics. Through cluster analysis, total 180 cotton genotypes were grouped into nine different clusters. Group 7 and group 8 consist of 15 and 03 genotypes respectively. Genotypes among these two groups represent the higher CLCuD resistance, maximum yield per plant with better fibre traits. Phenotypic evaluation of cotton genotypes for different morphological, yield and fibre traits provide the basis for exploitation of best performing genotypes in the future breeding programme.

**Keywords:** Genetic diversity, CLCuD, yield components, fibre traits, *Gossypium hirsutum* L.

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### 1. INTRODUCTION

Crop productivity is threatened by climate change; improving yields under changing climate scenarios is crucial. Global climate change i.e., increase in temperature and shortage of water have drastically reduces the plants eco-physiological performance (Gul, 2022). Cotton, the most ancient, cultivated crop gives the most suitable fibre for human. To increase yield with improved fibre quality while retaining other key agronomic traits, there is a need for cotton

researchers to develop innovative ideas. So, development of cotton breeds with sustained economic performance is utmost necessity of the country (Iqbal, 2020a).

A systematic utilization of genetic diversity is necessary to minimize the drastic ecological consequences of global climatic changes. Cotton is believed to have a high level of genetic variability that enhances its ability to adapt to harmful environmental changes. Use of closely related genotypes in hybridization programme is the reason for narrow genetic base (Esbroeck, 1999).



The morphological variation in consequent of genomic variation and eco-expressional variation of genes is a key aspect of biological evolution and breeding strategies of a crop. Morphological variation is first-hand information of a breed for identification. It can be used for accessing the genetic diversity. It is most important for plant breeders to select diverse parents for hybridization to achieve better yield under stress conditions (Zafar, 2021; Nasir *et al.*, 2021). A major constraint to cotton production in Pakistan is cotton leaf curl virus disease (CLCuD). It first appears in 1967 and there was an epidemic of CLCuD in 1992-93, which lowered Pakistan's harvest from 9.05 million bales to 8.04 million bales. (Saeed, 2014). Also, Breeders aim to improve the fibre quality of upland cotton, but selecting traits accurately is quite difficult. Fibre quality is a complex quantitative trait under the control of multiple genes and highly dependent on environmental conditions (Sun, 2017). Crop traits should be improved by exploiting genetic divergence between genotypes through morphological characteristics, as morphological characteristics are highly influenced by environmental factors (Manan, 2022). Therefore, genetic diversity may be exploited to develop climate resilient cotton varieties with high CLCuD-resistance having superior yield and fiber quality. To cope with the ranked genetic erosion of cotton due to global climate change, a

recent study of genetic diversity was necessary for smart breeding strategy. For this purpose, gene pool of 180 cotton genotypes with different origins was characterized with objective to evaluate the better performing cotton genotypes for CLCuD, fibre, yield and yield components.

## 2. MATERIALS AND METHODS

A total of 180 cotton genotypes were planted in the research area of Cotton Research institute (CRI), Multan, Pakistan located at 30.015° latitude, 71.44° longitude and 189 m elevation from sea level and having dry semiarid agro-climatic weather conditions. Plot was maintained at 200 sq.ft with P × P distance 30cm and R × R at 75cm under augmented design. Recommended agronomic management practices for cotton were applied as described in the Cotton Calendar Guide by CRI, Multan, 2021([https://www.agripunjab.gov.pk/campaign\\_cotton2020-21](https://www.agripunjab.gov.pk/campaign_cotton2020-21)).

## 3. Data collection

Data of five guarded plants from three randomly selected locations in the plot were recorded for CLCuD (%), Plant height (cm), plant yield (g) and yield components (no. of bolls/plant, boll weight (g) along with GOT% and fibre traits (Staple length, staple strength and micronaire value). Fibre traits were analysed on Uster HVI Spectrum 1, at Fibre testing lab, CRI, Multan. Scoring of CLCuD was done as described by

**Table 1. Grading for CLCuD.**

Disease index (%)	Severity grade	Symptoms	Remarks
0	0	Asymptomatic	Resistant
1-20	1	Thickening of primary veins	Highly tolerant
21-30	2	Thickening of secondary and tertiary veins	Tolerant
31-50	3	Vein thickening, leaf curling or enation or both.	Susceptible
>50	4	Stunting along with vein thickening, leaf curling/enation	Highly susceptible

The average disease rating grade (ADRG) was calculated by using the formula:

ADRG= Sum of all disease rating grades ÷ Total number of plants, and percent disease intensity (PDI) was calculated for each entry/plot by using the following formula: PDI=(Average disease rating÷Maximum disease rating grade)×100

Nazeer, 2014 given in the following Table 1.

#### 4. Statistical analysis

Analysis of variance was performed to check the significant differences of traits. To check the performance of genotypes, similarities and difference among genotypes, biplots and hierarchical clustering were done by using R software. Association among studied traits were assessed by correlation analysis (Package cor and corplot in R) (Merriam, 2022).

#### 5. RESULTS

The analysis of variance showed the significant difference for morphological, yield and fibre traits among 180 genotypes presented in Table 2. To check the performance of these genotypes, biplot was constructed and variation indicated by PC1 (26%) and PC2 (15.5%) for morphological, yield and fibre traits (Figure 1). Biplot analysis showed strong positive association between TNB, YPP and PH while negative associated with CLCuD. Similarly, SL and SS were also strongly associated but negatively with GOT and M. Strongly associated traits were showed less angle among corresponding lines while angle more than 90 ° had strong negative

SS while contrasting genotypes were 39 and 56 but they performed best for GOT and M. Similarly, genotype 14 revealed high score for CLCuD but the contrasting genotypes for that trait were 72, 77, 32 and 35 (Figure 1).

Cluster analysis was used for the classification of genotypes based on their similarities and differences (Fig. 2a). Cluster analysis classified the genotypes into 9 different groups shown in Fig 2a. Mean value for each trait of different groups is presented in Fig. 2b. Group 7 and 8 consisted of 15 and 3 number of genotypes, respectively, that performed best for yield per plant (> 80 g), total number of bolls (> 30) staple length (> 26.5 mm) and staple strength (> 30 g/tax). Group 8 also showed less susceptibility (< 40 %) to cotton leaf curl disease. Similarly, group 1 and 3 consisted of 61 genotypes that performed outstanding for GOT (> 41 %). Information related to association will help in the improvement of the desired trait during selection procedure. Corplot (Figure 3) revealed that YPP was found significant and exhibited positive correlation with PH, TNB, BW, SL and SS while negative association with CLCuD. Similarly, PH and TNB were also positively correlated with TNB and SS. Among fibre traits, GOT was

**Table 2: Mean square of morphological, yield and fibre traits of 180 cotton genotypes grown under normal condition for the year 2021.**

Source of Variation	DF	CLCuD (%)	PH (cm)	TNB	BW (g)	Y/P (g)	GOT (%)	SL (mm)	M (ug/inch)	SS (g/tax)
Block	5	1470	1593.3	170.4	2.27	651.01	73.5	20.8	0.32	8.51
Treatment	183	1972.51	393.2 ***	118.5 ***	0.63 ***	885.2 ***	15.6 **	8.08 ***	0.28 ***	7.30 ***
Control	3	24.71	274.08 *	65.3 **	0.58 ***	76.5 *	2.6 *	2.71*	0.22 **	1.53*
Control + Control Vs Block	180	2004.9	395.2 ***	119.4 ***	0.64 ***	898.7 ***	15.8 ***	8.17 ***	0.28 ***	7.3 ***
Residuals		8.78	5.9	11.4	0.03	2.4	1.4	0.78	0.03	0.5

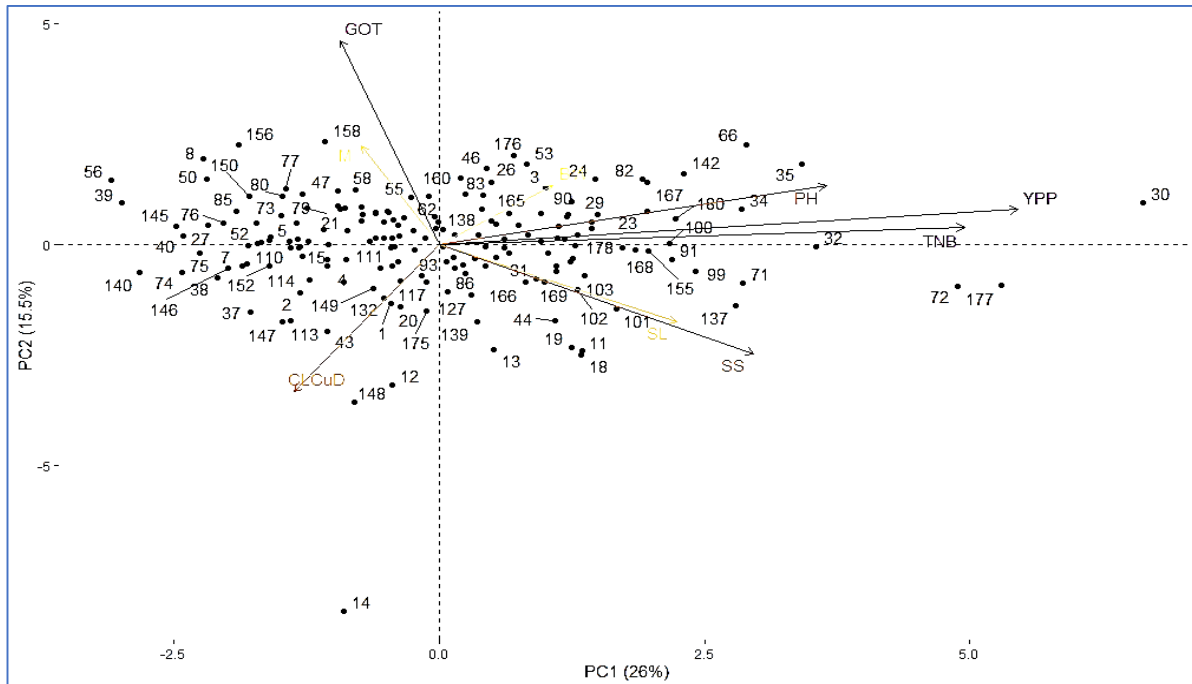
\*, \*\*, \*\*\* indicates significant differences at  $p \leq 0.05$ ,  $p \leq 0.01$ ,  $p \leq 0.001$  and (NS) indicates non-significant. Degree of freedom (DF), Cotton leaf Curl disease (CLCuD), Plant height (PH), Total no. of bolls (TNB), Yield per plant (Y/P), Ginning out turn (GOT), Staple length (SL), Mike (M), Staple strength (SS).

association. Less variation was found for BW and M due smaller length of the corresponding lines. Genotypes 72 and 77 performed best for TNB, YPP, PH, SL and

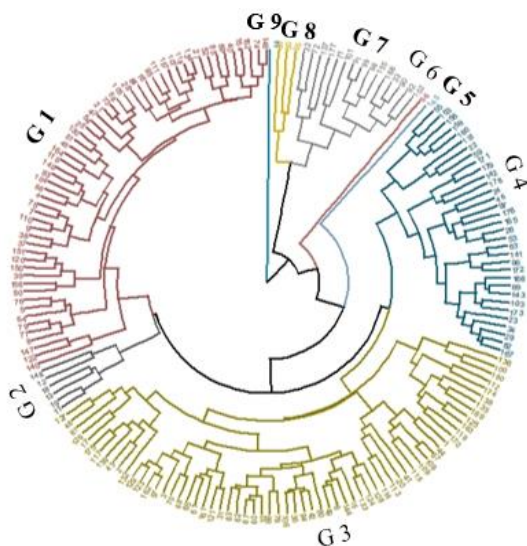
positive and significantly correlated with SS while negatively with M. Similarly, SL was positively correlated with SS and

negatively with M. It showed the increase in SL and SS with increase in GOT%.

2022). Seed cotton yield in cotton is mainly affected by the potential of genotype and climatic factors such as biotic and abiotic



**Figure 1.** Biplot analysis of cotton leaf curl disease (CLCuD), morphological i.e. Plant Height (PH), Total Number of Bolls (TNB), Boll Weight (BW), Yield Per Plant (YPP) and fibre traits i.e. Ginning Out Turn (GOT), Staple Length (SL), Mike (M) and Staple Strength (SS) among 180 cotton genotypes. Length of the arrows shows the extend of variation for the respective traits.



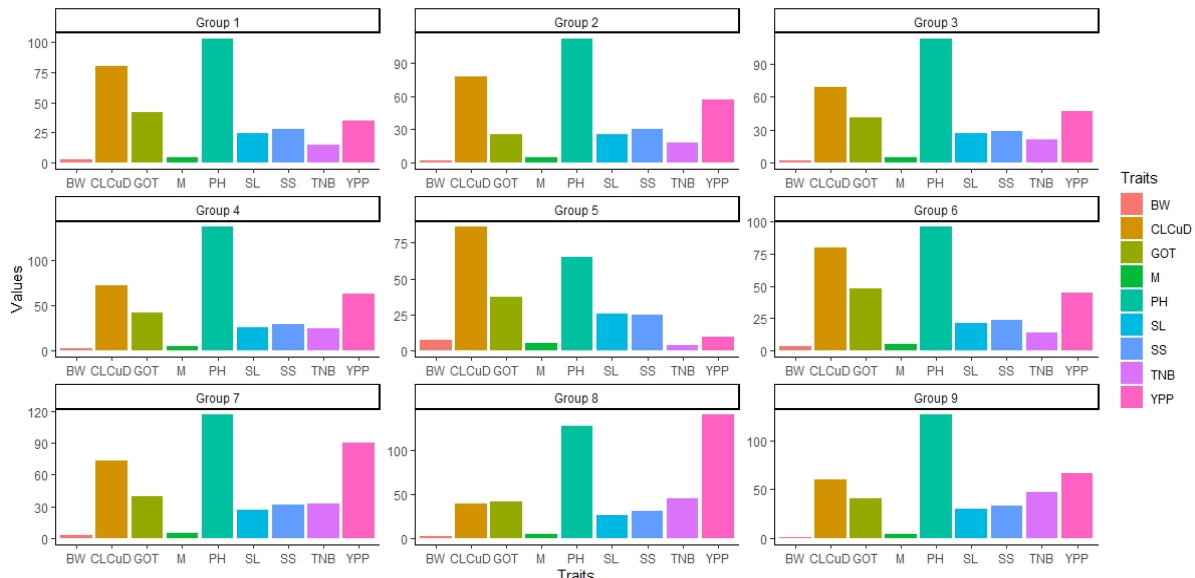
**Figure 2a.** Cluster analysis among 180 genotypes grown under field conditions. Colour shows the classification of the groups 1 to 9

## 6. DISCUSSION

The assessment of genetic diversity and the test of varietal distinctness are traditionally done through morphological traits (Kumar,

stresses and planting time (Farid, 2017). In the current study, 180 cotton genotypes were studied for different morphological, yield and fibre traits. Normal distribution of the traits estimated by Shapiro–Wilk test and that same method was used in barley (Jamil, 2020). Significant variation was present among the genotypes for all the traits as presented in Table 1. These results are in accordance with the Ekinçi, 2017.

In case of biplot analysis, genotypes near the vectors were considered poor performers, whereas genotypes at the opposite end were considered best performers for that specific trait (Hakeem, 2021). For example, genotype 30, 72 and 177 were far from the origin vector and found best for total number of bolls, plant yield and fibre traits while on the other hand genotype 39 and 56 were poor for these specific traits but high for ginning out turn

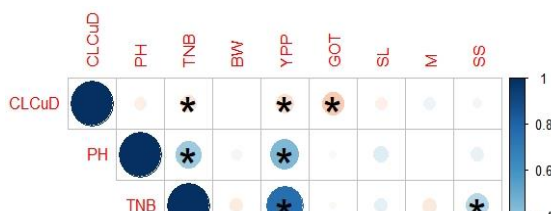


**Figure. 2b.** Visualization of mean values of each group obtained through cluster analysis. Traits are cotton leaf curl disease (CLCuD), morphological i.e. Plant Height (PH), Total Number of Bolls (TNB), Boll Weight (BW), Yield Per Plant (YPP) and fibre traits i.e. Ginning out turn (GOT), Staple Length (SL), Mike (M) and Staple Strength (SS)

and micronaire as presented in Fig.1. Also, genotype 14 was poor for the CLCuD resistance due to high scoring while genotype 72 and 77 showed high resistance against CLCuD. Genotypes that are present far from the origin are better performing for that specific trait and may be selected and considered more variant from breeding point of view. (Aziz, 2018). In order to cope with biotic and abiotic stresses, genotypes must have genetically superior qualitative and quantitative characteristics (Bakhtawar *et al.*, 2015). The purpose of cluster analysis is to group the genotypes that belong to the closely related traits (Spasova,

2016). Nine different groups can be seen among 180 cotton genotypes as presented in fig. 2a. Group 7 and 8 consisted of the genotypes that perform best for the total no. of bolls, yield per plant, fibre length and fibre strength. Genotypes from this group can be selected for the utilization in future breeding programme for these traits. Similarly, group 7 reflects the genotypes with low susceptibility to CLCuD. Wide range of mean values for different traits that was grouped differentially can be observed in Fig.2b. Different grouping of cotton genotypes for different traits was also reported by Cetin and Guvercin, 2022.

The association of the traits revealed the positive correlation of plant yield with plant height, total no. of bolls, boll weight, staple length and staple strength as presented in Fig.3. While negation association of plant yield was observed in case of CLCuD. Positive correlation of seed cotton yield with fibre yield and fibre fines was observed by Mawblei, 2022. Whereas negative association of plant yield with fibre strength was described by Chapepa, 2020. In a study, positive association of fibre yield was observed with plant yield and fibre fineness (Saeed, 2014). Thus, genotypes with better yield and fibre traits



**Figure 3.** Corplot of correlation among cotton leaf curl disease (CLCuD), morphological i.e. Plant Height (PH), Total Number of Bolls (TNB), Boll Weight (BW), Yield Per Plant (YPP) and fibre traits i.e. Ginning out turn (GOT), Staple Length (SL), Mike (M) and Staple Strength (SS) among 180 cotton genotypes. Blue colour for positive correlation and pink for negative, size of the circle show the magnitude of correlation. \* indicates significant ( $P < 0.05$ ) and without sign (\*) indicates non-significant ( $P \geq 0.05$ ).

with high CLCuD resistance can be bred to obtain the cotton ideotype with biotic and abiotic stress tolerance. Breeding programs rely on genetic diversity to overcome unexpected effects due to climatic changes on crops. Furthermore, evaluation and classification of genotypes through PCA biplot and cluster analysis provides better understanding for the development of climate smart cotton genotypes with crop yield improvement.

## 7. CONCLUSIONS

Massive use of selective cotton cultivars of narrow genetic base over the years have led towards the inbreeding depression. Cotton breeding is critically dependent on genetic variability under changing climatic conditions. Proper evaluation of variability and finding more diverse/distant genotypes is the solution to enhance the performance of breeding programme. In our study, genotype 30, 72 and 177 were found more distant for the yield and fibre traits and preferable for hybridization programme.

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