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Original Research Article

IMPACT OF HEAT STRESS ON AGRO-MORPHOMETRIC AND FIBERRELATED TRAITS IN INDIGENOUS UPLAND COTTON GENOTYPES UNDER SEMI-ARID CONDITIONS

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Abstract: *To understand the impact of heat stress on agro-morphological and fiber quality-related traits in cotton, nine locally developed cotton genotypes were grown under heat stress conditions (Late sowing) at the cotton research station, Bahawalpur. Genotypes were laid-out under randomized complete block design (RCBD) in triplicates, where plant to plant and bed to bed distance was maintained as 30 cm and 75 cm, respectively. Data was collected from selected, guarded plants for agronomic as well as fiber quality-related traits. The results unveiled the presence of significant variations for studied traits under high temperature conditions. The correlation analysis revealed the significant association of seed cotton yield with plant population (0.403**), monopodial branches per plant (0.267**), fiber strength (0.070*), CLCuV incidence percentage (-0.475**), fiber length (-0.447**), nodes per plant (-0.186*), sympodial branches per plant (-0.186*), and fiber fineness (-0.077*). The multivariate approaches i.e., Principal component, biplot, and cluster analysis classify and characterize cotton genotypes on the basis of their heat tolerance capacity. Moreover, these multivariate analyses showed that BH-377, BH-272, and BH-283 were the most heat tolerant genotypes while BH-283 and BH-284 showed comparatively good CLCuV tolerance. Therefore, these genotypes should be recommended for sowing in heat and CLCuV affected areas of Pakistan after their large-scale, multilocation testing.*

Keywords: CLCuV tolerance, high temperature, correlation, multivariate testing

Introduction

Cotton, the white gold, is one of the most significant cash crops world due to its diverse utilization in the textile and cooking oil industries (Salimath *et al.*, 2021). It is cultivated in more than eighty countries to fulfill the needs of their textile and oil sectors. In 2020-21, it was cultivated on an area of 31.11 million hectares and 111.79 million 480lb bales of cotton were produced with an average of 782 kg per hectare (USDA, 2022). China, India, the U.S.A., Brazil, and Pakistan are the top five largest cotton-producing countries, contributing 78% of the global cotton production. However, climatic change in recent years resulted in a grievous reduction in cotton production due to the onsets of several insect/pest infestation and abiotic stresses. Among these, heat stress is one of the deadliest stresses which mostly accompany drought stress. It could have detrimental effects on cotton yield and quality by altering the normal growth pattern and physio-chemical functioning of plants. Although, Pakistan is among the one of the major cotton producing countries in the world, however, the suitable temperature for cotton growing areas in Pakistan (38 °C/26 °C) is far higher than the highest cotton-producing areas of the world (China 29 °C/18 °C, U.S.A 30 °C/24 °C, and India 35 °C/22 °C) (Saleem *et al.*, 2021). Throughout the initial vegetative phase (June-July), the maximum temperature remains 44 °C to 47 °C and may reach up to 49 °C in cotton-growing areas of Pakistan.

Heat stress in cotton, like other crops, drastically affects the growth and development of the plants, especially the early reproductive stage (Salman *et al.*, 2019). The most susceptible parts to heat stress in cotton are the flowers and squares. High temperature along with less availability of irrigation water could

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lead to complete crop failure. The optimum temperature for cotton growth and development lay somewhat between 26 ℃ to 35 ℃ (Conaty *et al.*, 2012; Lokhande & Reddy, 2014). The higher temperature could lead to flower and square shedding, reduced pollination efficiency and time, reduced boll weight, and lastly, decreased seed cotton yield (Xu *et al.*, 2020). Similarly, the average pollen germination temperature is 28 C and the temperature above this range could hamper pollen germination, pollen tube elongation, photosynthetic activity, stomatal conductance, boll abscission, and ultimately the cotton yield (Salman *et al.*, 2019). It is reported that for every 1 C increase over the optimum temperature in the field, 110 kg per hectare yield is reduced (Singh *et al.*, 2007).

There might be several reasons for the gradual reduction in cotton yield over the years including climate change, the outbreak of different diseases, poorly tested, unapproved and substandard seeds, higher rates of inputs, and deterioration of land due to intensive cultivation. Many of these problems are due to the narrow genetic base of newly developed cotton varieties (Munir *et al.*, 2020). Therefore, the very first step to develop heat-tolerant cotton varieties is to evaluate the existing cultivated germplasm against stress conditions and the selection of diverse parents to be used in the hybridization program. For this, different statistical approaches could be used but multivariate analysis provides the best possible solution for the selection of genotypes. It is considered one of the best methods to evaluate crop genotypes worldwide under stressed and non-stressed conditions (Munir *et al.*, 2020, Yousaf *et al.*, 2021a, Rahman*et al.*, 2022). Therefore, multivariate model-based approaches i.e., Principal component and cluster analysis were applied to screen cotton genotypes for their tolerance against high temperature.

Materials and Methods

Study Material and Location

The current investigational study was carried out at the research area of Cotton Research Station, Bahawalpur (29°23'10.4"N 71°39'08.8"E). The experimental material consisted of nine cotton genotypes i.e., BH-184, BH-272, BH-283, BH-284, BH-287, BH-297, BH-320, BH-377, and CIM-600 of indigenous origin. These nine genotypes were sown under randomized complete block design in three replications. The sowing was done on May 28, 2021, through hand held seed drill @ 2 seeds per hill, latter at early seedling stage thinned to one healthy, seedling. The genotypes were believed to experience high-temperature stress (40℃-45℃) from the date of sowing to boll formation, where the single-day temperature may raise up to 47℃ - 48℃. Each genotype was sown in a four-rowed 10-meter plot with net plot size of 15cm^2. During the whole growing season, 200 kg/ha nitrogen, 110 kg/ha phosphorus, and 60-65 kg/ha potash were applied to the genotypes. Other standard crop management practices like the application of preemergence herbicides and hoeing were carried out to ensure plant health.

Data Collection:

Data were recorded for different morphological and fiber quality-related traits including plant height (PH), nodes per plant (N/P), monopodial branches per plant (M/P), sympodial branches per plant (S/P), number of bolls per plant (B/P), CLCuV incidence percentage (CLCuV), plant population per hectare (PP ha^{-1}), percentage of lint (%), fibre length (FL), fiber fineness (FF), fiber strength (FS) and seed cotton yield (SCY). The data were recorded from ten different, fully guided plants per genotype per replication. The fiber quality-related traits were measured through High-Volume Instrument (1 X USTER HVI 900 A). Lint percentage (%) was measured with the following formula;

$$\text{Lint Percentage } (\%) = \frac{\text{weight of lint otained after ginning per 1o selected plants}}{\text{Total weight of seed cotton from 10 plants (seed + lint)}} \times 100$$

Moreover, the CLCuV incidence percentage (CLCuV) was calculated as below;

$$\text{CLCuV incidence percentage} = \frac{\text{Number of Infected Plant Units}}{\text{Total Number of Units Assesed (Healthy + Infected)}} \times 100$$

Statistical Data Analysis:

The obtained data were statistically analyzed for analysis of variance and correlation coefficient analysis (Steel *et al.*,1997) by using two statistical packages i.e., Statistix 8.1 and XLSTAT 22.0. Furthermore, two multivariate analyses i.e., Principal component (PC) and cluster analysis (CA) were carried out to characterize cotton genotypes under heat stress conditions (Sneath & Sokal, 1973). For this, XLSTAT statistical tool was used. For the illustration of data, Microsoft Excel (Version 2021) and OriginPro (Version 21) were used.

Metrological Conditions during the trial (2021):

The research trial was conducted in 2021 (May 2021 to November 2021) at the research area of Cotton

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Research Station, Bahawalpur. During the whole experiment, daily metrological data including minimum/maximum temperature, relative humidity, and rainfall was recorded through a weather observatory installed at Regional Agricultural Research Institute (RARI), Bahawalpur. The highest maximum temperature was observed in the months of June and July, where the average maximum temperature for the month was recorded as high as 47.9 ℃ and 44.9 ℃, respectively (Figure 1). Moreover, the highest relative humidity was also observed in these months (84.1%, 83.9%), respectively. The line graph drawn between the maximum/minimum temperature and days after sowing depicts the maximum temperature from 21 days after sowing to 81 days after sowing (Figure 2). These were the most critical days which could determine the overall performance of the genotypes by coinciding with the development of square and boll formation. Such a high temperature could drastically affect the overall crop yield and lint quality of the cotton crop.

Results

Analysis of Variance (ANOVA)

The results obtained through ANOVA revealed the presence of substantial genetic variations among cotton genotypes for studied traits i.e. plant height (PH), nodes per plant (N/P), monopodial branches per plant (M/P), sympodial branches per plant (S/P), number of bolls per plant (B/P), CLCuV incidence percentage (CLCuV), plant population per hectare (PP ha^{-1}), percentage of lint (%), fiber length (FL), fiber fineness (FF), fiber strength and ultimately, seed cotton yield (SCY) under heat stress conditions (Table 1).

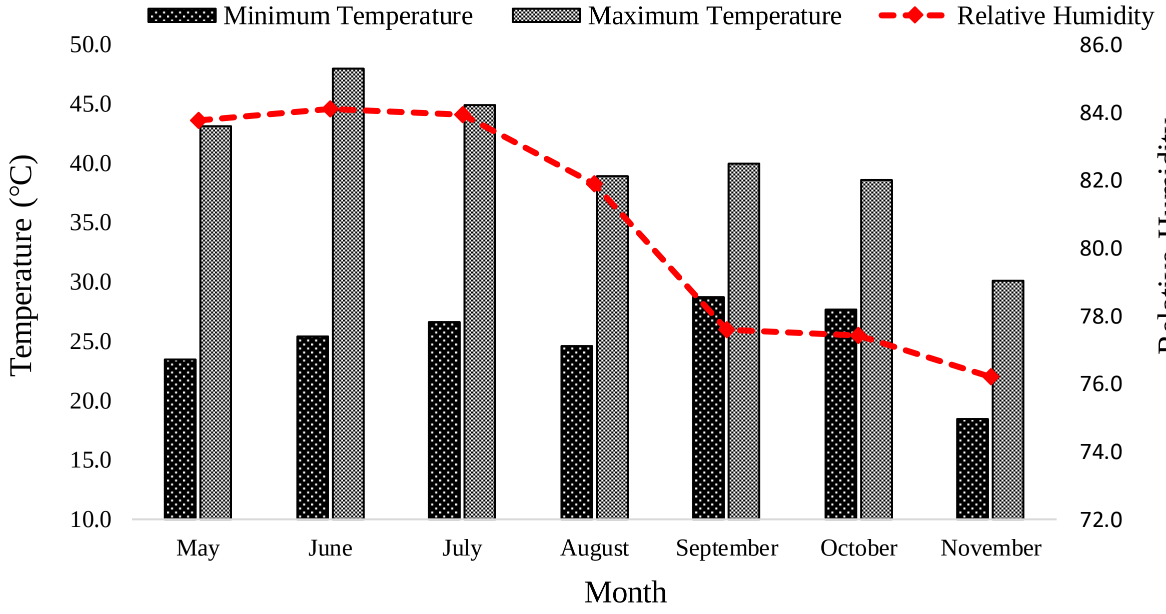

Figure 1: Metrological data of complete cotton growing season

Correlation Coefficient Analysis

The correlation coefficient analysis was executed to find the relationship between seed cotton yield and associated parameters under high temperature conditions. The correlation analysis showed a positive correlation of seed cotton with plant population per hectare (0.403*) monopodial branches per plant (0.267*) and fiber strength (0.070*) (Table 2 & Figure 3). However, seed cotton yield was observed to have a significant negative correlation with CLCuV incidence percentage (-0.475*), fiber length (-0.447*), nodes per plant (-0.186*), sympodial branches per plant (-0.186*), and fiber fineness (0.077*). There were, however, few traits i.e., plant height and bolls per plant that had a negative but non-significant association (-0.008^{NS}; -0.005^{NS}) with seed cotton yield, respectively.

Principal Component Analysis (PCA)

The PCA was applied to investigate the magnitude of variations among the cotton genotypes for yield and associated parameters under heat stress. The PCA extracted eight principal components (PCs) based on variations present in the data, among the first five PCs have eigenvalue more than 1, hence having significant variations up to 88.3% of the overall data (Table 3 and Figure 4). The individual highest variations were depicted by PC1 (34.7%) and PC2 (19.4%), respectively.

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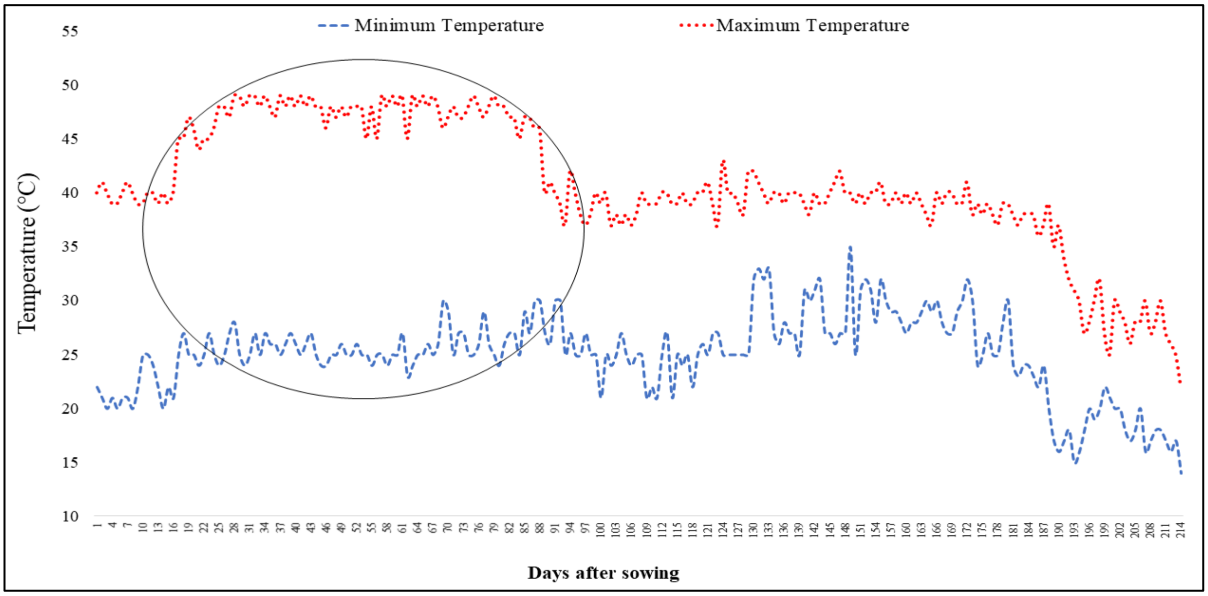
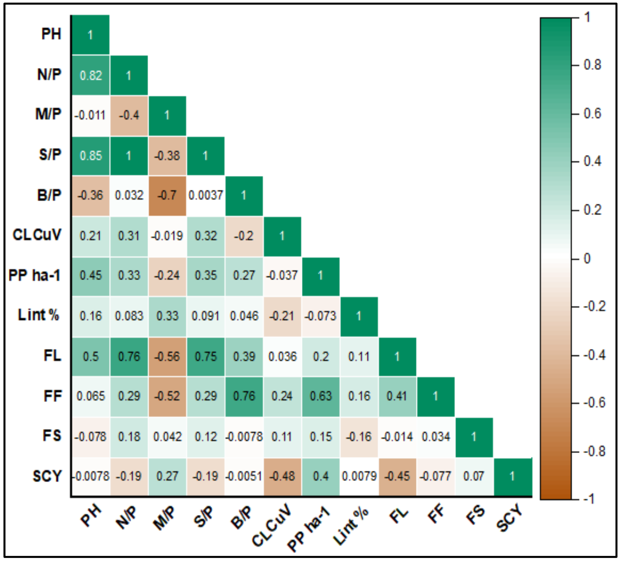


Figure 2: Variation in Temperature for whole cotton growing season (Circle indicates the maximum variations and highest average temperature)

The Correlation/factor loading between principal components and plant traits is represented in Table 5. The first principal component (PC1) showed 4.2 eigenvalue and maximum contribution by plant height (0.684), nodes per plant (0.912), monopodia(-0.613), sympodia(0.913), fiber length (0.852), and fiber fineness (0.610), respectively (Table 4). Similarly, in PC2, which has an eigenvalue of 2.3 and contributed 19.4% in variability, the most significant plant trait was the number of bolls per plant (0.910). Plant population per hectare and seed cotton yield were among the most significant traits in principal component 3, which accounted for 14.5% in total variations. In PC4 and PC5, which shared a contribution of 11.4% and 8.4%, lint percentage and CLCuV were the most associated traits.



	PH	N/P	M/P	S/P	B/P	CLCuV	PP ha-1	Lint %	FL	FF	FS	SCY
PH	1											
N/P	0.82	1										
M/P	-0.011	-0.4	1									
S/P	0.85	1	-0.38	1								
B/P	-0.36	0.032	-0.7	0.0037	1							
CLCuV	0.21	0.31	-0.019	0.32	-0.2	1						
PP ha-1	0.45	0.33	-0.24	0.35	0.27	-0.037	1					
Lint %	0.16	0.083	0.33	0.091	0.046	-0.21	-0.073	1				
FL	0.5	0.76	-0.56	0.75	0.39	0.036	0.2	0.11	1			
FF	0.065	0.29	-0.52	0.29	0.76	0.24	0.63	0.16	0.41	1		
FS	-0.078	0.18	0.042	0.12	-0.0078	0.11	0.15	-0.16	-0.014	0.034	1	
SCY	-0.0078	-0.19	0.27	-0.19	-0.0051	-0.48	0.4	0.0079	-0.45	-0.077	0.07	1

Figure 3: Graphical Representation of Correlation between traits in cotton genotypes under heat stress

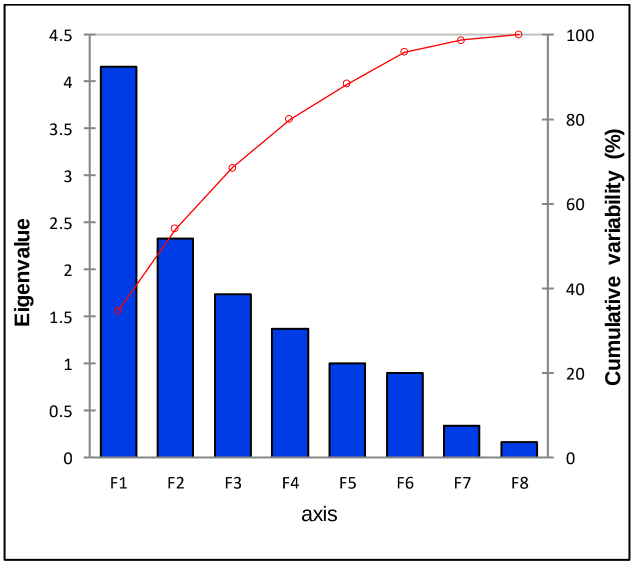


Figure 4: Scree plot of Principal ComponentAnalysis in cotton genotypes

The squared cosines of the plant traits showed the PC having the highest value of a plant trait/variable. The results showed that PC1 has the highest squared cosines values for plant height (0.468), nodes per plant (0.831), monopodia(-0.376),sympodia (0.833), fiber length (0.726), and fiber fineness (0.372),

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respectively (Table5). None of the other PCs had the highest values for these traits. Similarly, PC2 had the maximum value for the number of bolls per plant (0.828), PC3 had the highest squared cosines value of plant population per hectare (0.435), and seed cotton yield (0.750), respectively. The highest squared cosines values for lint percentage (0.578) were reported in PC4 and CLCuV incidence percentage (0.272) in PC5, respectively.

Biplot Analysis

Biplot analysis was applied to find the direction and magnitude of the variations in the plant traits. Furthermore, characterization of cotton genotypes was carried out based on their stability and variations. The PC1/PC2 biplot covers the 54.1% variations presented in the data.

Table 1: Mean Square (MS) values of selected traits of cotton genotypes under heat stress conditions

SOV	df	PH	N/P	M/P	S/P	B/P	CLCuV	PP ha^{-1}	Lint %	FL	FF	FS	SCY
Replication	2	43.82	2.37	05.48^{e-4}	2.33	5.59	1.23	3615400	0.14	0.018	0.01	0.01	5560.1
Genotypes	8	682.37**	33.70*	2.08**	30.92**	51.48**	11.78*	1.19e+7**	18.37**	2.29**	0.96**	70.75**	40343.1**
Error	16	102.48	11.62	0.58	9.29	15.01	6.56	7332084	0.06	0.014	0.07	0.04	13835.8

****: Significant at 1%, *: Significant at 5%, NS: Non-significant, PH**:Plant Height (cm), **N/P**: Nodes per plant, **M/P**: Monopodial branches per plant, **S/P**: Sympodial branches per plant, **B/P**: Number of bolls per plant, **CLCuV**: CLCuV incidence percentage, **PP ha^{-1}**: Plant population per hectare, **Lint %**: Lint percentage, **FL**: Fiber length, **FF**: Fiber fineness, **FS**: Fiber strength, **SCY**: Seed cotton yield

Table 2: Correlation coefficient analysis between selected traits of cotton genotypes under heat stress conditions

Variables	PH	N/P	M/P	S/P	B/P	CLCuV	PP ha^{-1}	Lint %	FL	FF	FS
N/P	**0.815**	**1**									
M/P	-0.011	**-0.398**	**1**								
S/P	**0.850**	**0.997**	**-0.384**	**1**							
B/P	**-0.362**	**0.032**	**-0.699**	0.004	**1**						
CLCuV	**0.209**	**0.305**	-0.019	**0.315**	**-0.201**	**1**					
PP ha-1	**0.449**	**0.333**	**-0.242**	**0.352**	**0.269**	**-0.037**	**1**				
Lint %	**0.156**	**0.083**	**0.330**	**0.091**	**0.046**	**-0.214**	**-0.073**	**1**			
FL	**0.501**	**0.763**	**-0.559**	**0.752**	**0.392**	**0.036**	**0.196**	**0.112**	**1**		
FF	**0.065**	**0.290**	**-0.520**	**0.289**	**0.759**	**0.243**	**0.626**	**0.161**	**0.412**	**1**	
FS	**-0.078**	**0.181**	**0.042**	**0.122**	-0.008	**0.109**	**0.147**	**-0.156**	**-0.014**	**0.034**	**1**
SCY	-0.008	**-0.186**	**0.267**	**-0.186**	-0.005	**-0.475**	**0.403**	**0.008**	**-0.447**	**-0.077**	0.070

Values in bold are significant at 5% probability level, PH: Plant Height (cm), **N/P**: Nodes per plant, **M/P**: Monopodial branches per plant, **S/P**: Sympodial branches per plant, **B/P**: Number of bolls per plant, **CLCuV**: CLCuV incidence percentage, **PP ha^{-1}**: Plant population per hectare, **Lint %**: Lint percentage, **FL**: Fiber length, **FF**: Fiber fineness, **FS**: Fiber strength, **SCY**: Seed cotton yield

Table 3: Eigenvalues, variability % and Cumulative variability % in cotton genotypes through Principal Component Analysis

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigenvalue	4.2	2.3	1.7	1.4	1.0	0.9	0.3	0.2
Variability (%)	34.7	19.4	14.5	11.4	8.4	7.5	2.8	1.4
Cumulative %	34.7	54.1	68.5	80.0	88.3	95.9	98.6	100.0

Table 4: Factor Loading/ Correlation between Plant traits and Principal Components in cotton genotypes under heat stress

Traits/PCs	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
PH	0.684	-0.616	0.316	0.075	-0.071	-0.184	-0.080	-0.040
N/P	0.912	-0.338	0.048	-0.018	-0.089	0.129	0.163	0.004
M/P	-0.613	-0.568	0.283	0.090	0.364	0.064	-0.121	0.248
S/P	0.913	-0.362	0.061	0.004	-0.084	0.063	0.145	-0.013
B/P	0.345	0.910	-0.038	0.128	0.036	0.104	0.117	0.096

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CLCuV	0.298	-0.311	-0.492	-0.423	0.522	-0.295	0.178	0.056
PP ha^{-1}	0.510	0.239	0.660	-0.301	0.122	-0.244	-0.281	-0.067
Lint %	0.049	-0.109	0.262	0.760	0.497	0.262	0.076	-0.132
FL	0.852	0.044	-0.190	0.285	-0.198	0.188	-0.170	0.227
FF	0.610	0.608	0.096	-0.025	0.475	-0.146	-0.028	0.033
FS	0.090	-0.032	0.098	-0.622	0.174	0.748	-0.056	-0.041
SCY	-0.274	0.116	0.866	-0.156	-0.143	-0.049	0.319	0.112

Table 5: Squared Cosine values of Plant traits as revealed through PCA in cotton genotypes under heat stress

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**
PH	**0.468**	0.379	0.100	0.006	0.005	0.034	0.006	0.002
N/P	**0.831**	0.115	0.002	0.000	0.008	0.017	0.027	0.000
M/P	**0.376**	0.323	0.080	0.008	0.133	0.004	0.015	0.061
S/P	**0.833**	0.131	0.004	0.000	0.007	0.004	0.021	0.000
B/P	0.119	**0.828**	0.001	0.016	0.001	0.011	0.014	0.009
CLCuV	0.089	0.097	0.242	0.179	**0.272**	0.087	0.032	0.003
PP ha-1	0.260	0.057	**0.435**	0.091	0.015	0.060	0.079	0.004
Lint %	0.002	0.012	0.069	**0.578**	0.247	0.068	0.006	0.017
FL	**0.726**	0.002	0.036	0.081	0.039	0.035	0.029	0.052
FF	**0.372**	0.370	0.009	0.001	0.225	0.021	0.001	0.001
FS	0.008	0.001	0.010	0.387	0.030	**0.559**	0.003	0.002
SCY	0.075	0.013	**0.750**	0.024	0.021	0.002	0.102	0.013

Biplot analysis showed that seed cotton yield was significantly associated in a positive way with the number of bolls, plant population and monopodia while a negative correlation of seed cotton yield was observed with sympodia, nodes per plant, CLCuV, plant height, staple length and as revealed by the angle between corresponding lines (Figure 5). Moreover, maximum variations were observed in the bolls per plant, monopodia, PH, sympodia, and nodes per plant as their corresponding lines were at a maximum distance from the center of origin. Biplot analysis also unveiled the behavior of cotton genotypes in biplot under heat stress conditions. PC1/PC2 biplot showed that two cotton genotypes were present at the center of origin and one genotype BH-284 was present at maximum distance from the origin of the graph in the direction of the line that corresponded to seed cotton yield.

Hierarchical Cluster Analysis

Another multivariate analysis used to identify and categorize heat tolerant and heat susceptible cotton genotypes was Hierarchical Cluster Analysis or Hierarchical Clustering. Cluster analysis categorized cotton genotypes into three clusters based on genotypic similarities and mean values for each trait under these clusters are given in Table 6. The genotypes within the cluster were much similar within the group while different from the genotypes of other clusters/groups. Cluster one was comprised of three genotypes i.e., BH-284, BH-320, and BH-184 (Figure 6). This group had the lowest mean values for plant height, nodes per plant, sympodial branches per plant, plant population per hectare, fiber fineness, and finally the seed cotton yield (Table 6). On the other side, mean values for CLCuV incidence percentage and fiber length were highest in this cluster. Cluster two consisted of three other cotton genotypes i.e., BH-297, BH-287, and CIM-600 were, having intermediate mean values for most of the traits. The third and last cluster included again three genotypes i.e., BH-377, BH-272, and BH-283, and the group had the highest mean values for bolls per plant, plant population per hectare, fiber fineness, fiber strength, and seed cotton yield.

Table 6: Class means of three clusters through agglomerative hierarchical clustering in cotton genotypes

Class / Plant Traits	**Class 1**	**Class 2**	**Class 3**
Plant Height	86.8	107.6	97.8
Nodes per plant	20.7	22.6	21.7
Monopodial branches per plant	1.7	1.7	1.7
Sympodial branches per plant	16.3	18.6	17.4
Number of bolls per plant	21.2	19.9	22.2

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CLCuV incidence percentage	9.4	9.3	9.3
Plant Population per hectare	25534.7	28165.8	29840.2
Lint percentage	36.6	38	36.4
Fiber length	28.8	28.6	28.7
Fiber Fineness	4.1	4.3	4.9
Fiber Strength	98.6	95.6	99.6
Seed cotton yield	1172.2	1243.9	1339.7

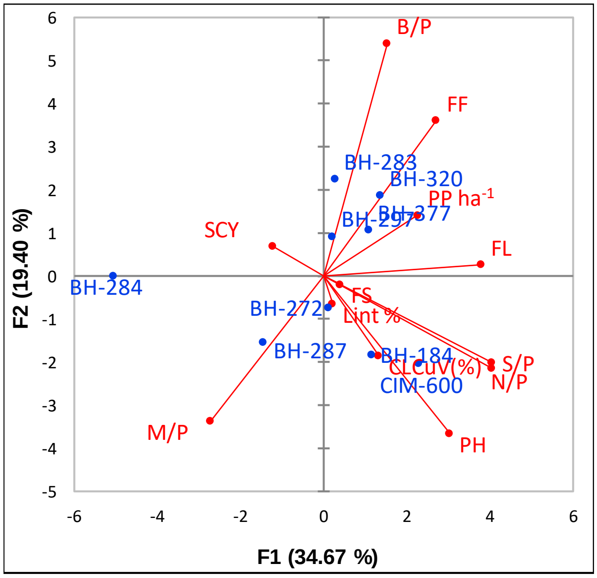

Figure 5:PC1/PC2 Cummulative Bipot between plant traits and cotton genotypes under heat stress

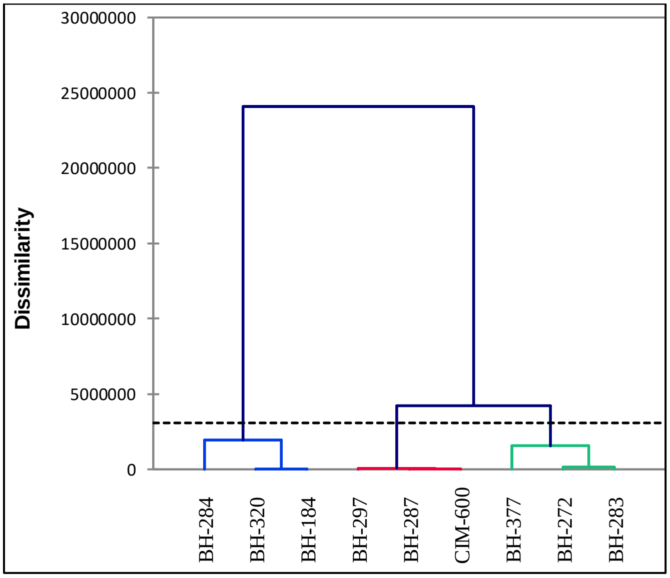

Figure 6: Dendrogram of cotton genotypes based on agglomerative hierarchical clustering

Discussion

Estimation and exploration of genetic variations present in the cultivated germplasm is one of the preliminary for every new breeding program. The success of every new breeding program depends upon the extent of variability present in the available germplasm. It gives the opportunity to select and exploit the desirable set of genes in a diverse population for the improvement of the crop for a specific trait under a range of biotic and abiotic stresses including CLCuV, heat, and drought stresses. As seed cotton yield is a complex, polygenic trait, therefore, direct selection is not suitable for its improvement. It is, therefore, pivotal to select hybridizing parents from diverse germplasm resources based on associated traits. Hence, exploration of available germplasm for the variations depicted among the agro-morphological and fiber quality-related traits is one of the key steps for crop improvement. The results obtained from analysis of variance (ANOVA) revealed the presence of highly significant variations among cotton genotypes for agronomically important morphological and fiber quality-related traits under heat stress conditions.

However, the genetic diversity for the number of nodes per plant and CLCuV incidence percentage was significant only. Similar observations were also reported by Bhatti *et al.* (2020a), Bhatti *et al.* (2020b), Hassan *et al.* (2021) and Sahar *et al.* (2021) who showed the presence of significant variations among cotton genotypes that could be used to improve seed cotton yield.

Correlation coefficient analysis was adopted to investigate the relationship between different parameters of cotton genotypes under heat stress conditions. Correlation analysis is one of the most basic statistical approaches utilized by researchers to explore the association between different plant traits under different circumstances including heat stress (Mumtaz *et al.*, 2018; Yousaf *et al.* 2021a; Yousaf *et al.*, 2021b; Riaz *et al;* 2021 and Rahman *et al.*, 2022). In the current experimental study, correlation analysis unveiled anexpressively positive association of seed cotton yield with plant population per hectare, monopodial branches per plant, and fiber strength. This might be due to the fact that semi-spreading/Semi-bushy types of cotton genotypes with more monopodial branches required less net per plant area, which increases their plant population and source capacity, resulting in more seed cotton yield per unit area. On the other hand, a significantly negative association of seed cotton yield was

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recorded with fiber length, CLCuV incidence percentage, nodes per plant, sympodial branches per plant, and fiber fineness as cotton genotypes with good quality traits and high CLCuV attack had to compensate over yield. Our findings were in complete agreement with the results of Rehman*et al.*, (2020), Sarwar *et al.* (2021), and Shaheen *et al.* (2021) who reported that seed cotton yield could be improved through the positive selection based upon plant architecture and monopodial branches per plant while negative selection for CLCuV incidence percentage and fiber length.

Genetic diversity assessment through multivariate analysis-based approaches is one of the most frequently used statistical methods for the classification and characterization of crop species (Yousaf *et al*., 2017; Khan *et al*., 2017; Yousaf *et al.* 2018). Principal component analysis categorizes cotton genotypes into eight principal components (PCs), the first five PCs having the eigenvalue of more than one.

The first two PCs were the most important ones, contributing 54.1% in total variability. The maximum variability in these PCs was due to plant height, nodes per plan, monopodia, sympodia, fiber length, fiber fineness, and bolls per plant. It means that transgressive sergeants for these traits must be in consideration while selecting hybridizing parents. Moreover, PC1/PC2 biplot analysis verified the results obtained through correlation analysis and depicted that the maximum variation present in the data was due to five plant traits i.e., monopodia, sympodia, nodes per plant, plant height, and the number of bolls per plants. Likewise, cotton genotypes BH-248 contributed maximally to the genetic variations in the same way the variables situated at maximum distance from the origin of the biplot are considered highly divergent and the variables neighboring to the origin are considered as stable (Saeed *et al.*,2018). Similar results were also described by Khan *et al.* (2020) and Zafar *et al.* (2021) who showed the utilization of PCA for the assessment of genetic diversity in cotton genotypes.

Cluster analysis, another multivariate approach, classified cotton genotypes into three classes i.e., cluster-I, cluster-II, and cluster-III based on their performance under heat stress conditions. The cluster-I was characterized as the cluster of heat susceptible cotton genotype's group while cluster-III was designated as the cluster of cotton genotypes having the highest heat tolerance based on the performance of their seed cotton yield and related traits. So, to produce a population with maximum variation and greater genetic gain, the genotypes from cluster-I & III must be introgressed. Several researchers used cluster analysis to characterize different cotton genotypes under a range of environmental conditions using morpho-molecular and fiber quality-related traits and found it very useful in categorizing cotton genotypes (Manan*et al*., 2021; Sikder *et al.*, 2020; Munir *et al.*, 2020; Eldessouky*et al.*, 2021).

Conclusion and Recommendations

Evaluation of multivariate analysis approaches like principal component analysis, biplot analysis, and Agglomerative Hierarchical Clustering provides in-depth knowledge of genotypes with diverse genetic makeup. This could greatly help the breeders to select genotypes that better suit their breeding objectives. The current study revealed that an efficient selection of parental cross should consider several correlated traits i.e., monopodial branches per plant, CLCuV incidence percentage, fiber length, nodes per plant, and sympodial branches per plant. Furthermore, a cross between BH-272 and BH-320 must be constituted to broaden the genetic base of the cotton crop to create maximum variations. Moreover, BH-272 and BH-283 could be recommended to heat-prone areas after intensive, multilocation testing.

Conflict of interest

The authors declared absence of conflict of interest.

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