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Original Research Article

EVALUATION OF UPLAND COTTON GENOTYPES FOR MORPHOMETRIC, PHOTOSYNTHESIS-RELATED TRAITS AND PARAMETERS RELATED TO ENZYMATIC AND NON-ENZYMATIC ANTIOXIDANT ACCUMULATION

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Abstract: *To develop new crop varieties, the evaluation of existing germplasm is the basic step based on the agro-morphological, physiological, biochemical traits and molecular traits. The current study was designed to evaluate ten cotton genotypes based on key morpho-physiological and biochemical traits. Cotton genotypes were arranged in triplicates using a randomized complete block design (RCBD) with plant-to-plant and bed-to-bed distances of 30 cm and 75 cm, respectively. Data from fully guarded, mature plants was collected. The results obtained through ANOVA revealed the presence of significant variations in the studied plant parameters. The correlation analysis revealed a significant relationship between seed cotton yield and net photosynthetic rate (0.92**), tannins (0.80**), malondialdehyde (0.73*), total oxidant status (-0.86**) and hydrogen peroxide (-0.84**). Multivariate analysis approaches, i.e., principal component, biplot, and cluster analysis, were used to classify and characterize cotton genotypes based on their performance. These analyses revealed that BH-341 and BH-254 were the most productive cotton genotypes. Therefore, these genotypes could be recommended for cultivation in core-cotton areas following extensive multilocation testing.*

Keywords: Correlation, Multivariate Analysis, Antioxidants, Photosynthetic Rate, Glycine Betaine

Introduction

Cotton is universally recognized as a pivotal crop, having a wide-reaching influence on the world and specific significance to countries like Pakistan. Globally, cotton drives the textile industry, serving as the primary raw material for clothing, bedding, and other fabric products. Its economic impact is profound, providing employment to millions and acting as a key commodity in international trade (Cororaton et al., 2008). In many developing nations, cotton represents a critical source of revenue, shaping economic policies and trade relations. The cotton crop has a wide range of uses, influencing various sectors across the globe. The most notable use of cotton is in textiles. Cotton's breathable, absorbent, and durable properties make it a primary raw material in the textile industry. It is employed extensively in manufacturing clothing, bedding, upholstery, and other fabric products, satisfying consumer demand on a global scale (Khanzada et al., 2020). Apart from clothing, cotton by-products find uses in several industrial applications. Cottonseed oil, for instance, is incorporated into the production of items like soap, cosmetics, and lubricants. Furthermore, cottonseed

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meal, rich in protein, is a valuable source of animal feed, particularly in dairy farming (Wanapat et al., 2013). Cotton's absorbent quality also renders it suitable for medical supplies such as bandages, swabs, and surgical dressings, highlighting its role in healthcare.

Cotton is the most significant industrial crop in natural fiber and oil production (Salimath et al., 2021). In 2020–21, it was grown on 31.42 million hectares and produced 111.48 million 480-pound bales, averaging 773 kg ha^{-1} globally (USDA, 2022). For Pakistan, cotton holds a distinctive place, being the mainstay of the agricultural and industrial sectors. It is one of the largest cotton producers in the world, contributing significantly to Pakistan's GDP and export earnings. Cotton cultivation provides livelihoods to a substantial segment of Pakistan's population, including farmers, ginners, spinners, and textile workers. Additionally, the cotton industry in Pakistan plays a vital role in attracting foreign investment and building industrial infrastructure. During 2021–2022, the cultivated area under cotton in Pakistan was 1.93 million hectares, and an average of 731 kilograms per hectare was produced, producing 8.329 million bales (ESP, 2021–2022). Although Pakistan's per-hectare cotton production is very close to the global average, it lags far behind the major cotton-producing nations, such as Australia (2,217 kg^{-1}), China (19,765 kg ha^{-1}), Turkey (1804 kg ha^{-1}), Brazil (17,220 kg ha^{-1}), and the United States (957 kg ha^{-1}) (USDA, 2022). High input costs, inaccessibility of inputs, high disease and insect-pest infestation rates, drought stress, heat stress, lack of mechanized harvesting, and inaccessibility of quality seed are the primary causes of Pakistan's low cotton yield.

Evaluating existing crop germplasm is essential in developing new varieties as it provides a comprehensive understanding of existing crops' genetic diversity, characteristics, and potential. This understanding is vital for identifying traits that can be exploited to breed crops with enhanced disease resistance, nutritional content, or other desirable attributes. In this complex process, statistical methods such as ANOVA, correlation coefficient analysis, cluster analysis, and principal component analysis play crucial roles. Therefore, the current study was designed to evaluate the existing approved cotton varieties along with the potential candidate lines.

Methodology

Experimental Location and Site

The current study was conducted at Cotton Research Institute, Bahawalpur's research area, during the 2022-23 crop year. The genotypes included in the study were BH-341, BH-243, BH-348, BH-313, BH-254, BH-188, BH-200, BH-224, BH-184, BH-600. The experiment was conducted under a Randomized complete block design (RCBD) with three replicates. Sowing was done with the help dibbler at the rate of two seeds per hill. At the seedling stage, the crop was thinned to one seedling only for proper growth and development. Each genotype consisted of two rows of 5-meter length per replication. The plant-to-plant and row-to-row distance was maintained at 25 cm and 75 cm, respectively. Standard agronomic and plant protection measures were carried out for all the genotypes under study.

Data Recording and Measurement

At maturity, several plants' morphological traits, i.e., the number of balls (NB), plant height (PH), monopodial branches per plant (MB), sympodial branches per plant (SB), nodes per plant (NP), ball weight (BW) and lint yield of cotton (Y) parameters were recorded/measured. Measurement of important physiological traits, including net photosynthetic rate (Pn), stomatal conductance (Ci), and total chlorophyll contents (Total Chl), was also carried out using the Infrared Gas Analyzer (IRGA). Furthermore, key biochemical traits, i.e., Hydrogen per Oxide (H2O2), Total Oxidants Status (TOS), Total Carotene (TC), Sugars, Tannins (Tan), Malondialdehyde (MDA), Glycine Betaine (GB), Peroxidase (POD), Catalase (CAT), Superoxide Dismutase (SOD) and Total Antioxidant Capacity (TAC) were also measured using mass spectrometry.

Statistical Analysis

The recorded data of measured traits were subjected to analysis of variance (ANOVA) to examine the variations among the cotton genotypes based on morphological, physiological, and biochemical traits (Steel *et al.*,1997). Moreover, correlation coefficient analysis was executed to evaluate the relationship between seed cotton yield and other related traits (Steel *et al.*,1997). Two multivariate approaches, i.e., principal component analysis (PCA) and cluster analysis (CA), were also applied to categorize and classify the cotton genotypes based on their performance (Sneath & Sokal, 1973). To execute the operations, statistical packages, i.e., Statistix 8.1 and XLSTAT, were used to analyze the data statistically. Furthermore, Microsoft Excel and OriginPro were used to illustrate the results obtained.

Results and Discussion

Analysis of Variance

The results obtained through the analysis of variance (ANOVA) unveiled the incidence of highly significant variations among cotton genotypes for studied plant morphological, physiological, and biochemical traits, including no of bolls, plant height,

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monopodial branches, sympodial branches, nodes per plant, net photosynthetic rate, stomatal conductance, total chlorophyll contents, hydrogen peroxide, total oxidants status, total carotene, sugars, tannins, malondialdehyde, glycine betaine, peroxidase dismutase, catalase, superoxide dismutase, total antioxidant capacity and yield per plot (Table 1). However, variations in total chlorophyll contents and Monopodial Branches for cotton genotypes were significant, but the variations for Sugars contents were insignificant at 1% and 5%, respectively. Similar results were also found by Zafar *et al.* (2022), Shafique *et al.* (2023), Hussain *et al.* (2023), and Yousaf *et al.* (2023), who showed the presence of significant variations in cotton genotypes for morpho-physiological and biochemical traits and emphasized on the utilization of diverse cotton germplasm to make proper selection.

Correlation Coefficient Analysis

Correlation coefficient analysis is one of the most commonly used statistical approaches to evaluate the strength and direction of the linear relationship between two quantitative variables. The current study determined the correlation coefficients to draw the quantitative relationship between key morpho-physiological and biochemical traits in cotton genotypes (Figure 1). The results revealed the presence of a significantly positive correlation between cotton yield with the net photosynthetic rate ($r = 0.92^{**}$), tannins ($r = 0.80^{**}$), and malondialdehyde ($r = 0.73^{**}$) while a significantly negative correlation with total oxidant status ($r = -0.86^{**}$) and hydrogen peroxide ($r = -0.84^{**}$). Similarly, seed cotton yield also showed a positive correlation with glycine betaine (r = 0.63), superoxide dismutase (r = 0.63), stomatal conductance (r = 0.61), total carotenoid contents (r = 0.61), peroxidase (r = 0.50) but these correlations were not significant (Figure 1). Aslam et al. (2022) also showed that seed cotton yield could be increased by making the selection based on highly correlated traits like net photosynthetic rate. Similarly, traits like total oxidative status and hydrogen peroxide are negatively correlated because the more oxidative damage to the cell, the more sensitive the genotype and, consequently, lower the yield (Hasanuzzaman et al., 2021).

Table 1: Mean Square (MS) values of key cotton traits in ten cotton genotypes

SOV	Replication	Treatment	Error
Degree of Freedom (df)	2	9	18
No of Bolls (NB)	1.9603	36.444**	5.5896
Plant Height (PH)	2.977	294.208**	17.608
Monopodial Branches (MB)	1.76633	0.4637*	0.16004
Sympodial Branches (SB)	0.1013	12.0794**	3.378
Nodes per Plant (NP)	0.75033	16.66726**	4.38626
Net Photosynthetic Rate (Pn)	6.5823	91.7363**	12.8446
Stomatal Conductance (Ci)	1.633	171.319**	1.041
Total Chlorophyll Contents (Total Chl)	0.09961	0.58612*	0.21767
Hydrogen peroxide (H_2O_2)	0.01433	5.708**	0.01433
Total Oxidants Status (TOS)	3137	9801460**	1419
Total Carotene (TC)	1.312	513.102**	0.259
Sugars	0.2943	26.9319^{NS}	0.6277
Tannins (Tan)	82917.9	$1.648\times10^{7**}$	28114.8
Malondialdehyde (MDA)	8.03	5070.35**	21.5
Glycine Betaine (GB)	0.4423	29.0376**	0.1986
Peroxidase (POD)	0.2	25870.2**	37.5
Catalase (CAT)	18.63	4249.72**	28.41
Superoxide Dismutase (SOD)	6.433	295.985**	77.841
Total Antioxidant Capacity (TAC)	0.00794	2.92305**	0.01333
Yield\Plot (Y)	0.12933	1.14626**	0.09748

: Significant at 1%, *: Significant at 5%, NS: Non-significant, **NB: No. of Bolls, **PH***: Plant Height (cm),* **MB***: Monopodial Branches,* **SB***: Sympodial Branches,* ***NP****: Nodes per plant,* ***Pn****: Net Photosynthetic Rate,* ***Ci****: Stomatal Conductance,* ***Total Chl****: Total Chlorophyll Contents plant,* **H_2O_2***: Hydrogen peroxide,* ***TOS****: Total Oxidants Status,* ***TC****: Total Carotene, Sugar,* ***Tan****: Tannins,* **MDA***:*

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Malondialdehyde, **GB***: Glycine Betaine,* ***POD****: Peroxidase,* ***CAT****: Catalase,* ***SOD****: Superoxide Dismutase,* ***TAC****: Total Antioxidant Capacity,* ***Y****: Yield/Plot*

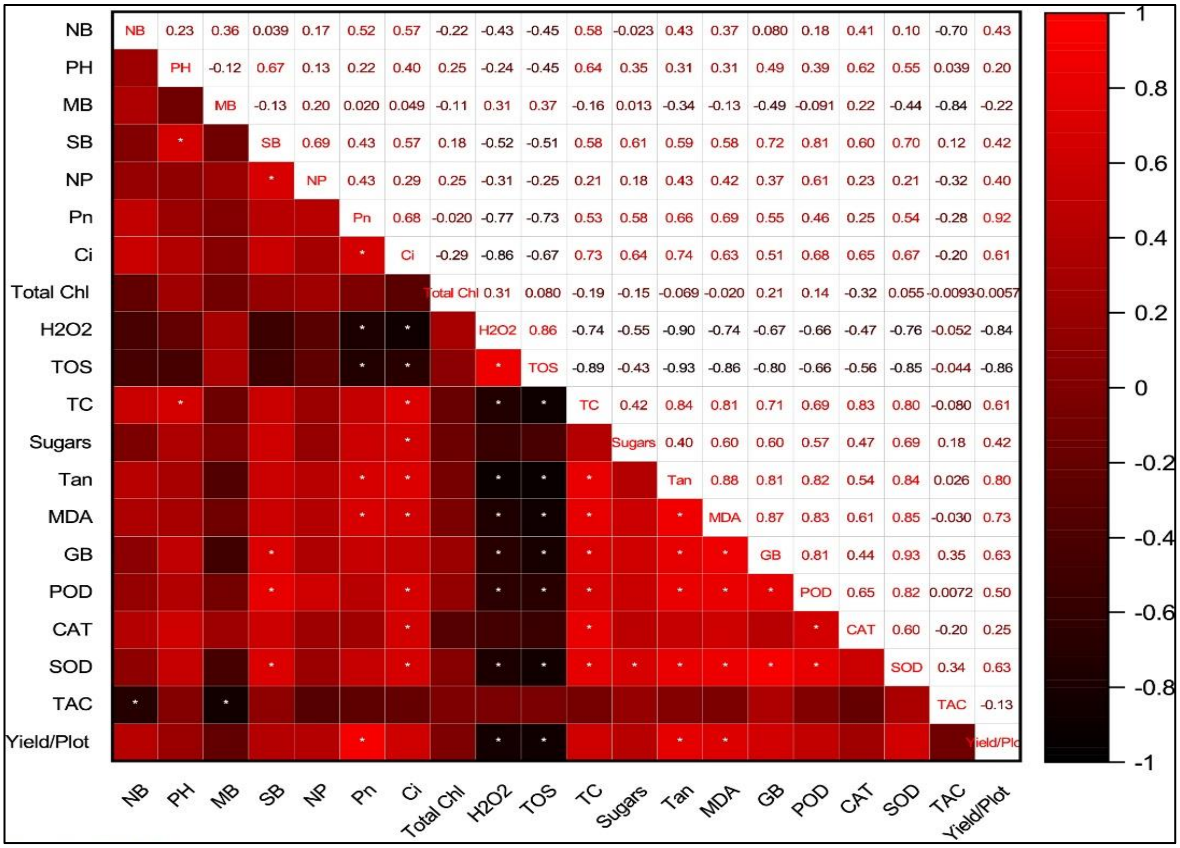

Figure 1: *Correlation coefficient analysis between key plant traits in cotton genotypes*

NB: No. of Bolls, **PH***: Plant Height (cm),* **MB***: Monopodial Branches,* **SB***: Sympodial Branches,* ***NP****: Nodes per plant,* **Pn***: Net Photosynthetic Rate,* ***Ci****: Stomatal Conductance,* **Total Chl***: Total Chlorophyll Contents plant,* ***H₂O₂****: Hydrogen peroxide,* ***TOS****: Total Oxidants Status,* ***TC****: Total Carotene, Sugar,* ***Tan****: Tannins,* **MDA***: Malondialdehyde,* **GB***: Glycine Betaine,* ***POD****: Peroxidase,* ***CAT****: Catalase,* ***SOD****: Superoxide Dismutase,* ***TAC****: Total Antioxidant Capacity,* ***Y****: Yield/Plot*

Cluster Analysis

Cluster analysis is the multivariate analysis extensively used in plant sciences to categorize, classify or characterize genotypes based on their performance under given conditions. In the current study, ten cotton genotypes were analyzed for cluster analysis. The results are unrevealed that cluster analysis categorizes ten cotton genotypes into four groups or clusters (Figure 2). The first cluster comprised only one genotype, i.e., BH-341, and the cluster is characterized by the group of second highest seed cotton yield (2.53 kg plot^{-1}), including the higher values for the key traits including the number of Bolls (47.0), Plant Height (164.0), Monopodial Branches (1.2), Net Photosynthetic Rate (28.0), Stomatal Conductance (29.0) and Sugars (24.7) (Table 2). The cluster-2, which consisted of three cotton genotypes, i.e., BH-184, BH-313, and BH-243, was the group of poorest performing genotypes with a seed cotton yield of 2.23 kg plot^{-1} and had the lowest values for most of the studied traits including plant height (148.5 cm), sympodial branches per plant (16.1), ball weight (BW), net photosynthetic rate (22.7), stomatal conductance (8.7), total carotene (35.1), sugars (17.1), malondialdehyde (170.6), glycine betaine (16.9), peroxidase (738.1), catalase (652.3), superoxide dismutase (142.4) and highest values for hydrogen peroxide (8.06), total oxidants status (7574.9), respectively (Table 2).

The third cluster is characterized as the most productive group of genotypes with seed cotton yield of 2.68 kg plot^{-1} and highest values for traits including Sympodial Branches (19.4), Nodes per Plant (24.8), Total Chlorophyll Contents (1.87), Total Carotene (64.0), Tannins (12735.8), Malondialdehyde (268.7), Glycine Betaine (24.2), Peroxidase (954.8), Superoxide Dismutase (166.5) and lowest value for Monopodial Branches (0.6) (Table 2 & Figure 3). This

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cluster is comprised of two genotypes, including BH-254 and BH-348. The last cluster, cluster-4, is the second lowest productive but the largest by the number of genotypes group comprised four cotton genotypes, including BH-200, BH-188, BH-224, and CIM-600. The group has the highest value for total antioxidant activity (5.98) and the lowest value for the number of bolls (39.9). Several researchers employed cluster analysis in cotton to categorize genotypes under different conditions (Mumma et al., 1999; Sezener et al., 2006; Sarwar et al., 2021; Alabady et al., 2008). The cluster analysis help in selecting the genotypes based on the cluster averages of the genotypes included in the cluster.

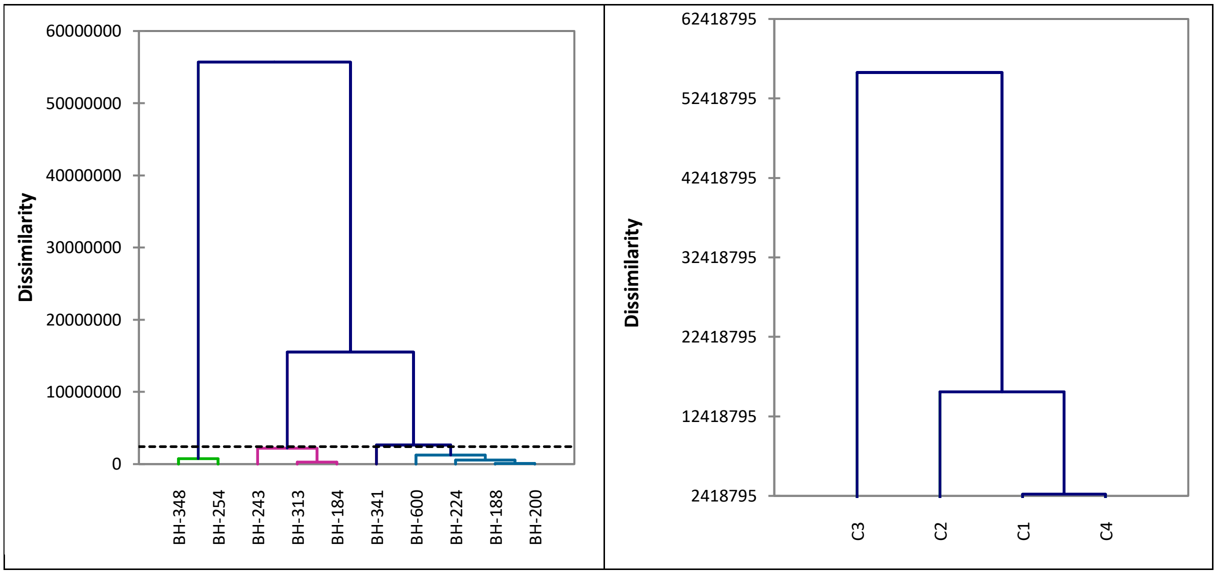

Figure 2: *Dendrogram of cotton genotypes based on cluster analysis*

Table 2: Cluster means for morpho-physiological and biochemical traits in cotton genotypes under study

Class	Class-1	Class-2	Class-3	Class-4
No of Bolls (NB)	47.0	41.7	44.3	39.9
Plant Height (PH)	164.0	148.5	158.2	158.2
Monopodial Branches (MB)	1.2	1.0	0.6	0.7
Sympodial Branches (SB)	17.9	16.1	19.4	19.3
Nodes per Plant (NP)	22.3	23.3	24.8	23.9
Net Photosynthetic Rate (Pn)	28.0	22.7	26.9	22.9
Stomatal Conductance (Ci)	29.0	8.7	22.0	18.4
Total Chlorophyll Contents (Total Chl)	1.47	1.76	1.87	1.74
Hydrogen per Oxide (H_2O_2)	5.47	8.06	4.98	6.62
Total Oxidants Status (TOS)	4697.3	7574.9	3066.7	6410.6
Total Carotene (TC)	59.3	35.1	64.0	46.4
Sugars	24.7	17.1	20.3	21.2
Tannins (Tan)	9437.0	6510.1	12735.8	8836.0
Malondialdehyde (MDA)	232.2	170.6	268.7	202.3
Glycine Betaine (GB)	20.7	16.9	24.2	20.9
Peroxidase (POD)	843.0	738.1	954.8	881.9
Catalase (CAT)	715.3	652.3	706.7	691.5
Superoxide Dismutase (SOD)	161.3	142.4	166.5	157.8
Total Antioxidant Capacity (TAC)	4.41	4.88	5.19	5.98
Yield\Plot (Y)	2.53	2.23	2.68	2.26

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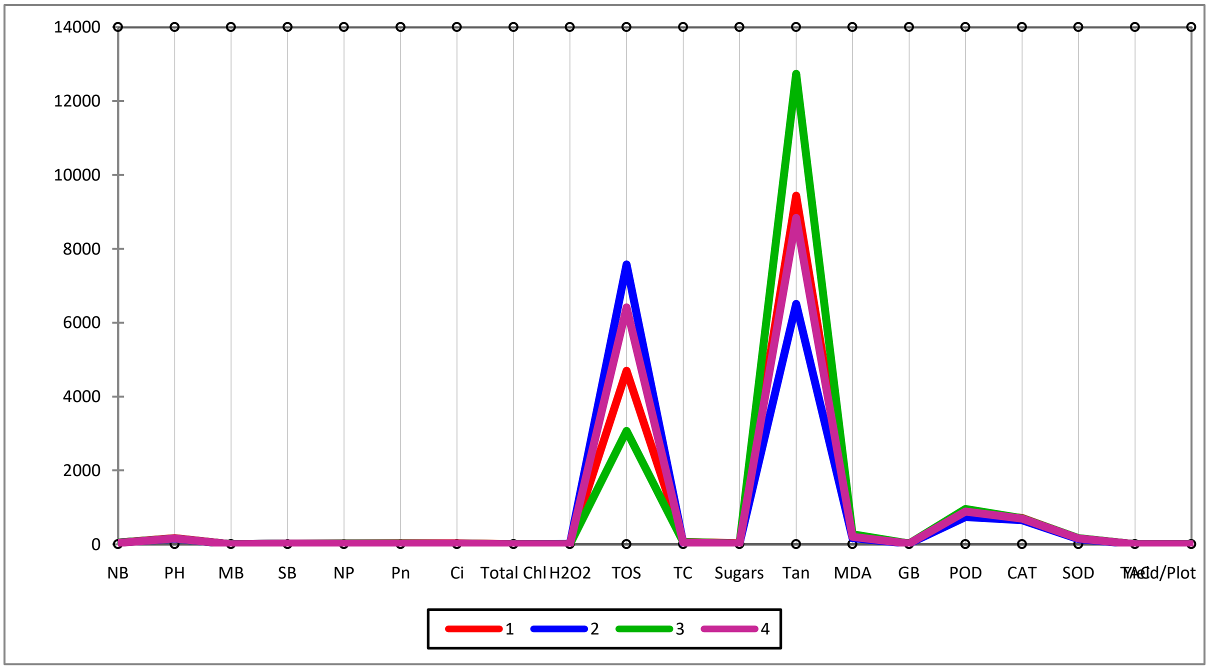

***Figure 3**: Profile Plot from cluster analysis*

Principal Component Analysis (PCA)

Principal Component Analysis (PCA) has become a significant statistical tool in the analysis of cotton genotypes, offering a method to understand the complex relationships within genetic data. It is particularly useful when you have a large set of correlated variables, as it allows you to transform the dataset into a set of linearly uncorrelated variables called principal components. Its extensive applications in this field range from identifying key morphological and physiological traits to genetic diversity analysis. By highlighting the most influential traits, researchers have been able to concentrate on factors that directly impact yield and quality. Furthermore, PCA has been instrumental in assessing genetic diversity, enabling an understanding of population structure within and between cotton species.

In the current study, the PCA extracted nine principal components (PCs) based on their performance and diversity of plant traits related to morphology, phonology, physiology, and biochemistry. The data in Table 3 and Figure 4 shows that only five of these nine PCs had an eigenvalue larger than 1. Therefore these significant PCs will be discussed in detail. These five PCs accounted for 90.328% of the variance in the data, as depicted in Table 3.

The PCA analysis displayed that PC1 accounted for 52.258% of the total variation in the data and plant height, sympodial branches per plant, net photosynthetic rate, stomatal conductance, hydrogen peroxide, total oxidants status, total carotene, sugars, tannins, malondialdehyde, glycine betaine, peroxidase, catalase, and superoxide dismutase are the most important contributing parameters (Table 4 & 5). In PC2, which contributed 14.627% to the variability in the data and has an eigenvalue of 2.925, three traits, i.e., number of bolls, monopodial branches per plant, and total antioxidant capacity, were the major contributing traits. Nodes per plant and total chlorophyll contents were the key features of principal component 3, which account for 9.427% variability in the data. PC4 and PC5 contributed 8.150% and 5.866% to the total variability with eigenvalues 1.630 and 1.173, respectively (Table 4). No parameters could make an impact on these two principal components.

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

	F1	F2	F3	F4	F5	F6	F7	F8	F9
Eigenvalue	10.452	2.925	1.885	1.630	1.173	0.818	0.579	0.353	0.184
Variability (%)	52.258	14.627	9.427	8.150	5.866	4.092	2.896	1.763	0.922
Cumulative %	52.258	66.884	76.312	84.462	90.328	94.420	97.315	99.078	100.00

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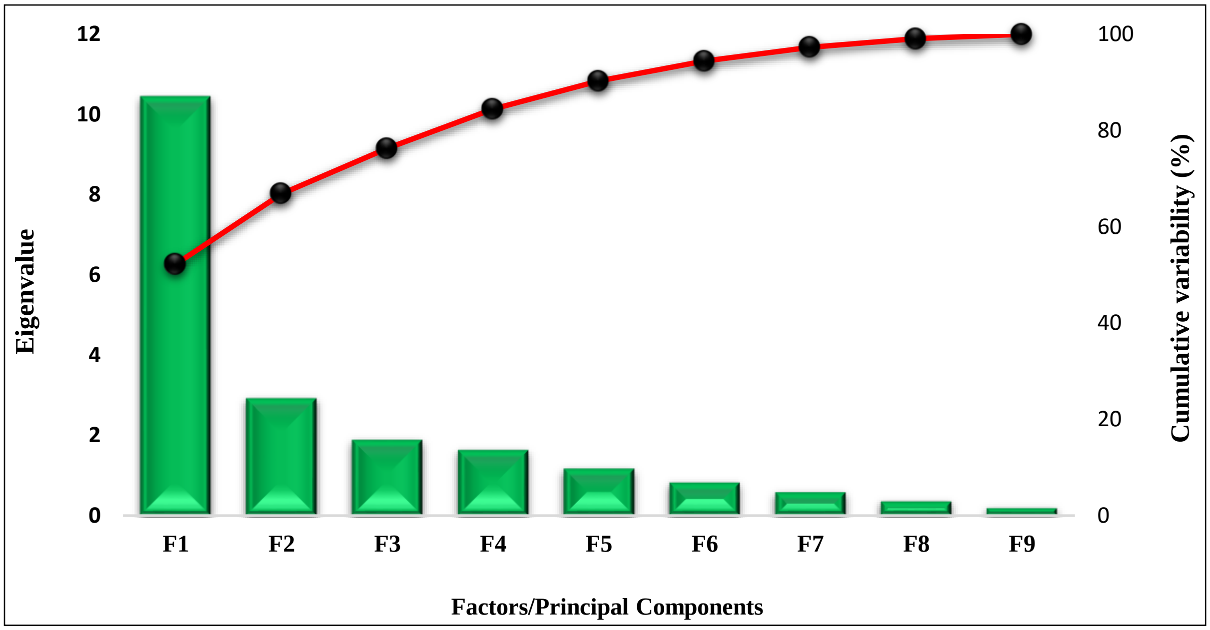

Figure 4*: Scree plot of Principal Component Analysis in cotton genotypes*

Table 4: Correlations between plant traits and principal components as derived from PCA

Plant Traits	F1	F2	F3	F4	F5
No of Bolls (NB)	0.422	-0.759	-0.202	0.011	-0.360
Plant Height (PH)	0.528	0.104	0.422	0.410	-0.424
Monopodial Branches (MB)	-0.208	-0.836	0.362	0.106	0.246
Sympodial Branches (SB)	0.750	0.175	0.539	0.061	0.140
Nodes per Plant (NP)	0.450	-0.214	0.550	-0.473	0.194
Net Photosynthetic Rate (Pn)	0.753	-0.275	-0.178	-0.405	0.131
Stomatal Conductance (Ci)	0.823	-0.289	-0.118	0.176	0.181
Total Chlorophyll Contents (Total Chl)	-0.054	0.288	0.604	-0.502	-0.398
Hydrogen per Oxide (H_2O_2)	-0.884	0.034	0.368	0.083	-0.139
Total Oxidants Status (TOS)	-0.920	-0.046	0.259	0.063	0.236
Total Carotene (TC)	0.889	-0.111	-0.078	0.298	-0.297
Sugars	0.650	0.125	0.095	0.193	0.571
Tannins (Tan)	0.931	0.033	-0.167	-0.141	-0.102
Malondialdehyde (MDA)	0.914	-0.001	-0.017	-0.094	0.031
Glycine Betaine (GB)	0.864	0.416	0.098	-0.100	-0.055
Peroxidase (POD)	0.853	0.081	0.337	-0.023	0.128
Catalase (CAT)	0.682	-0.258	0.210	0.604	-0.023
Superoxide Dismutase (SOD)	0.909	0.360	-0.001	0.115	-0.005
Total Antioxidant Capacity (TAC)	-0.004	0.951	-0.197	0.159	0.123
Yield\Plot	0.794	-0.104	-0.282	-0.443	-0.027

Table 5: Contribution of the variables (%) in different principal components

Plant Traits	F1	F2	F3	F4	F5
No of Bolls (NB)	1.707	**19.681**	2.161	0.007	11.066
Plant Height (PH)	**2.672**	0.368	9.425	10.328	15.335
Monopodial Branches (MB)	0.413	**23.878**	6.956	0.685	5.174
Sympodial Branches (SB)	**5.389**	1.052	15.429	0.228	1.668
Nodes per Plant (NP)	1.939	1.559	**16.041**	13.709	3.206
Net Photosynthetic Rate (Pn)	**5.425**	2.580	1.689	10.063	1.455
Stomatal Conductance (Ci)	**6.488**	2.856	0.745	1.903	2.801
Total Chlorophyll Contents (Total Chl)	0.028	2.829	**19.370**	15.484	13.514
Hydrogen per Oxide (H_2O_2)	**7.471**	0.039	7.192	0.423	1.645
Total Oxidants Status (TOS)	**8.107**	0.073	3.545	0.244	4.751
Total Carotene (TC)	**7.561**	0.420	0.320	5.437	7.538
Sugars	**4.043**	0.534	0.478	2.275	27.837
Tannins (Tan)	**8.293**	0.036	1.481	1.216	0.888
Malondialdehyde (MDA)	**7.986**	0.000	0.015	0.546	0.081
Glycine Betaine (GB)	**7.135**	5.906	0.506	0.610	0.261
Peroxidase (POD)	**6.965**	0.224	6.040	0.031	1.394
Catalase (CAT)	**4.449**	2.276	2.342	22.392	0.044
Superoxide Dismutase (SOD)	**7.903**	4.429	0.000	0.814	0.002
Total Antioxidant Capacity (TAC)	0.000	**30.887**	2.050	1.557	1.281
Yield\Plot (Y)	**6.026**	0.373	4.215	12.048	0.060

To observe the pattern of association between maize hybrids and investigated traits across cotton genotypes, PC1/PC2 biplot was generated using principal component analysis. The PC1/PC2 biplot analysis revealed total antioxidant capacity, monopodial branches per plant, sympodial branches per plant, glycine betaine, superoxide dismutase, hydrogen peroxide, and total oxidants status to be the most distinguishing characteristics among cotton genotypes (Figure 5). The biplot also showed that two cotton hybrids, BH-341 and BH-254, were the most productive. Moreover, five cotton genotypes, including BH-341, BH-243, BH-348, BH-313, and BH-254, showed maximum contribution toward variability in the data (Table 5). Isong et al., 2017 and Sarwar et al. 2020 used principal component analysis to categorize cotton genotypes based on agronomically important traits and found it convincing to group the cotton genotypes based on their performance.

Table 6: Contribution of the cotton genotypes (%) in different principal components

Genotypes	F1	F2	F3	F4	F5	F6	F7	F8	F9
BH-341	**6.94**	15.30	5.61	7.25	0.51	48.04	2.69	3.39	0.29
BH-243	**22.90**	4.28	8.55	4.57	0.80	0.71	13.07	1.26	33.86
BH-348	**25.30**	0.16	16.07	0.53	3.37	9.56	1.16	25.91	7.94
BH-313	**14.59**	6.04	15.63	16.07	2.89	10.40	17.05	4.97	2.37
BH-254	**13.32**	0.01	3.49	18.72	40.28	1.38	2.38	10.20	0.23
BH-188	0.21	6.48	1.43	3.86	0.51	5.06	**54.08**	8.07	10.29
BH-200	2.82	1.59	21.36	9.49	**37.37**	0.29	0.16	0.00	16.91
BH-224	4.62	**17.02**	13.73	2.91	4.27	6.92	7.90	32.62	0.01
BH-184	**9.20**	22.59	0.10	5.48	2.32	15.34	1.51	5.42	28.05
BH-600	0.11	**26.53**	14.02	31.13	7.68	2.32	0.00	8.16	0.06

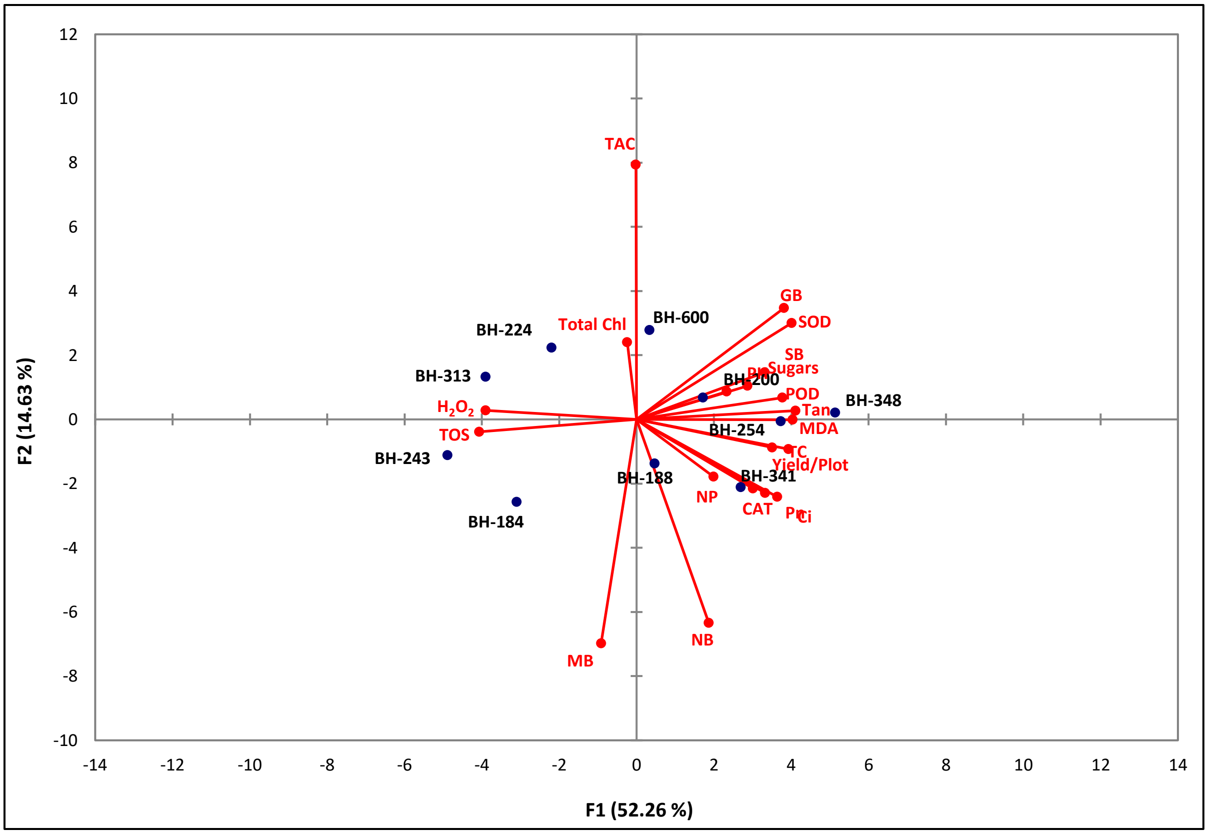

***Figure 5:** PC1/PC2 Cumulative Biplot between plant traits and cotton genotypes under heat stress*

Conclusion

The experimental results indicated the presence of significant variations in the studied plant parameters in ten cotton genotypes. The correlation analysis revealed a significantly positive correlation of seed cotton yield with net photosynthetic rate, tannins, malondialdehyde, stomatal conductance, and total carotene. Three multivariate analysis approaches, i.e., principal component, biplot, and cluster analysis, were used to categorize cotton genotypes based on their performance. These analyses revealed that BH-341 and BH-254 were the most productive cotton genotypes. Therefore, these genotypes could be recommended for cultivation in core-cotton areas following extensive multilocation testing.

Declarations

Data Availability statement

All data generated or analyzed during the study are included in the manuscript.

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

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Conflict of interest

The authors declared absence of conflict of interest.

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