Global Research journal of Natural Science and Technology (GRJNST)
Volume: 04 - Issue 1 (2026)
p.ISSN: 2790-7643 e.ISSN: 2790-7651

Evaluation of Morphometric and Physiological Divergence Present in Cultivated Cotton Germplasm

Sabir Hussain
Regional Agricultural Research Institute, Bahawalpur
Muhammad Irfan Yousaf*
Cotton Research Station, Bahawalpur
Muhammad Jamil
Cotton Research Institute, Multan
Muhammad Nouman Manzoor
Department of Plant Breeding and Genetics, The Islamia University of Bahawalpur
Saqib Saleem
Potato Research Station, Sahowali, Sialkot
Musarrat Shaheen
Cotton Research Institute, Khanpur
Imran Akhtar
Regional Agricultural Research Institute, Bahawalpur
Imran Akram
Regional Agricultural Research Institute, Bahawalpur
Ghulam Murtaza
Soil Fertility Multan
Muhammad Shah Jahan Bukhari
Agricultural Research Station, Bahawalpur
Mahreen Khalid
Regional Agricultural Research Institute, Bahawalpur
Syed Waqar Hussain Shah
Entomological Research Sub-Station, Bahawalpur

*Corresponding Author: irfanpbg.uaf@gmail.com
DOI: https://doi.org/10.53762/grjnst.04.01.28

Abstract: *Cotton (Gossypium hirsutum L.) is a major fiber crop of Pakistan; however, its productivity has declined in recent years due to climatic stress, pest pressure, and limited genetic improvement. The present study was conducted to assess genetic diversity and identify superior cotton genotypes using multivariate statistical approaches. Eleven cotton genotypes were evaluated at the Cotton Research Station, Bahawalpur, under a randomized complete block design with three replications. Data were recorded for key agronomic, physiological, yield, and fiber quality traits, including plant height, number of nodes, monopodial and sympodial branches, green bolls, open bolls, net photosynthetic rate, ginning out turn, fiber length, and seed cotton yield. Analysis of variance revealed significant genetic*

CC BY

variability among genotypes for most traits, particularly plant height, monopodial branches, net photosynthetic rate, fiber length, ginning out turn, and yield. Correlation analysis showed that seed cotton yield was strongly and positively associated with net photosynthetic rate (r = 0.95**), open bolls (r = 0.80**), number of nodes (r = 0.78**), and plant height (r = 0.75**), while a strong negative correlation was observed between yield and fiber length (r = –0.96**), indicating a trade-off between yield and fiber quality. Cluster analysis grouped the genotypes into three distinct clusters, with Cluster-2 exhibiting superior performance for yield and yield-related traits. Principal component analysis explained 85.31% of total variation through the first three principal components, highlighting net photosynthetic rate, yield, and nodal traits as major contributors to genetic divergence. Overall, the study identified promising genotypes (VH-373 and BH-224) with high yield potential and provided useful selection criteria for cotton improvement programs.

Keywords: *Upland cotton, multivariate analysis, PCA, cluster analysis, correlation*

Introduction

Upland cotton (*Gossypium hirsutum*) is an important crop due to its essential source of fiber production for the survival of the textile industry. It contributes significantly to Pakistan's Gross Domestic Product (GDP), with estimates around 0.7% to 8.5%, supporting the agricultural and industrial sectors. But a gradual decrease in cotton production in Pakistan has been observed over the last few years (Khalid & Amjad, 2019). In 2025, the cotton area is lowered due to a decline in area in Sindh province. As a result of this decline, the production is lowered to 4.8 million (480 lbs.) bales. With domestic cotton use expected to decrease slightly, the import for 2025 has been lowered to 5.6 million bales (USDA, 2025). The actual area under cotton cultivation in Pakistan for 2025 is estimated at approximately 1.85 to 2.0 million hectares (USDA, 2025).

Globally, Pakistan contributes about 4% to total cotton production, performing better than several countries such as Turkey, Uzbekistan, Argentina, and the EU. However, its share remains lower than major producers like China, India, Brazil, the United States, and Australia (USDA, 2024-25). This production gap highlights the need to improve fiber quality and enhance yield potential to remain competitive. Strengthening germplasm, adopting modern breeding tools, and improving crop management can help Pakistan elevate its global position. Cotton production in Pakistan has declined significantly over the past decade, with expected production dropping to 6.9 million bales by the 2024-25 season, due to factors like climate change, obsolete techniques, lack of investment, and pests (Salahuddin et al., 2010). Climate change has intensified droughts, heatwaves, and erratic rainfall, while declining water availability further stresses production. Pest pressure remains a major constraint, with pink bollworm, whitefly, and jassids showing variable incidence across Punjab. These bottlenecks, along with old farming practices, poor-quality seed or unavailability of quality seed to the farmer, limited adoption of modern technologies, and weak research which continue to decline cotton productivity and sustainability.

The main objective for a plant breeder is to evaluate high-yielding varieties (Salahuddin et al., 2010). Improving cotton productivity requires multiple integrated approaches, with the first step being germplasm selection and identification of genetically diverse, stress-tolerant genotypes (Jarwar et al., 2019; Hussain et al., 2024a). Advanced statistical tools, including PCA, cluster analysis, biplots, and multiple comparison tests, etc, which enable precise evaluation of high-performing genotypes. This study was conducted to evaluate the performance of cotton germplasm at the Cotton Research Station, Bahawalpur. Data were recorded across multiple replications to ensure precise assessment of growth, yield, and stress-responsive traits. Such a comprehensive assessment facilitates the identification of the most resilient and high-performing genotypes, which can be prioritized in breeding programs to develop robust, high-yielding cotton varieties for sustainable production.

Material and Method

Location and Experimental Design

This experiment was conducted at the Cotton Research Station, Bahawalpur, located at southeast Punjab, which is the most cotton-cultivated division of Punjab, Pakistan. The climate as well as soil is suitable for this region. This experiment was laid out according to a Randomized Complete Block Design (RCBD), with each having three replications. The eleven genotypes were selected in this study, named as Tri Star, FH-1050, C-55, VH-373, BH-224, Sultan, BH-228, AZ-10, 666, AZ-8, and FH-490, and sown with the dibbling method, @three seeds per hill. At the early seedling stage, thinning was performed, and one healthy seedling was retained to maintain proper plant-to-plant spacing. All Agronomic and plant protection practices were carried out for all treatments.

Data measured

Data were recorded for key agronomic traits, including plant height (PH), number of nodes per plant (Nodes), number of monopodial branches (MNP), number of sympodial branches (SYMP), number of green bolls per plant (GB), number of open bolls per plant (OB), ginning out turn (GOT %), fiber length (FL), and Seed cotton yield (Yield).

Statistical analysis

The collected data was statistically analyzed for analysis of variance, multiple comparison, correlation coefficient analysis, cluster, and biplot analysis (Steel et al., 1997) using statistical analysis software such as Statistics 8.1, R/R-Studio, and Microsoft Excel for analysis of data and to illustrate the graphs.

Results and Discussion

Analysis of variance

The ANOVA results revealed significant differences among the eleven cotton genotypes, confirming the presence of significant suitable diversity. Genotypes showed a highly significant difference for plant height (530.78**), monopodial branches (0.55**), fiber length (1.66**), net photosynthetic rate (12.22**), GOT% (6.40**), and yield (5.81**). But the number of nodes (29.32^{NS}), Sympodial branches (19.60^{NS}), and open bolls (57.69^{NS}) showed a non-significant difference, suggesting limited genetic diversity for these traits among the tested genotypes. Green bolls (28.28*) per plant were significant, indicating the moderate genetic influence.

Table 1: Analysis of Variance for studied plant traits in eleven cotton genotypes

SOV	Replication	Genotype	Error
df	**2**	**10**	**20**
Plant height	45.09	530.78**	81.42
Nodes per plant	11.75	29.32^{NS}	21.35
Monopodial branches per plant	0.21	0.55**	0.078
Sympodial branches per plant	14.18	19.60^{NS}	20.71
Green Bolls	10.09	28.28*	9.15
Open Bolls	16.03	57.69^{NS}	51.79
Fiber Length	0.25	1.66**	3.30E-30
Net Photosynthetic rate	1.48	12.22**	0.15
Ginning Out Turn	0.27	6.40**	0.072

Seed Cotton Yield	0.039	5.81**	0.0001

The ANOVA results indicate that the eleven cotton genotypes possess meaningful exploitable genetic variability for key productivity, physiological, and quality traits, as evidenced by highly significant genotypic effects for plant height, monopodial branches, fiber length, net photosynthetic rate, GOT%, and seed cotton yield. This pattern suggests that selection can effectively target yield improvement through traits reflecting both plant vigor and lint productivity (GOT%), while also enabling improvement in fiber length, which is a major quality determinant in breeding programs (Mangi et al., 2024). In contrast, the non-significant variation for nodes per plant, sympodial branches, and open bolls implies that these characters were comparatively stable across the tested material, potentially due to a narrow genetic base for these traits in the selected genotypes or past selection that reduced variability, thereby limiting their usefulness as discriminating selection criteria within this specific set.

The significant genotypic differences for green bolls (moderate level) still support a measurable genetic impact on early fruiting and boll formation, which can contribute to yield under semi-arid conditions. Notably, the highly significant variation in net photosynthetic rate is particularly relevant because genotypic differences in photosynthetic performance are increasingly recognized as a pathway to improve cotton productivity and resilience under stress-prone environments, and recent work links photosynthetic efficiency and stress response to yield outcomes in cotton (Younas et al., 2025; Thompson et al., 2025; Hussain et al., 2023a). Therefore, the combination of significant yield, GOT%, fiber length, and photosynthetic variability confirms that these genotypes provide a useful breeding pool for simultaneous improvement of yield potential, lint percentage, and fiber quality, while traits showing non-significant differences may require broader germplasm introgression or multi-environment testing to reveal hidden variability (Mangi et al., 2024).

Correlation Coefficient Analysis

The correlation coefficient analysis unveiled the relationships among different plant traits including plant height (PH), number of nodes (Nodes), monopodial branches (MNP), sympodial branches (SYMP), net photosynthetic rate (Pn), fiber length (FL), ginning out-turn (GOT), open boll (OB), green boll (GB), and seed cotton yield. The results showed that seed cotton yield had the highest positive correlation with net photosynthetic rate ($r = 0.95^{**}$), followed by open bolls ($r = 0.80^{**}$), number of nodes ($r = 0.78^{**}$), and plant height ($r = 0.75^{**}$). However, seed cotton yield was found negatively correlated with fiber length ($r = –0.96^{**}$). Moderate positive correlations of cotton yield were observed with sympodial branches ($r = 0.600^{*}$), ginning out-turn ($r = 0.50^{*}$), and boll weight ($r = 0.38^{*}$). Net photosynthetic rate showed a positive relationship with the number of nodes ($r = 0.75^{**}$) and plant height ($r = 0.72^{**}$), contributing to seed cotton yield. However, fiber length showed the highest negative correlation with net photosynthetic rate ($r = –0.98^{**}$), reflecting an inverse relationship between yield and fiber quality. Monopodial branches had weak correlations with yield ($r = 0.22^{ns}$).

Table 2: Correlation coefficients among yield and quality traits of studied genotypes.

Variables	PH	Nodes	MNP	SYMP	GB	OB	Pn	FL	GOT
Nodes	0.562								
MNP	-0.001	0.304							
SYMP	**0.704**	0.600	-0.325						
GB	-0.028	0.106	-0.013	0.125					
OB	**0.784**	0.587	0.262	0.566	0.336				
Pn	**0.717**	**0.750**	0.156	0.451	0.283	**0.673**			

FL	**-0.698**	**-0.749**	-0.225	-0.435	-0.239	**-0.731**	**-0.977**		
GOT	0.078	0.392	**0.603**	-0.161	-0.042	0.180	0.531	**-0.618**	
Yield	**0.749**	**0.787**	0.217	0.600	0.380	**0.799**	**0.946**	**-0.954**	0.504

The correlation matrix indicates that, under the tested conditions, seed cotton yield is primarily driven by source strength and fruiting intensity, with the strongest positive association observed between yield and net photosynthetic rate, followed by open bolls, nodes, and plant height, collectively suggesting that genotypes with greater canopy development and higher carbon assimilation tend to set and mature more bolls and ultimately achieve higher yield. This agrees with recent studies showing that physiological performance and stress-response capacity are closely linked with yield outcomes across genotypes and environments (Thompson et al., 2025). However, the very strong negative correlation between yield and fiber length, along with the strongly negative association between FL and Pn, suggests a pronounced yield–quality trade-off, likely reflecting competition for assimilates between boll/fiber development and total fruit load, an issue increasingly emphasized in modern cotton improvement where selection for higher productivity can inadvertently constrain certain fiber attributes if not managed through balanced indices and parent choice (Scarpin et al., 2023; Younas et al., 2025). Meanwhile, yield's moderate positive correlations with number of sympodial branches and GOT% indicate that both fruiting branch development and lint proportion still contribute meaningfully to productivity, whereas the weak relationship of monopodia with yield implies limited value of monopodial branching as a direct selection proxy in this specific germplasm set; overall, these relationships support prioritizing Pn, boll opening, node production, and plant stature for yield enhancement while simultaneously using multi-trait selection to prevent deterioration of fiber length (Lamlom et al., 2024; Hugar et al., 2024)

Cluster Analysis

The cluster analysis categorized the eleven cotton genotypes into three distinct clusters based on their performance across plant height, number of nodes, monopodial branches, sympodial branches, net photosynthetic rate, fiber length, ginning out turn, open boll, green boll and seed cotton yield. The dendrogram, using Euclidean distance and Ward's method, divided the genotypes into three clusters with cluster-1 (Tri Star, FH-1050, C-55, BH-228, BH-90, AZ-28), cluster-2 (VH-373, BH-224), cluster-3 (Sultan, AZ-10, FH-490) as shown in Figure 1. Cluster 2 showed the highest mean values for seed cotton yield (5.612 kg/plot), plant height (151.667cm), number of nodes (41.333), sympodial branches (36.833), net photosynthetic rate (29.167µmol m^{-2} s^{-1}), and open bolls (33.167), identifying this cluster as the most superior in terms of overall productivity (Table 3). However, Cluster 1 exhibited intermediate performance, with moderate plant height (134.167 cm), node count (39.333), sympodial branch number (33.722), green bolls (7.778), and yield (4.798 kg/plot), suggesting balanced growth and yield potential. On the other hand, Cluster 3 recorded the lowest values for most traits, including plant height (115.556cm), net photosynthetic rate (25.44µmol m^{-2} s^{-1}), open bolls (24.00), and yield (2.936 kg/plot), indicating poor yield performance of member genotypes. However, Cluster 3 showed relatively higher fiber length (29.17mm), suggesting a possible trade-off between yield and fiber quality.

Table 3: Cluster analysis grouping of cotton genotypes based on yield and quality traits.

Cluster	Cluster-1	Cluster-2	Cluster-3
Plant height	134.16	151.67	115.56
Nodes per plant	39.33	41.33	37.000

Monopodial branches per plant	0.38	0.00	0.000
Sympodial branches per plant	33.72	36.9	32.33
Green Bolls	7.78	4.33	5.22
Open Bolls	29.56	33.16	24.00
Net Photosynthetic rate	28.00	29.16	25.44
Fiber Length	28.36	27.78	29.17
Ginning Out Turn	**34.56**	**33.5**	**35.47**
Seed Cotton Yield	4.79	5.62	2.94

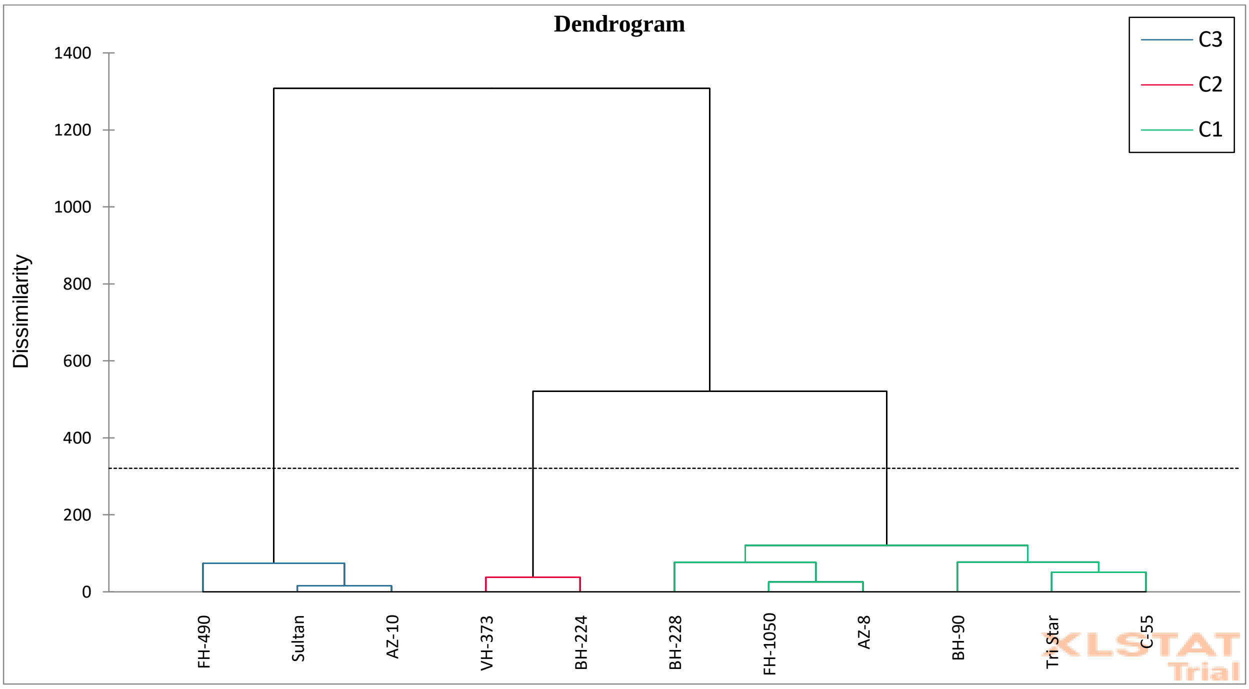


Figure 1: Dendrogram generated through cluster analysis showing genetic divergence.

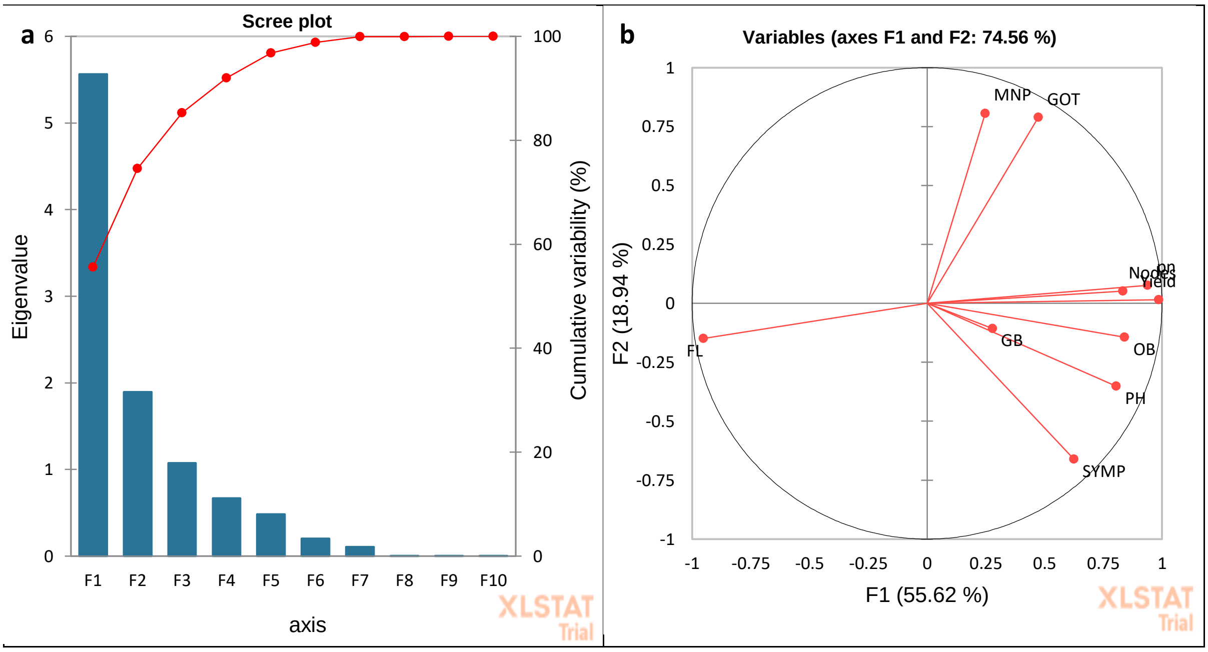
The cluster analysis grouped the eleven cotton genotypes into three distinct clusters, revealing clear genetic divergence based on yield, morphological, physiological, and fiber quality traits. Cluster-2 (VH-373 and BH-224) emerged as the most superior group, exhibiting the highest mean values for seed cotton yield, plant height, number of nodes, sympodial branches, net photosynthetic rate, and open bolls, indicating that enhanced canopy development and reproductive capacity collectively contributed to superior productivity. This clustering pattern supports previous findings that yield improvement in cotton is strongly associated with plant vigor, fruiting branch number, and photosynthetic efficiency, which together enhance assimilate production and boll retention (Thompson et al., 2025). Cluster-1 displayed intermediate performance with balanced vegetative growth and moderate yield, suggesting stable adaptability and potential utility in breeding programs targeting both yield and stability. In contrast, Cluster-3 recorded the lowest values for most yield-contributing traits but showed relatively higher fiber length and ginning out turn, indicating a potential trade-off between productivity and fiber quality. Such inverse relationships between yield and fiber attributes have been widely reported in cotton breeding studies, where resource allocation dynamics influence lint development versus boll load (Scarpin et al., 2023; Hussain et al., 2024b; Javed et al., 2024). Overall, the clear separation of genotypes into three clusters highlights substantial genetic diversity and suggests that hybridization between high-yielding Cluster-2 genotypes and fiber-quality-oriented Cluster-3 lines may broaden the genetic base and enhance simultaneous improvement of yield and quality traits.

Principal Component Analysis (PCA)

Principal Component Analysis (PCA) revealed substantial genetic diversity among the studied genotypes. The Scree plot indicated that the first three principal components (PC1, PC2, PC3) had eigenvalues greater than one, collectively explaining 85.306% of the total variation (Figure 2). The first principal component (PC1) showed the highest eigenvalue (5.562) and alone accounted for 55.623% of the total variation. The PC2 and PC3 principal components contributed 18.935% and 10.748% of the variation, respectively, further confirming their importance in describing genetic diversity. The remaining principal components (PC4-PC10) had eigenvalues less than one and contributed only minor proportions to total variability, indicating limited practical importance (Table 4). The cumulative variance exceeded 96% by PC5 and approached 100% by PC9, showing that later components added little additional information.

Table 4: Eigenvalues, proportion of variance, and cumulative variance explained by the principal components of cotton genotypes

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**
Eigenvalue	5.562	1.89	1.07	0.66	0.48	0.20	0.10	0.005	0.004	0.000
Variability %	55.62	18.93	10.74	6.68	4.82	2.03	1.06	0.05	0.039	0.000
Cumulative %	55.62	74.56	85.30	91.9	96.8	98.8	99.9	99.9	100.0	100.0



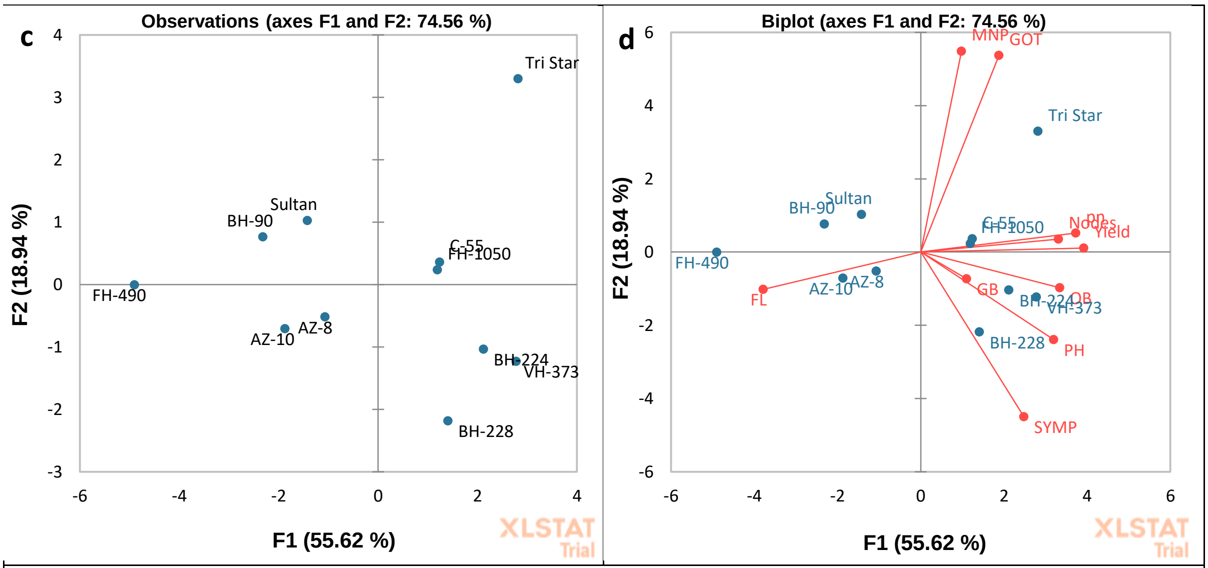


Figure 2: Principal Component Analysis in eleven cotton genotypes **(a)** Screeplot of Principal Component Analysis **(b)** Variable biplot **(c)** Observation biplot **(d)** Combined PCA Biplot

The individual variable indicates that in PC1, net photosynthetic rate and the number of nodes strongly positively correlated with seed cotton yield (Figure 2). However, fiber length showed a strong negative association with yield. Furthermore, in PC2, monopodial branches and ginning out turn indicate a positive correlation with yield. However, fiber length showed a negative correlation. In an individual observation plot, the genotypes Tri Star, VH-373, BH-228, BH-224, and FH-490 showed a strong divergence, as indicated by observations far from the mean (Figure 2).

The combined PCA biplot (PC1 = 55.62%, PC2 = 18.94%) explains 74.56% of the total variation. Genotypes located near traits showed a strong association with those traits. BH-224 and VH-273 are close to Yield, net photosynthetic rate, and number of nodes, indicating better growth and productivity. Tri-Star lies near the monopodial branches and ginning out tern, showed a strong association with those traits. FH-490 is close to the fiber length as shown in Figure 2.

The Principal Component Analysis (PCA) demonstrated pronounced genetic variability among the eleven cotton genotypes, with the first three principal components explaining 85.31% of the total variation, indicating that most of the genetic divergence can be effectively summarized within a reduced dimensional framework. PC1 alone accounted for 55.62% of the total variability, reflecting that a major proportion of variation among genotypes is governed by a core group of agronomic and yield-related traits, while PC2 (18.93%) and PC3 (10.74%) further captured secondary sources of differentiation. The presence of eigenvalues greater than one for PC1, PC2, and PC3 confirms their statistical and biological relevance in describing diversity, whereas subsequent components (PC4–PC10) contributed minimal additional variation, suggesting limited practical importance for genotype discrimination. Such dominance of the first few principal components is commonly reported in cotton diversity studies, where yield, plant architecture, and physiological traits collectively drive most of the observed variability (Hugar et al., 2024; Yousaf et al., 2024; Yousaf et al., 2022). The rapid accumulation of cumulative variance beyond 96% by PC5 further indicates redundancy among later components and validates the efficiency of PCA in summarizing complex multivariate datasets. Overall, these findings confirm substantial genetic divergence within the studied germplasm and highlight the usefulness of

PCA in identifying superior and contrasting genotypes for strategic parent selection in cotton breeding programs aimed at improving yield and fiber-related traits (Scarpin et al., 2023).

Conclusion

The present investigation confirmed the existence of substantial genetic diversity among the evaluated cotton genotypes under the agro-climatic conditions of Bahawalpur. Significant variation for key agronomic, physiological, yield, and fiber traits indicates ample scope for selection and genetic improvement. Seed cotton yield was primarily influenced by net photosynthetic rate, number of open bolls, nodal count, and plant height, suggesting that these traits should be prioritized in selection strategies. The strong negative association between yield and fiber length highlights a potential trade-off, emphasizing the need for balanced breeding approaches to improve both productivity and fiber quality simultaneously. Multivariate analyses effectively differentiated the genotypes, with cluster and PCA results consistently identifying Cluster-2 genotypes, particularly VH-373 and BH-224, as superior performers for yield and related traits. These genotypes can be exploited directly in varietal development or used as parental material in future breeding programs. Overall, the findings provide a strong scientific basis for germplasm selection and contribute to the development of high-yielding, resilient cotton cultivars for sustainable cotton production in Pakistan.

Author’s Contribution

MIY; *Conceptualization and Execution,* **MIY, MNM, SS, SWHS,** *Data retrieval, Writing – original draft;* **MJ, MS, IA, GM, IA**; *Writing – review & editing,* **SJB, MK, SH**; *Data Visualization and Analysis;*

References

Khalid, M., & Amjad, I. (2019). Combining Ability and Heterosis Studies In Upland Cotton (Gossypium Hirsutum L.). *Bulletin of Biological and Allied Sciences Research*, *2019*(1), 20. https://doi.org/10.54112/bbasr.v2019i1.20

USDA (United States Department of Agriculture) (2025). Cotton and Products Update. USDA Foreign Agricultural Service USDA

https://share.google/onjcHTiG1xntA7pXZ

USDA (United States Department of Agriculture) (2025). Cotton and Products Update. USDA Foreign Agricultural Service USDA

https://www.fas.usda.gov/data/production/commodity/2631000

Salahuddin, S., Abro, S., Kandhro, M., Salahuddin, L., Laghari, S., & Pakistan, S. (2010). Correlation and Path Coefficient Analysis of Yield Components of Upland Cotton (Gossypium hirsutum L.) Sympodial Nuclear Institute of Agriculture. *Biotechnology & Genetic Engineering*, *8*, 71–75.

Jarwar, A. H., Wang, X., Iqbal, M. S., Sarfraz, Z., Wang, L., Ma, Q., & Shuli, F. (2019). Genetic divergence on the basis of principal component, correlation, and cluster analysis of yield and quality traits in cotton cultivars. *Pakistan Journal of Botany*, *51*(3), 1143–1148. https://doi.org/10.30848/PJB2019-3(38)

Mangi, N., Iqbal, M. S., Shuli, F., Iqbal, M. T., Alharthi, B., Jatoi, G. H., ... & Sun, X. (2024). Empowering cotton breeding programs through the strategic exploration and exploitation of phenotypic diversity of genetic resources under climate change conditions. Plant Stress, 13, 100548.

Younas, M., Zafar, M., Hussain Babar, B., Jamil, M., Ashraf, M. S., Habib, I., Hussain, A., Idrees, M., Waqar, S., Shah, H., Shaheen, M., Khan, A. G., Tauseef, M., & Yousaf, M. I. (2025). Role of Photosynthetic Rate and Transpiration Efficiency in Fibre and Lint Yield Improvement of Upland Cotton Genotypes in Clay-Loamy Soils. *Global Research Journal of Natural Science and Technology (Grjnst)*, *3*(2), 3–5.

Thompson, A. L., Thorp, K. R., & Herritt, M. T. (2025). Identifying seed cotton yield and abiotic stress response in cotton (*Gossypium hirsutum* L.) grown in the Arizona low desert. *Crop Science*, *65*(2), e70058.

Scarpin, G. J., Dileo, P. N., Winkler, H. M., Cereijo, A. E., Lorenzini, F. G., Muchut, R. J., ... & Paytas, M. (2023). Genetic progress in seed and fiber quality traits of cotton in Argentina. *Field Crops Research*, *302*, 109106.

Lamlom, S. F., Yehia, W. M. B., Kotb, H. M. K., Abdelghany, A. M., Shah, A. N., Salama, E. A., ... & Abdelsalam, N. R. (2024). Genetic improvement of Egyptian cotton (Gossypium barbadense L.) for high yield and fiber quality properties under semi arid conditions. *Scientific Reports*, *14*(1), 7723.

Hugar, A. A., Nidagundi, J. M., Fakrudin, B., Neelagiri, Y. L., Muniswamy, S., Hosamani, A. C., ... & B, K. (2024). Genetic divergence and hybrid potential for yield and fiber quality in cotton

Hussain, A., Jamil, S., Bilal, M., Nadeem, A., Kausar, S., Umer, F., Akram, F., Haq, A. U. L., Quyum, M. A., Butt, B., Qamar, M. J., Iqbal, R. A., Ahmad, R. T., Shakir, M. S., Hussain, S., & Yousaf, M. I. (2024a). Impact of water stress on cotton physiology, ROS accumulation and antioxidant activity in upland cotton genotypes. Biological and Clinical Sciences Research Journal, 5, 919.

Hussain, S., Aslam, M. Z., Yousaf, M. I., Iqbal, J., Bukhari, M. S. I., Ali, F., Ashfaq, M., Qamar, M. I., Farooq, M. R., Hafeez, Z., Akhtar, I., & Shah, S. W. H. (2023a). Quantitative effects of heat stress on fiber-related and agronomically important parameters in cotton (*Gossypium hirsutum* L.). Biological and Clinical Sciences Research Journal, 4, 210.

Younas, M., Zafar, M., Babar, B. H., Jamil, M., Munir, M. K., Iqbal, M. M., ... & Hussain13, S. (2025). Multivariate Analysis of Elite Bt Cotton Genotypes for Seed Cotton Yield and Fiber Quality Traits Under Semi-Arid Conditions. *Plant Biotechnology*, *3*, 101-111.

Javed, I., Ashraf, S., Parveen, N., Jamil, M., Ghaffar, W., Sardar, A., Qamar, M. J., Farooq, M. R., Saleem, S., Habib, F., Akram, M. I., Javeed, Z., Khalid, M., Latif, M. I., Rauf, A., Hussain, F., Ali, B., Hassan, W., Manzoor, N., Yousaf, M. I., & Hussain, S. (2024). Role of photosynthetic stability and physio-chemical attributes in the selection of improved cotton genotypes in actual field conditions. Biological and Clinical Sciences Research Journal, 5, 199.

Hussain, S., Khan, M. M., Talib, I., Khalid, M., Zubair, M., Murtaza, G., Akhtar, I., Qamar, M. J., Farooq, M. R., Ashfaq, M., Bukhari, M. S. J., Shah, S. W. H., Ali, B., Nayab, S. F., Akram, M. I., Nazar, S., Kausar, S., Asif, M., Jamil, S., Rehman, S., Saleem, M., Luqman, M., & Yousaf, M. I. (2024b). Genetic characterization and performance evaluation of elite cotton strains for morphological and physio-chemical traits under heat stress conditions. Biological and Clinical Sciences Research Journal, 5, 725.

Steel, R. G. D., Torrie, J. H. and Dickey, D. A. (1997). Principles and Procedures of Statistics: A Biometrical Approach, 3rd Ed. McGraw Hill Book Co., New York.

Yousaf, M. I., Ghani, A., Zubair, M., Talib, I., Kausar, S., Akhtar, I., Murtaza, G., Rehman, S., Bukhari, M. S. J., Nazar, S., Qamar, M. J., Akram, F., Ashfaq, M., Shah, S. W. H., Ali, B., Sharif, S., Luqman, M., Asif, M., Jamil, S., Sattar, A., Hafeez, Z., Khalid, M., & Hussain, S. (2024). Role of antioxidants accumulation and photosynthetic stability for sustainable cotton production and fibre quality under water stress conditions. Biological and Clinical Sciences Research Journal, 5, 726.

Yousaf, M. I., Hussain, Q., Alwahibi, M. S., Aslam, M. Z., Khalid, M. Z., Hussain, S., Zafar, A., Shah, S. A. S., Abbasi, A. M., Mehboob, A., Riaz, M. W., & Elshikh, M. S. (2022). Impact of heat stress on agro-morphological, physiochemical and fiber related parameters in upland cotton (*Gossypium hirsutum* L.) genotypes. Journal of King Saud University – Science, 35, 102379.