

## GENETIC CHARACTERIZATION OF ELITE COTTON STRAINS FOR THEIR YIELD POTENTIAL AND FIBER QUALITY TRAITS

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### ABSTRACT

Cotton (*Gossypium hirsutum* L.) is a pivotal cash crop supporting global textile industries and rural livelihoods, especially in major producing countries such as Pakistan. This study aimed to assess the genetic diversity of ten elite cotton genotypes using multivariate statistical techniques under arid field conditions of Bahawalpur. The evaluation focused on key morphological, physiological, and fiber quality traits to identify high-performing genotypes suitable for future breeding. A randomized complete block design with three replications was implemented, and traits such as plant height, number of nodes per plant, number of sympodial branches per plant, total number of bolls per plant, boll weight, seed cotton yield, ginning Out turn, staple length, fiber strength and fiber fineness were measured. Analysis of variance revealed significant genotypic variation across most traits, indicating substantial genetic diversity. Cluster analysis effectively distinguished genotypes with superior combinations of yield and fiber attributes. Genotypes BH-422, BH-408, BH-184, and CIM-600 demonstrated promising yield and fiber characteristics, making them ideal candidates for breeding programs targeting high productivity and fiber excellence. The findings underscore the potential of integrating multivariate analysis for strategic genotype selection to meet the dual objectives of yield maximization and lint quality improvement.

**Keywords:** Cluster analysis, physiological traits, agronomic performance, genotypic variability

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### INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is globally recognized as one of the most critical cash crops, not only for its economic contribution but also for its role in sustaining rural livelihoods. It serves as the backbone of many economies, particularly in cotton-producing countries like Pakistan, India, China, the United States, and Brazil, where millions of farmers, laborers, and industries depend on its cultivation and processing (USDA, 2025). The fiber produced from cotton is a raw material for the textile sector, while its by-products, including cottonseed oil and

meal, further enhance its industrial significance (Liu *et al.*, 2012). In Pakistan, cotton is often referred to as "white gold" due to its profound contribution to national GDP and foreign exchange earnings, accounting for nearly 60% of the country's total export earnings (Hussain *et al.*, 2025). However, despite its critical importance, the cotton sector faces significant challenges such as climatic fluctuations, pest pressures, and declining soil fertility, which directly impact yield potential and fiber quality traits (Mollaee *et al.*, 2019).

Over the years, the demand for superior cotton fiber quality has intensified globally, driven by the evolving requirements of the textile industry and international markets. High fiber quality, characterized by parameters such as fiber length, strength, fineness, and uniformity, is pivotal for manufacturing premium fabrics and ensuring competitive advantage in global trade (May, 2024). Simultaneously, maximizing yield potential remains a priority to meet the growing raw material demand for the spinning industry (Yousaf *et al.*, 2023). These dual objectives of enhancing yield and improving fiber quality necessitate the adoption of advanced breeding strategies and precise genetic characterization of available germplasm. Identification and utilization of elite cotton genotypes exhibiting superior performance for both yield and fiber quality traits can accelerate the development of resilient, high-performing cultivars suitable for diverse agro-ecological zones (Manan *et al.*, 2022).

Genetic characterization, especially when integrated with robust multivariate analyses, plays a crucial role in unraveling the complex interactions between yield-contributing and fiber quality traits in cotton (Joshi *et al.*, 2023). Techniques such as Principal Component Analysis (PCA) and cluster analysis allow breeders to assess genetic diversity, classify genotypes, and identify promising parental lines for targeted hybridization programs (Singh, 2022; Hussain *et al.*, 2024). Previous studies have demonstrated that genotypes exhibiting a favorable combination of agronomic and fiber attributes significantly contribute to enhancing overall crop productivity and fiber marketability (Rahman *et al.*, 2022). Moreover, understanding trait interrelationships helps in the formulation of effective selection criteria, enabling breeders to simultaneously improve multiple traits and achieve substantial genetic gains.

Considering the pivotal role of elite cotton strains in sustainable cotton improvement programs, it becomes imperative to perform their comprehensive genetic characterization under field conditions. This approach not only helps in identifying superior genotypes but also supports the cotton breeding pipeline by providing essential data on trait stability and genotype performance across environments (Aslam *et al.*, 2022). The present study, therefore, aims to evaluate the genetic diversity of elite cotton strains with a specific focus on yield potential and fiber quality parameters. By deploying multivariate statistical techniques, the study endeavours to dissect the genetic relationships among traits and categorize the genotypes effectively, thus providing valuable insights for breeders to enhance cotton productivity and fiber excellence in future breeding initiatives.

## MATERIALS AND METHODS

### Experimental Site and Environmental Conditions

The present research trial was conducted during the cotton growing season of 2024 at the experimental fields of Cotton Research Station, Bahawalpur, Pakistan (29.3954° N, 71.6833° E). The region is characterized by an arid climate with extreme summer temperatures, often exceeding 45°C during peak flowering and boll-setting stages, and low annual rainfall ranging between 100–200 mm. The experimental field had sandy clay loam soil, and all standard agronomic practices recommended for cotton cultivation were followed uniformly across the study. The physio-chemical properties of the soil and irrigation water used in this study are presented in Table 1.

**Table 1.** Properties of Soil and Irrigation Water at the Experimental Site.

Parameters	Value
Soil Texture	Sandy Clay Loam
pH	7.8
EC (dS/m)	4.9
Organic Matter (%)	0.74
Available Phosphorus (ppm)	7.5
Available Potassium (ppm)	85
Zinc (ppm)	1.35
TSS in irrigation water (ppm)	1145
SAR	6.8
RSB	1.45
Chloride (meq/L)	4.3

### Plant Material and Experimental Design

The experimental material consisted of ten elite cotton genotypes, namely: BH-220, BH-248, BH-313, BH-402, BH-406, BH-408, BH-417 and BH-422 including two approved check varieties i.e., BH-184 and CIM-600. These genotypes were selected from the advanced breeding program of Cotton Research Station, Bahawalpur, based on preliminary evaluations for yield potential and fiber quality attributes. The trial was laid out in a Randomized Complete Block Design (RCBD) with three replications to ensure reliable statistical inference. Each experimental unit consisted of four rows, each 30 feet in length. The plant-to-plant spacing was maintained at 30 cm, while row-to-row distance was kept at 75 cm to ensure adequate aeration and sunlight interception. Manual dibbling was employed for sowing at a rate of two seeds per hill, followed by thinning at the early vegetative stage to maintain optimum plant density. Standard crop management practices were uniformly adopted across the experimental field, including timely irrigation, fertilizer application at the recommended rate of 200:100:50 kg ha<sup>-1</sup> of N:P:K, and pest control measures. Weeds were managed through both manual weeding and herbicide application as per crop requirement.

### Data Collection

Data were collected from ten randomly selected, well-guarded plants per genotype in each replication to avoid border effects. The following morphological, physiological, and fiber quality traits were recorded during the study i.e., Plant height, number of nodes per plant, number of sympodial branches per plant, total number of bolls per plant, boll weight, seed cotton yield, ginning Out turn, staple length, fiber strength and fiber fineness. Fiber quality parameters were assessed using High Volume Instrument (HVI) at the Fiber Testing Laboratory, Cotton Research Institute, Multan. For physiological measurements, traits such as net photosynthetic rate, transpiration rate and stomatal conductance were recorded using the CI-340 Handheld Photosynthesis System (CID Bio-Science, Inc.).

### Statistical Analysis

The collected data were statistically analyzed using Statistix 8.1, XLSTAT, and OriginPro 2023 software packages. Analysis of Variance (ANOVA) was performed to detect significant differences among genotypes for the studied traits (Steel *et al.*, 1997). Trait associations were explored through Pearson's correlation coefficient analysis to determine relationships between yield and fiber quality attributes (Yousaf *et al.*, 2023). To better understand the multivariate relationships and genotype performance, Cluster analysis was employed following the method used by Hussain *et al.* (2023a). Genotypes were categorized into clusters based on their overall performance using agglomerative hierarchical clustering.

## RESULTS AND DISCUSSION

### Analysis of Variance

The analysis of variance (ANOVA) demonstrated highly significant ( $p < 0.01$ ) genetic differences among the tested cotton genotypes for all the studied traits, except for boll weight, which showed significance at the  $p < 0.05$  level (Table 2). The maximum variation was recorded for seed cotton yield, followed by plant height and total bolls per plant, indicating the presence of substantial genetic diversity in these traits, which are crucial for yield enhancement. Significant differences were also observed for physiological parameters, with stomatal conductance and net photosynthetic rate displaying notable variability, reflecting genotypic differences in gas exchange efficiency and photosynthetic activity. Such variation is essential for selecting genotypes with improved photosynthetic capacity and water-use efficiency under field conditions (Javed *et al.*, 2024; Younas *et al.*, 2025a; Younas *et al.*, 2025b).

Moreover, fiber quality traits such as fiber strength, fiber length, and fiber fineness also showed significant genotypic variation, indicating ample scope for improving lint quality through breeding. The significant variation in GOT further supports the potential for enhancing fiber recovery from seed cotton. These findings align with earlier reports by Afzal *et al.* (2024) and Younas *et al.* (2025c), who emphasized that genetic variability for yield and fiber traits is the cornerstone for selecting high-performing genotypes. The presence of wide genetic diversity among the elite genotypes in this study suggests their suitability for future breeding programs aimed at simultaneous improvement of yield potential and fiber quality, ensuring the development of superior cotton cultivars adapted to diverse agro-climatic conditions.

**Table 2.** Mean Square (MS) values of studied cotton traits in ten cotton genotypes.

Sov	Replications	Genotypes	Error
df	2	9	18
Plant Height	42.03	593.26**	81.89
Number of Nodes per Plant	17.03	80.75**	6.47
Number of sympodial branches per Plant	0.93	12.38**	3.89
Total Bolls	0.1333	17.6**	4.8
Net Photosynthetic Rate	62.5	18.63**	6.05
Stomatal Conductance	3491.76	1831.9**	703.2
Transpiration Rate	0.13	0.398**	0.1
Fiber length	0.54	0.42**	0.11
Fiber strength	5.59	37.56**	11.43
Fiber Fineness	0.01	0.18**	0.06
Ginning out turn	0.35	4.53**	1.66
Boll weight	0.03	0.05*	0.028
Yield	700064	852670**	44284

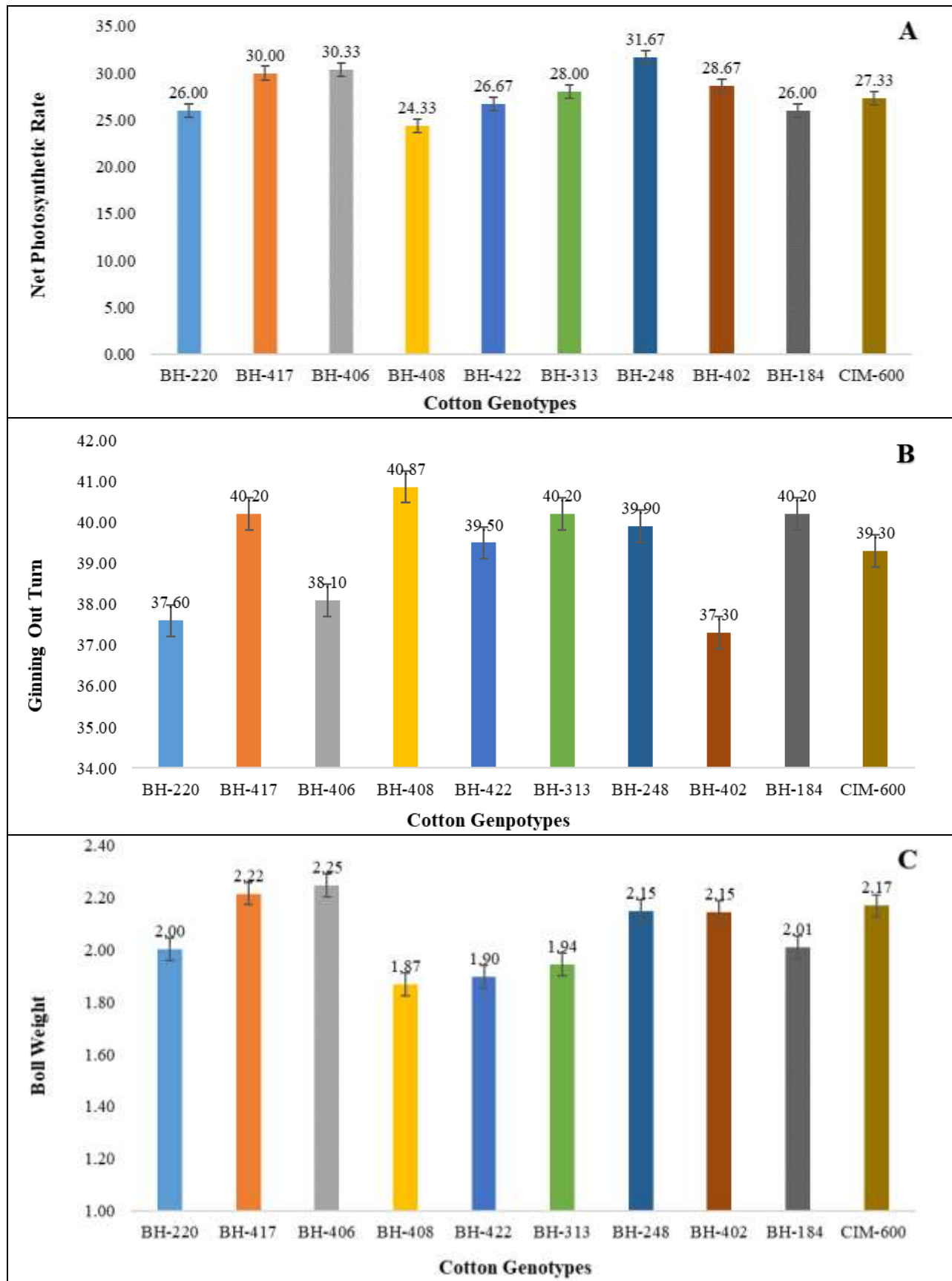
### Mean Performance of Cotton Genotypes for Morphological, Physiological, and Fiber Quality Traits

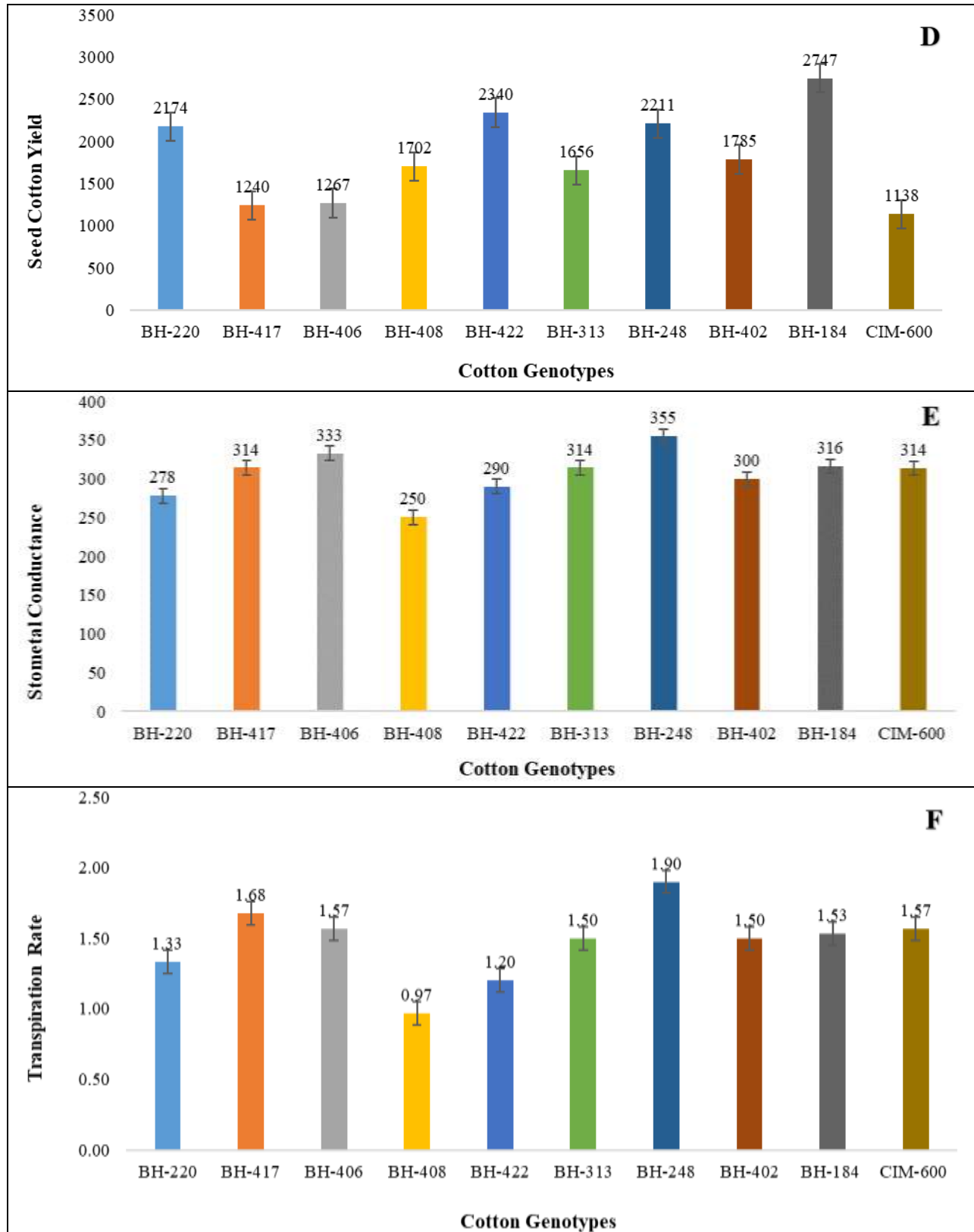
The evaluation of mean performance among the tested cotton genotypes revealed substantial variability for all studied traits, indicating wide genetic diversity within the germplasm (Table 3). Plant height ranged from 96 cm in genotype BH-220 to 144.33 cm in BH-406 and BH-313, indicating significant genotypic differences in plant architecture. A similar trend was observed for the number of nodes per plant, where BH-406 recorded the highest (26), while BH-226 showed the lowest (9). The total number of bolls per plant, a direct yield-contributing trait, was notably higher in BH-402 (74.6) and BH-408 (74.3), reflecting their superior boll-setting capacity. These findings align with the observations of Hussain *et al.* (2024), who emphasized that plant height and boll number are critical traits in maximizing cotton yield potential.

In terms of physiological attributes, BH-248 exhibited the highest stomatal conductance ( $355 \text{ mmol m}^{-2} \text{ s}^{-1}$ ) and transpiration rate ( $1.9 \text{ mmol m}^{-2} \text{ s}^{-1}$ ), indicating better gaseous exchange and potential for enhanced photosynthetic activity under field conditions. The net photosynthetic rate was highest in BH-407 ( $31.67 \text{ } \mu\text{mol m}^{-2} \text{ s}^{-1}$ ), suggesting its superior physiological efficiency.

**Table 3.** Mean performance of studied cotton traits in ten cotton genotypes.

Traits/ Genotypes	PH	Nodes	Sympodia	TB	FL	FS	FF	FF
BH-220	96 ± 2.08	9 ± 0.57	17.6 ± 2.33	39.6 ± 4.3	28.9 ± 0.58	98.4 ± 1.84	4.63 ± 0.08	4.63 ± 0.08
BH-417	123.3±3.33	19.3±1.20	22.6±0.88	63.3±5.7	28.7±0.27	97.73±1.23	4.7±0.25	4.7±0.25
BH-406	144.3±9.68	26±1.52	21.6±2.96	45.6±0.6	28.7±0.23	104.6±0.29	4.13±0.03	4.133±0.03
BH-408	133.3±6.01	20.3±2.3	21.6±4.25	74.3±0.8	28.6±0.16	100.1±2.71	4.16±0.06	4.16±0.06
BH-422	126±4.93	17.3±0.88	18±0.57	46.4±0.3	28.4±0.35	97.3±2.16	4.53±0.03	4.53±0.03
BH-313	144±7.02	23±2.30	20.6±2.33	41.5±0.3	28.1±0.69	95±0.11	4.6±0.05	4.6±0.05
BH-248	121.3±1.85	18.3±0.33	18±1	59.7±0.3	28.7±0.23	98.6±3.30	4.4±0.05	4.4±0.05
BH-402	131.6±1.85	25.3±1.45	17±1	74.6±0.3	28.9±0.46	98.6±2.65	4.56±0.28	4.56±0.28
BH-184	117.6±5.04	14.6±2.02	18±0.57	45.8±0.3	28.1±0.22	92.33±0.58	4.73±0.03	4.73±0.03
CIM-600	120±2.88	15.3±1.76	19.3±0.88	40.3±0.7	29.3±0.13	93.2±0.90	4.06±0.21	4.06±0.21





**Fig. 1.** Performance of cotton genotypes based on (A) Net Photosynthetic rate (B) Ginning Out Turn (C) Boll Weight (D) Seed cotton yield (E) Stomatal conductance (F) Transpiration rate. Capped bars above means represent the  $\pm$  SE of three replicates.

Regarding fiber quality traits, CIM-600 outperformed other genotypes with the highest fiber length (29.36 mm), while BH-406 demonstrated the strongest fiber strength (104.63 g tex<sup>-1</sup>). However, fiber fineness values remained fairly uniform across genotypes, with minor variations. Notably, the economic traits such as seed cotton yield were highest in BH-184 (2747.25 kg ha<sup>-1</sup>) and BH-422 (2340.25 kg ha<sup>-1</sup>), confirming their potential as promising candidates for future breeding efforts. These results are consistent with findings by Munir *et al.* (2020), who reported that combining superior physiological performance with desirable fiber qualities leads to enhanced cotton yield and lint value. Overall, the variation in genotype performance highlights the potential for selecting high-yielding and high-fiber-quality genotypes for targeted breeding programs aimed at improving cotton productivity and fiber excellence.

### Correlation Coefficient Analysis

The correlation coefficient analysis (Fi. 1) elucidated significant relationships among physiological parameters i.e., photosynthetic rate (Pr), stomatal conductance (Ci), transpiration rate (Tr); agronomic traits i.e., plant height (PH), number of nodes (Nodes), sympodial branches (SB), total number of bolls (TB), boll weight (BW); fiber quality traits i.e., fiber length (FL), fiber strength (FS), fiber fineness (FF), ginning out-turn (GOT) and seed cotton yield (Yield) in the ten cotton genotypes evaluated under semi-arid conditions. Yield exhibited a strong negative correlation with SB ( $r = -0.69^*$ ,  $p \leq 0.05$ ) while negative but non-significant correlation was found with PH ( $r = -0.42$ ), Nodes ( $r = -0.45$ ), SL ( $r = -0.54$ ) and BW ( $r = -0.53$ ). Yield exhibited a positive yet non-significant correlation with FF ( $r = 0.55$ ,  $p \leq 0.05$ ). Pr showed strong positive correlations with Ci ( $r = 0.86^{**}$ ,  $p \leq 0.01$ ) and Tr ( $r = 0.86^{**}$ ,  $p \leq 0.01$ ), reflecting their interdependence in driving photosynthetic efficiency, but its negative correlation with Yield ( $r = -0.31$ ) suggests that excessive gas exchange may lead to water loss, limiting yield potential under semi-arid stress, a trade-off noted by Schwinning and Ehleringer (2001). Fiber quality traits like FL and FS were negatively correlated with Yield ( $r = -0.54$  and  $-0.31$ , respectively), highlighting a yield-quality trade-off, indicating that higher lint recovery may come at the expense of overall seed cotton yield (Majumdar *et al.*, 2019). Notably, Tr had a strong positive correlation with Ci ( $r = 0.93^{**}$ ,  $p \leq 0.01$ ), Pr ( $r = 0.86^{**}$ ,  $p \leq 0.01$ ) and BW ( $r = 0.68^*$ ,  $p \leq 0.01$ ) suggesting that higher transpiration supports reproductive growth, while PH and Nodes were positively correlated ( $r = 0.92^{**}$ ,  $p \leq 0.01$ ), reinforcing their structural contribution to yield through increased fruiting positions (Anjum *et al.*, 2001). These correlations underscore the need for a balanced selection approach in breeding programs to optimize both yield and quality traits in *Gossypium hirsutum* under semi-arid conditions.

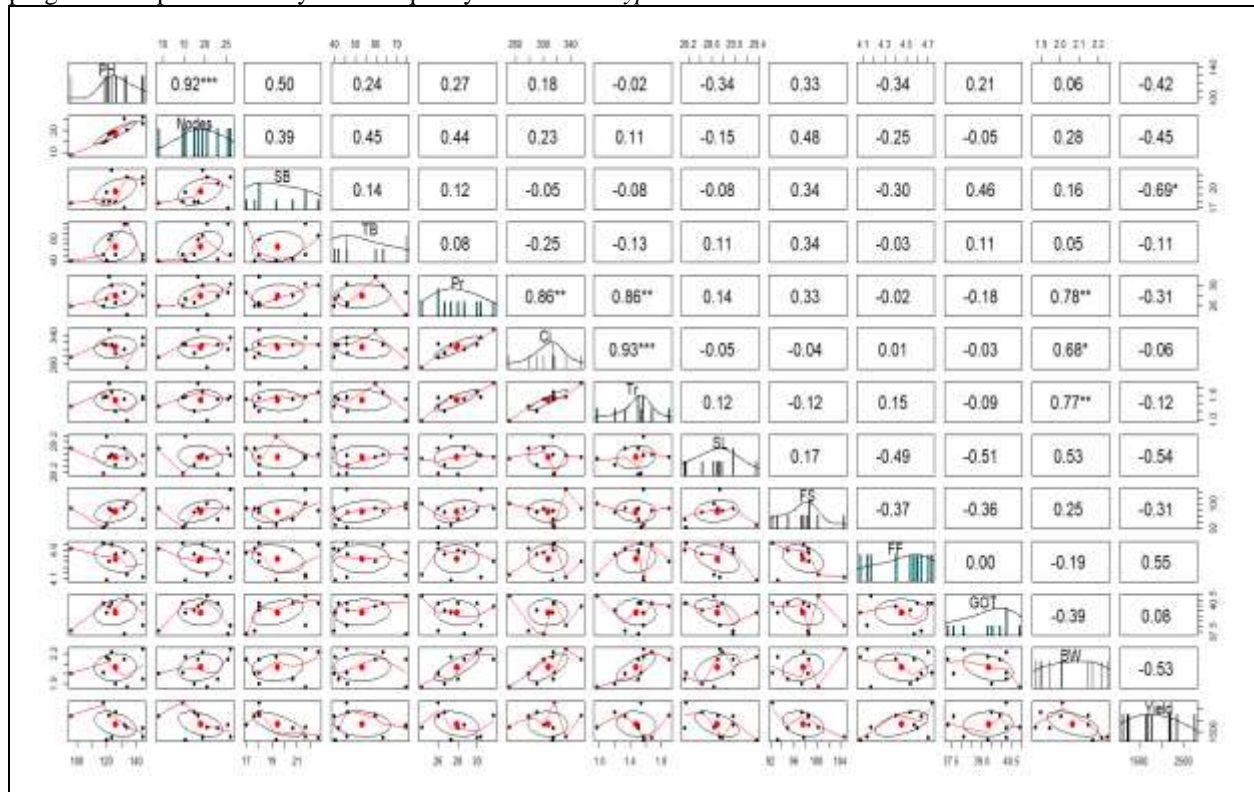
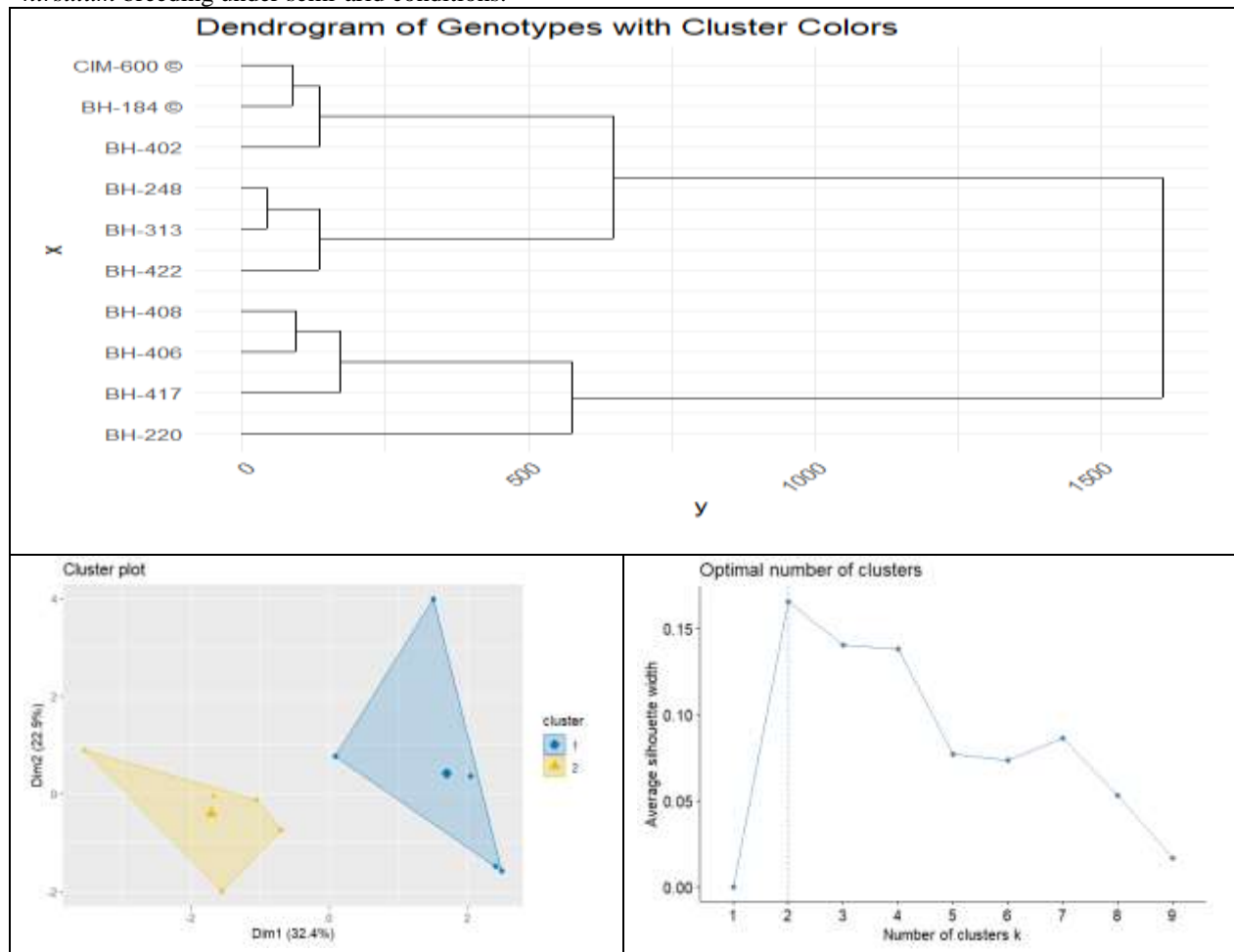


Fig. 2. Correlation Matrix of studied plant traits in ten cotton genotypes.

### Cluster Analysis

The cluster analysis, as depicted in the dendrogram of genotypes with cluster colors (Figure 3a), cluster diagram (Figure 3b) and the optimal number of clusters plot (Figure 3c), categorized the ten cotton genotypes into two distinct clusters based on their physiological and yield-related traits under semi-arid conditions at the Cotton Research Station, Bahawalpur. The optimal number of clusters plot, using the silhouette method, identified two clusters ( $k = 2$ ) as the most appropriate grouping, with the highest average silhouette width of approximately 0.15, indicating a robust separation between clusters, though the relatively low silhouette value suggests some overlap in trait performance among genotypes (Jarwar *et al.*, 2019). The dendrogram, constructed using Euclidean distance, further supported this grouping by dividing the genotypes at a height of approximately 750, with Cluster-1 comprising BH-422, BH-313, BH-248, BH-402, BH-184 and CIM-600 and Cluster-2 including the check varieties. Cluster 1, forming a larger and more cohesive group, likely includes genotypes with superior yield-related traits such as higher sympodial branches and boll weight, as well as efficient physiological parameters like photosynthetic rate, given their tight clustering, which suggests genetic similarity in traits contributing to productivity under semi-arid stress (Fischer *et al.*, 1978). In contrast, Cluster-2, consisting of BH-408, BH-402, BH-417 and BH-220, showed greater divergence from the elite strains, potentially reflecting lower yield potential or limited adaptation to the semi-arid environment, a pattern consistent with studies where checks often underperform compared to elite lines under stress conditions (Ali *et al.*, 2023). This clustering pattern highlights the genetic diversity between the elite strains and checks, providing a strategic basis for selecting high-performing genotypes like BH-184 and BH-422 from Cluster 1 for yield-focused breeding programs, while the distinct separation of Cluster 2 suggests that CIM-600 and BH-184 may serve as contrasting parents for hybridization to introduce diverse traits in *Gossypium hirsutum* breeding under semi-arid conditions.



**Fig. 3.** Cluster Analysis in Cotton Genotypes (a) Dendrogram (b) Cluster Diagram (c) Optimal number of cluster diagram

## Conclusion

The present study demonstrated significant genetic variability among elite cotton genotypes for both yield-related and fiber quality traits under field conditions. The use of multivariate analyses, including PCA and cluster analysis, provided valuable insights into trait interrelationships and genotype classification. Notably, genotypes such as BH-402, BH-408, BH-184, and CIM-600 exhibited exceptional performance, making them promising candidates for cotton improvement programs. The diversity observed in physiological and morphological parameters suggests ample opportunity for targeted breeding to enhance crop productivity and fiber characteristics. These findings highlight the critical role of genetic characterization in optimizing selection strategies and developing resilient, high-yielding cultivars tailored to meet the evolving demands of the textile industry and climate-adaptive agriculture.

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