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# ASSESSMENT OF YIELD AND QUALITATIVE TRAITS OF VARIOUS ADVANCED LINES OF COTTON *(GOSSYPIUM HIRSUTUM L.)*

***[1]Muhammad Ameen Halo, [2]Wahid Dino Sipio*, [3]Muhammad Aqib Rajput, [4]Nawab Jan Baloch, [5]Arif Ali Laghari, [6]Rida Sajid, [7]Jan Muhammad Keerio***

*[1]Plant Breeding & Genetics, Sindh Agriculture University Tandojam, Sindh, Pakistan*

*[2, 3, 4, 5, 7] Cotton Research Institute, Agriculture Research Center (ARC), Tandojam, Sindh, Pakistan*

*[6]Department of Horticulture, Faculty of Agriculture Pir Mehr Ali Shah Arid Agriculture University Rawalpindi, Pakistan*

****Corresponding Author:** wahidsipio@hotmail.com*

**Article Info**

**Abstract**

The present study was conducted at Cotton Research Institute, Agriculture Research Center (ARC), Tandojam during the Kharif season, 2023, with the objective of evaluating the yield and quality attributes of selected advanced cotton lines (*Gossypium hirsutum* L.). The analysis of variance revealed that traits such as plant height (cm), number of sympodial and monopodial branches plant$^{-1}$, number of bolls plant$^{-1}$, boll weight (g), seed cotton yield plant$^{-1}$ (g), and ginning out turn GOT (%) exhibited highly significant differences ($p<0.01$), while staple length (mm) and seed index (g) showed no statistically significant variation. In terms of average performance, genotype PC/35/23 was characterized by a shorter plant height (83.67 cm), the highest GOT % (42.05), and the most sympodial branches (19.00). The highest monopodial branches plant$^{-1}$ (2.33) was observed in PC/30/23, whereas PC/33/23 had the fewest (1.00). PC/31/23 produced the most bolls plant$^{-1}$ (22.00), and PC/34/23 yielded the highest seed cotton output (66.19 g). Furthermore, seed cotton yield plant$^{-1}$ demonstrated a statistically significant positive correlation with plant height ($r = 0.571^{**}$), boll weight ($r = 0.674^{**}$), and staple length ($r = 0.474^{*}$). Heritability estimates indicated strong genetic control for plant height and seed cotton yield plant$^{-1}$, moderate for boll weight and sympodial branches plant$^{-1}$, and lower for bolls plant$^{-1}$. Overall, PC/35/23 showed superiority in fiber quality traits such as GOT % and staple length, while PC/34/23 stood out in terms of productivity.

**Keywords:**
*Cotton, ANOVA, Correlation, Heritability, Genetic diversity.*

## INTRODUCTION

Cotton (*Gossypium hirsutum* L.) holds a pivotal role in global agriculture, serving as both the leading natural fiber crop and the second-largest oilseed source following soybean (*Glycine max L.*). It is cultivated extensively in tropical and subtropical climates across more than 80 countries, including major producers such as the United States, India, China, Brazil, Turkey, and Australia (Coban et al., 2016). In Pakistan, cotton is regarded as a strategic cash crop that underpins the country's textile industry, which contributes significantly to foreign exchange earnings and employment. Despite its economic importance, the national yield averages remain considerably lower than the genetic potential of existing cultivars, highlighting the urgent need for genetically improved lines that combine enhanced yield performance with superior fiber quality (Rajper et al., 2015).

The development of high-performing cotton genotypes is a strategic priority for sustaining the fiber industry and mitigating the adverse effects of environmental stresses. In this context, genotypic evaluation of morpho-yield and quality-related traits has emerged as an essential approach to identify lines with promising agronomic performance (Sarwar et al., 2021). Traits such as plant height, number of sympodial and monopodial branches, boll weight, seed cotton yield, lint percentage, fiber length, and resistance to pests and abiotic stressors are central to defining genotype adaptability and commercial utility (Zhou et al., 2019). These traits, often heritable, offer valuable selection criteria in breeding programs aimed at improving productivity, fiber characteristics, and resilience under diverse environmental conditions.

Understanding the relationships among these traits is crucial for effective selection in cotton improvement programs. Correlation analysis, both at genotypic and phenotypic levels, provides insight into the nature and strength of associations among yield and fiber traits (Sahito et al., 2016). It helps breeders determine whether simultaneous improvement in multiple traits is possible or whether trade-offs must be managed. For instance, positive correlations between seed cotton yield and fiber traits such as boll weight, plant height, or staple length indicate potential for concurrent genetic improvement (Ali et al., 2020). Conversely, negative associations may constrain genetic gains and necessitate careful breeding strategies.

The heritability of agronomic traits further informs breeding decisions by quantifying the extent to which phenotypic variation is genetically determined. Traits exhibiting high heritability are more likely to respond effectively to selection, as they are less influenced by environmental fluctuations (Morris et al., 2018; Saltz, 2017). Previous research has demonstrated that characteristics such as seed cotton yield and plant height often display high heritability, suggesting strong genetic control. On the other hand, traits with low heritability, including certain fiber properties and boll number, may require multi-environment trials or incorporation of molecular markers for effective selection (Choudhry et al., 2015.

Moreover, evaluating direct and indirect effects of traits contributing to yield enables the identification of key selection targets. Yield in cotton is a complex, polygenic trait, and indirect selection through strongly associated components like boll weight or sympodial branching may enhance breeding efficiency (Afiah & Ghoneim, 2013; Choudhry et al., 2015). These inter-trait relationships are not static and can vary across genotypes and environments, necessitating repeated evaluations under diverse agro-ecological conditions to ensure stable performance and adaptability (Munir et al., 2020; Nisar et al., 2022).

Thus, a comprehensive understanding of morpho-yield trait interactions, heritability estimates, and their correlation with yield is indispensable for formulating an efficient cotton improvement strategy. This study was designed to assess the genetic variability, phenotypic correlations, and heritability of key agronomic and fiber traits among selected advanced cotton lines under the agro-climatic conditions of Southern Pakistan. The insights derived aim to inform breeding decisions and contribute to the development of genotypes that meet the dual demands of high yield and fiber quality, while enhancing the sustainability and profitability of cotton cultivation in the region.

## MATERIALS AND METHODS

### Experimental site and plant material

The present study was conducted at Cotton Research Institute, Agriculture Research Center (ARC), Tandojam in order to work-out correlation and broad sense heritability for various yield and fibre traits of eight upland cotton (*Gossypium hirsutum* L) genotypes. The genotypes were: PC/29/23, PC/30/23, PC/31/23, PC/32/23, PC/33/23, PC/34/23, PC/35/23 and Shahbaz (Check Variety). The experiment was carried-out in a randomized complete block design (RCBD) with three replications. The observations were taken on ten randomly tagged plants from each genotype per replication. Thus, characters of forty plants were recorded. The characters studied were plant height (cm), sympodial branches plant$^{-1}$, monopodial branches plant$^{-1}$, number of bolls plant$^{-1}$, boll weight (g), seed cotton yield plant$^{-1}$ (g), ginning out turn GOT (%), staple length (mm) and seed index (g). All the cultural practices and inputs were adopted as recommended for healthy growth of the crop.

### Statistical analysis

The collected data was subjected to the statistical analysis (ANOVA) as adopted by Gomez & Gomez (1984). The means of genotypes for all the traits was compared by using the least significant difference (LSD) at 5% probability level. Correlation studies were determined according to Snedecor & cochron (1980). & Heritability in broad sense was using method proposed by Falconer, (1996).

## RESULTS & DISCUSSION

The cultivation of cotton (*Gossypium hirsutum* L.) stands as a cornerstone in global agriculture, providing the essential raw material for the textile industry. As the demand for cotton continues to rise, there is an imperative to enhance its productivity and quality. The development of advanced lines through breeding programs has emerged as a promising avenue to address this challenge. This study aims to assess the yield and qualitative traits of various advanced lines of cotton, shedding light on their potential for commercial cultivation. By delving into the intricacies of these genetic variations, we seek to contribute valuable insights that can inform and guide cotton farmers, breeders, and stakeholders towards sustainable and efficient cotton production. Through a comprehensive evaluation of both yield and qualitative characteristics, this research endeavors to provide a comprehensive understanding of the performance and potential of these advanced cotton lines, paving the way for advancements in cotton agriculture.

**Table 1. Mean squares from analysis of variance for various yield and fiber traits in upland cotton genotypes**

| Trait | Replications | Genotypes | Error |
|---|---|---|---|
| **Plant height (cm)** | 5.042 | 287.048** | 10.423 |
| **Sympodial branches plant$^{-1}$** | 2.166 | 14.184** | 1.881 |
| **Monopodial branches plant$^{-1}$** | 0.5 | 0.476$^{ns}$ | 0.261 |
| **Number of bolls plant$^{-1}$** | 0.791 | 10.452** | 3.22 |
| **Boll weight (g)** | 0.138 | 0.453* | 0.185 |
| **Seed cotton yield plant$^{-1}$ (g)** | 1.482 | 298.204** | 6.345 |
| **Ginning out turn (%)** | 0.226 | 68.406** | 2.242 |
| **Staple length (mm)** | 0.291 | 1.184$^{ns}$ | 2 |
| **Seed index (g)** | 0.305 | 0.181$^{ns}$ | 0.414 |

*** = Highly significant level at 1% of probability level,* $^{NS}$ *= Non-significant*

**Analysis of variance**

The results depicted that for different characteristics such as plant height (cm), number of sympodial branches plant$^{-1}$, number of monopodial branches plant$^{-1}$, number of bolls plant$^{-1}$, boll weight (g), seed cotton yield plant$^{-1}$ (g), ginning out turn GOT (%), were highly significant at $p<0.01$ except for staple length (mm) and seed index (g) showing non-significant (Table 1). This shows that the genetic resources used often have helpful genetic differences, which can be used in future breeding to improve upland cotton for different traits. Similar findings were reported by Siyal et al., (2024) and Nizamani et al. (2017), who also found significant differences ($P \leq 0.05$) among the varieties for all the traits studied.

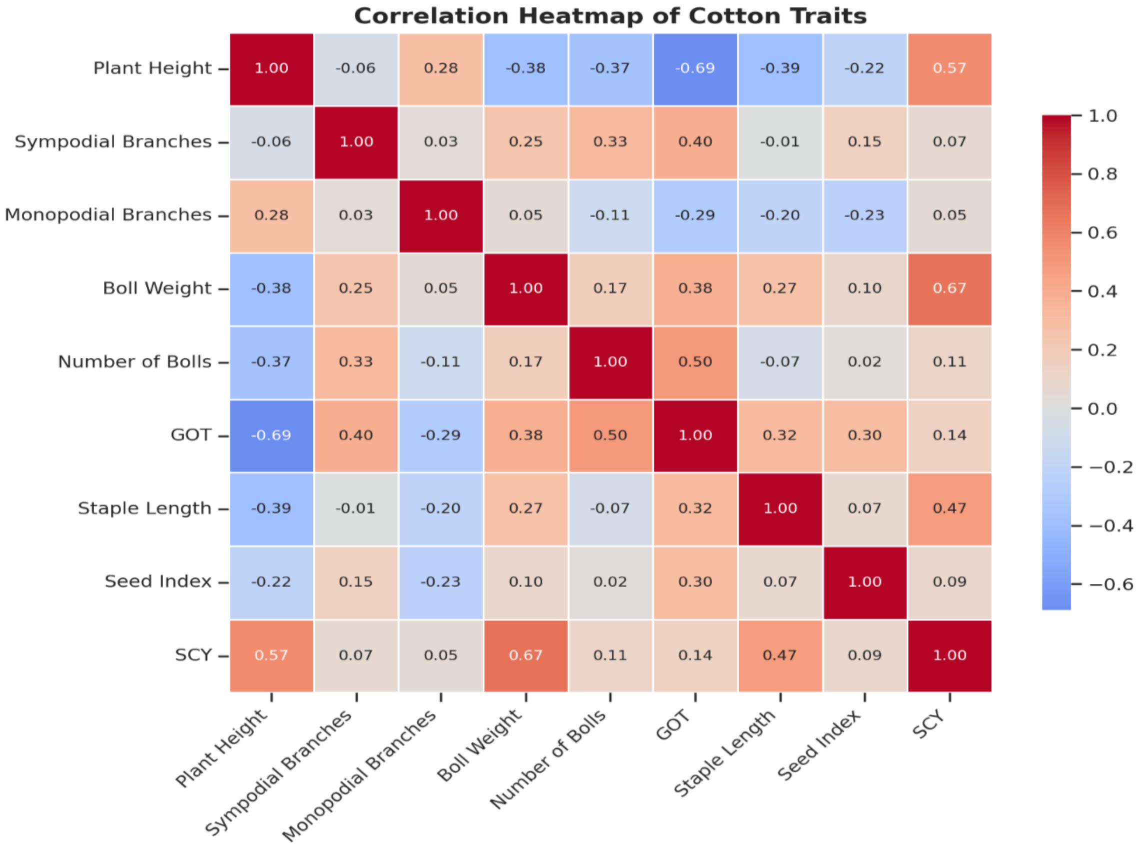
**Table 2. Mean performance of upland cotton genotypes for yield and fiber traits**

| **Genotypes** | **Plant height (cm)** | **Sympodial branches plant$^{-1}$** | **Monopodial branches plant$^{-1}$** | **Number of bolls plant$^{-1}$** | **Boll weight (g)** | **Staple length (mm)** | **G.O.T (%)** | **Seed cotton yield plant$^{-1}$ (g)** | **Seed index (g)** |
|---|---|---|---|---|---|---|---|---|---|
| **PC/29/23** | 108.33 | 15.00 | 1.33 | 21.66 | 3.34 | 28.33 | 39.52 | 50.31 | 7.83 |
| **PC/30/23** | 85.33 | 13.00 | 2.33 | 22.00 | 3.5 | 28.33 | 33.88 | 64.52 | 7.56 |
| **PC/31/23** | 93.00 | 13.33 | 1.33 | 22.00 | 3.15 | 29.00 | 36.32 | 56.80 | 8.40 |
| **PC/32/23** | 98.67 | 17.66 | 1.33 | 17.00 | 3.06 | 28.00 | 34.09 | 53.82 | 7.83 |
| **PC/33/23** | 88.33 | 13.33 | 1.00 | 19.33 | 2.96 | 28.33 | 36.46 | 51.80 | 8.00 |
| **PC/34/23** | 86.33 | 19.33 | 1.66 | 22.00 | 2.98 | 28.3 | 36.14 | 66.19 | 8.06 |
| **PC/35/23** | 83.67 | 19.00 | 1.33 | 9.66 | 3.04 | 29.00 | 42.05 | 54.88 | 7.86 |
| **Shahbaz** | 107.00 | 17.00 | 1.66 | 19.33 | 2.18 | 27.00 | 34.09 | 33.76 | 7.76 |
| **LSD 0.05 (%)** | 5.2232 | 2.2405 | 0.4179 | 2.8612 | 0.3516 | 1.1564 | 5.7177 | 9.7005 | 0.5260 |

**Mean performance**

Table 2 displays the results of eight upland cotton genotypes revealed significant differences in several agronomic and fiber traits, as supported by the ANOVA results. Among the genotypes, PC/29/23 recorded the highest plant height (108.33 cm), while PC/35/23 showed the lowest (83.67 cm), with plant height being highly significant ($p < 0.01$). For sympodial branches plant$^{-1}$, PC/34/23, PC/35/23, and PC/32/23 showed superior performance with 19.33, 19.00 and 17.66 branches, respectively, whereas PC/30/23 recorded the lowest (13.00 branches), again with highly significant variation. Although differences in monopodial branches plant$^{-1}$ were statistically non-significant, PC/30/23 produced the most (2.33 branches), while PC/33/23 had the fewest (1.00 branches). In terms of the number of bolls plant$^{-1}$, PC/30/23, PC/31/23 and PC/34/23 led with 22.00 bolls, while PC/35/23 produced the least (9.66), and the trait was highly significant ($p < 0.01$). Boll weight varied significantly ($p < 0.05$), with PC/30/23 (3.50 g) and PC/29/23 (3.34 g) outperforming others, whereas Shahbaz, PC/33/23 and PC/34/23 had the lowest weights (2.18 g, 2.96 g and 2.98 g, respectively). Regarding seed cotton yield plant$^{-1}$, which was highly significant ($p < 0.01$), PC/34/23 produced the highest yield (66.19 g), followed by PC/30/23 (64.52 g), while Shahbaz had the lowest (33.76 g). Ginning out turn % was also highly significant, with PC/35/23 showing the highest value (42.05%) and PC/30/23 the lowest (33.88%). Although staple length differences were statistically non-significant, PC/31/23 and PC/35/23 showed the longest staples (29.00 mm), and the check variety Shahbaz had the shortest (27.00 mm). For seed index, which was also non-significant, PC/31/23 had the highest value (8.40 g), followed by PC/34/23 (8.06 g), while PC/30/23 recorded the lowest (7.56 g). Overall, genotypes PC/34/23, PC/30/23, and PC/31/23 demonstrated superior performance across multiple traits, particularly in terms of yield and boll characteristics, making them promising candidates for cotton improvement programs. These findings are consistent with previous studies by Tariq et al. (2012), Rehman et al. (2016), Ali et al. (2020) and Siyal et al. (2024), which also highlighted the superior performance of specific genotypes across key agronomic and fiber traits.

**Figure.1 Correlation (r) coefficients among various traits in cotton genotypes**



Correlation Heatmap of Cotton Traits

| | Plant Height | Sympodial Branches | Monopodial Branches | Boll Weight | Number of Bolls | GOT | Staple Length | Seed Index | SCY |
|---|---|---|---|---|---|---|---|---|---|
| Plant Height | 1.00 | -0.06 | 0.28 | -0.38 | -0.37 | -0.69 | -0.39 | -0.22 | 0.57 |
| Sympodial Branches | -0.06 | 1.00 | 0.03 | 0.25 | 0.33 | 0.40 | -0.01 | 0.15 | 0.07 |
| Monopodial Branches | 0.28 | 0.03 | 1.00 | 0.05 | -0.11 | -0.29 | -0.20 | -0.23 | 0.05 |
| Boll Weight | -0.38 | 0.25 | 0.05 | 1.00 | 0.17 | 0.38 | 0.27 | 0.10 | 0.67 |
| Number of Bolls | -0.37 | 0.33 | -0.11 | 0.17 | 1.00 | 0.50 | -0.07 | 0.02 | 0.11 |
| GOT | -0.69 | 0.40 | -0.29 | 0.38 | 0.50 | 1.00 | 0.32 | 0.30 | 0.14 |
| Staple Length | -0.39 | -0.01 | -0.20 | 0.27 | -0.07 | 0.32 | 1.00 | 0.07 | 0.47 |
| Seed Index | -0.22 | 0.15 | -0.23 | 0.10 | 0.02 | 0.30 | 0.07 | 1.00 | 0.09 |
| SCY | 0.57 | 0.07 | 0.05 | 0.67 | 0.11 | 0.14 | 0.47 | 0.09 | 1.00 |

Figure.1 suggested that plant height had negative and significant correlations with the sympodial branches plant$^{-1}$ (r=-0.057$^{NS}$), monopodial branches plant$^{-1}$ (r=-0.284$^{NS}$). However, boll weight (r=-0.383*), number of bolls plant$^{-1}$ (r=-0.370*), ginning out turn (r=-0.689**), staple length (r=-0.392*) observed to have negative and significant association. Seed index (r=0.219$^{NS}$) showed non-significant association and seed cotton yield plant$^{-1}$ (r=0.571**) revealed highly significant and positive association. The results showed that the monopodial branches plant$^{-1}$ had a positive and non-significant correlation with boll weight (r=0.1445$^{NS}$) and seed cotton yield plant$^{-1}$ (r=0.1420$^{NS}$). Whereas, or sympodial branches plant$^{-1}$, ginning out turn observed significant and positive association as r=0.395* (Table 3). While staple length (r=-0.005$^{NS}$) depicted negative and non-significant association. Boll weight had a positive and significant association with ginning out turn (r=0.384**) and seed cotton yield plant$^{-1}$ (r=0.674**). Ginning out turn had a positive but non-significant correlation with staple length (r=0.316$^{NS}$), seed index (r=0.298$^{NS}$) and seed cotton yield plant$^{-1}$ (r=0.140$^{NS}$), respectively. The results showed that staple length had a non-significant correlation with staple length ($r=-0.0712^{NS}$) and significant with seed cotton yield plant$^{-1}$ ($r=0.474^{*}$). The results showed that seed cotton yield plant$^{-1}$ had a positive but non-significant correlation with ginning out turn ($r=-0.0695^{NS}$), staple length ($r=0.2701^{NS}$) and seed index ($r=0.0685^{NS}$). These findings are in line with the results suggested by Nizamani et al. (2017), Farias et al. (2016), Ahmad et al. (2016), Baloch et al. (2014) and Tabasum et al. (2015).

**Table 3. Heritability estimates in broad sense ($h^2$%) for various traits in cotton genotypes**

| Traits | Genotypic variance ($\sigma^2g$) | Phenotypic variance ($\sigma^2p$) | Heritability ($h^2$ %) |
|---|---|---|---|
| **Plant height (cm)** | 132.696 | 49.4891 | 68.131 |
| **Sympodial branches plant$^{-1}$** | 7.75 | 15.2798 | 50.72 |
| **Monopodial branches plant$^{-1}$** | 0.21429 | 0.4762 | 45 |
| **Number of bolls plant$^{-1}$** | 1.5179 | 13.79 | 11 |
| **Boll weight (g)** | 0.26799 | 0.4534 | 59.1 |
| **Seed cotton yield plant$^{-1}$ (g)** | 250.309 | 391.45 | 63.94 |
| **Ginning out turn (%)** | 3.3902 | 52.4289 | 6.46 |
| **Staple length (mm)** | 0.82143 | 2.8274 | 29.05 |
| **Seed index (g)** | 0.23304 | 0.648 | 35.96 |

## Heritability estimates

In the current study, heritability in the broad sense ($h^2$%) was estimated to assess the genetic contribution to various traits in cotton genotypes (Table 3). High heritability was observed for plant height (68.13%), seed cotton yield plant$^{-1}$ (63.94%), and boll weight (59.10%), suggesting these traits are mainly under genetic control and can be effectively improved through selection. Sympodial branches plant$^{-1}$ (50.72%) also showed moderate to high heritability, making it a promising trait for breeding. However, traits like monopodial branches plant$^{-1}$ (45%), seed index (35.96%), and staple length (29.05%) exhibited moderate heritability, indicating both genetic and environmental influence. Moreover, number of bolls plant$^{-1}$ (11%) and ginning out turn (6.46%) had low heritability, implying strong environmental effects, making direct selection less reliable for these traits. These findings align with results reported by Siyal et al. (2024), Abbas (2018), Dhivya (2014), and Farooq (2013), who also found high heritability in key yield and fiber traits. Such consistency across studies supports the potential for improving these traits through genetic selection.

## Conclusions

From the present study, it is concluded that PC/35/23 significantly provided greater GOT (%) as 42.05% as compared to check variety Shahbaz (34.09%). The staple length was larger in the genotype PC/31/23 as 29.00 mm followed by PC/35/23 (29.00 mm). More sympodial branches plant$^{-1}$ exhibited in the genotype's PC/34/23 (19.33), followed by PC/35/23 with 19.00 as compared to check variety Shahbaz.

PC/34/23 and PC/30/23 significantly performed better than other commercial lines in terms of maximum seed cotton yield plant$^{-1}$ with a weight of 66.19 g and 64.52 g. The correlations suggest that certain traits are interrelated, emphasizing the importance of considering multiple factors for cotton breeding and cultivation.

## Author’s contributions

Conceived and designed the experiments: WD Sipio & JM Keerio, Performed the experiments: MA Halo, Analyzed the data: MA Rajput & NJ Baloch, contributed reagents/materials/analysis tools: R Sajid & MA Rajput, Wrote the paper: WD Sipio & JM Keerio

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