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RESEARCH ARTICLE

Genetic Variability for Yield Related Traits in Some F_1 Crosses of Upland Cotton

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Abstract

Cotton is a vital fiber crop that significantly contributes to the agricultural economy. The improvement of high-yielding cotton varieties requires an understanding of genetic variation in key agronomic traits. This study aimed to evaluate the genetic diversity of selected upland cotton genotypes using statistical analysis. During the 2023 crop season, five cotton genotypes (Tipo-1, FH-Super, CIM-600 and FH-444) were evaluated in a field experiment laid out in a randomized complete block design (RCBD) with two replications. Data were recorded for yield related traits, including sympodial branches, monopodial branches, number of bolls per plant, plant height, seed cotton yield, seed index, boll weight, and ginning out turn percentage (GOT%). The results revealed that Tipo-1 X FH-444 showed the highest lint index, whereas FH-444 X Tipo-1 exhibited strong seed cotton yield. FH-Super X FH-Super and FH-Super X CIM-600 exhibited higher boll weight among genotypes. The collected data were statistically analyzed through ANOVA and mean graphs to determine and visualize the significance of genetic variation among genotypes. These findings provide valuable insights for cotton breeders in identifying promising genotypes for future breeding programs.

KEYWORDS
Genetic variation, Upland Cotton, Yield traits, ANOVA, Breeding program

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1 | INTRODUCTION

Cotton is a significant fiber crop in the domain and it belongs to the genus *Gossypium* and family *Malvaceae.* It is commonly referred to as "white gold," and is mostly grown for both oil and fiber in tropical and subtropical areas in world (Munir et al., 2016). It is highly valued for its various uses, including as a source of fiber, feed, protein, and oil. *Gossypium hirsutum* is grown on 95% globally cotton cultivation area. The remaining 5% of the world's cotton is supplied by *Gossypium arboreum* and *Gossypium herbaceum* (Erande et al., 2014).

Pakistan has ranked 5th in cotton production. Cotton was provisionally sown on an area of about 1.937 million hectares and total production of 8.329 million bales was noticed across the country with an average yield of 731kg/ha (GOP, 2022-23). The low production of cotton crops is caused by a variety of factors. A number of significant factors have had an impact on cotton production, including climate variation, the introduction of different insect pests, a decline in sowing area, and a slow promoting system (Hassan et al., 2021). The cotton crop in Pakistan during 2022-23 was severely damaged due to climatic changes such as shortage of irrigation water and heat wave. Cotton area sown increased to 2,144 thousand hectares against last year, but floods and insect pests such as pink bollworm, whitefly and thrips damaged the crop. (Government of Pakistan, 2022-23).

High yielding and better fiber quality traits have been effectively integrated into cotton cultivars. Genetic information for the inheritance of yield contributing traits should also be obtained from combining ability effects

(Tatineni et al., 1996). Cotton breeders around the world use a variety of breeding techniques to create new varieties of the crop. The selection of parents shows a important role in the success of a breeding program. Selecting the best hybrid crosses follows a successful breeding program involving the choice of capable parents (Queiroz et al., 2021). Plant breeders used diallel analysis extensively in early generations to identify parental varieties and hybrid crosses. It offers a productive and well-structured approach to finding appropriate parental genotypes and hybrid combinations, which in turn makes it easier for scientist to choose genotypes that interest them. Understanding of various gene action modes, heterotic effects, and combining ability estimation can help shape the genetic composition of the cotton crop (Nawaz et al., 2019).

In crop breeding, the evaluation of inbred lines and the growth of the population are significantly influenced by specific and general combining ability. Specific combing ability was defined by Sprague and Tatum (1942) as the mean performance of hybrid combinations in a particular cross, while average genotype sum was defined as general combing ability resulting in a sequence of crosses. Therefore, in a crossing, parents are considered to have good GCA if they show a superior average combining ability, and best SCA if they only show good combining in a single cross. Parameters related to strength, fineness and ginning qualities have been estimated using the GCA and SCA which helped in the selection to enhance these attributes (Khokhar et al., 2018).

Quantitative genetics plays a crucial role in determining the heritability of yield-contributing traits, which aids breeders in selecting superior genotypes. Analysis of variance (ANOVA) is a widely used statistical tool in plant breeding for evaluating genetic variability and treatment differences. ANOVA helps in assessing the significance of variations among genotypes, while mean graphs provide a visual representation of trait performance across different genotypes. These statistical techniques allow researchers to understand genetic control mechanisms and identify potential candidates for hybridization. Any crop improvement program should aim to select superior parents with high association across the majority of yield-contributing and quality parameters. The objective of the current study is to estimate the genetic variation in yield and yield related traits in upland cotton genotypes.

2. METERIAL AND METHOD

The research was performed at the Department of Plant Breeding and Genetics, University of Agriculture in Faisalabad, during crop season 2023, five cotton lines namely Tipo-1, C-1, FH-Super, CIM-600, and FH-444 were sown in pots in November 2022 in glass house of department. The required environmental conditions (temperature, humidity, and sunlight) were provided in glass house. Seeds were sow in according to complete randomized complete block design (RCBD) with two replications, in the field area. Five plants were specifically selected and labeled in each line for data collection. The row to row distance were kept 75 cm while plant to plant was maintain as 30 cm. From planting to harvest, all agronomic procedures (weeding, hoeing, thinning, plant protection techniques, and advised irrigation) was carried out to ensure proper crop growth. The following cotton genotypes and there F_1 were used in the study

1. Tipo-1
2. C-1
3. FH-super
4. CIM-600
5. FH-444

2.1. Data Collection

Data were recorded for each individual plant when they reached maturity. The following methodology was used to collect and analyze the data for each character.

2.1.1. Plant Height (cm)

Measured the height of five plants using a measuring tape. The plants were selected based on a standard criterion and their heights were recorded in centimeters from first node to apex when they had reached their final height.

2.1.2. Number of Monopodial Branches

From a row, a random sample of five mature plants were taken, and indirect fruit-bearing branches was recorded for each plant. The mean value was calculated for monopodial branches for data analysis.

2.1.3. Number of Sympodial Branches

Sympodial branches are the cotton plant's direct fruiting branches. When the selected plants matured, the sympodial branches on each plant was determined. For each replication, we calculated the average sympodial branches per plant.

2.1.4. Number of bolls

The total number of bolls on five mature plants were counted at harvest. The mean value for number of boll was calculated for data analysis.

2.1.5. Number of Seeds per boll

The total seeds of five separately collected bolls were counted manually after ginning and the divided by 5. This was done for five plants from each row then average was taken to get single value from each row.

2.1.6. Seed Cotton Yield

An electric balance was used to measure the yield of seed cotton on an individual plant basis. Seed cotton was picked from five guarded plants and placed in separate bags. The average yield was calculated for further analysis.

2.1.7. Seed Index

From every plant, 100 seeds were selected at random. A balance was used to weigh the seeds, and the mean weight was computed. Then, additional analysis was conducted using this mean weight.

2.1.8. Boll Weight

By dividing the number of picked bolls from the total quantity of yield of seed, the average weight of the bolls was determined. For statistical analysis, the average boll weight from each plant in a row in each replication was determined.

2.1.9. Ginning out-turn Percentage (%)

Each genotype's seed cotton yield was processed at the ginnery using a single roller electrical ginning machine. Each sample's yielded lint weight was measured, and the supplied formula was used to calculate the lint percentage.

$$GOT\ \% = \frac{weight\ of\ lint}{weight\ of\ seed\ cotton} \times 100$$

2.1.10. Lint Index

The lint index is a metric used to determine the quantity of cotton fiber (known as lint) that can be obtained from a cottonseed. The higher the lint index, the more fiber can be extracted from the seed cotton, and the better the quality of the cotton. Lint index was calculated by using following formula.

$$lint\ index = \frac{seed\ index\ \times\ lint\%}{100 - lint\ \%}$$

2.2. Statistical Analysis

Collected data were subjected to statistical analysis for further examination (Steel et al. 1981). The bar graphs using Microsoft Excel were generated to show the mean values.

3. RESULTS & DISCUSSION

Significant variations between the genotypes for the investigated traits were revealed by the analysis of variance.

3.1. Number of Monopodial Branches

Monopodial branches show a critical character in the overall growth and architecture of the cotton plant. An increase in the number of monopodial branches on a cotton plant can result in higher growth and delayed harvesting. The mean graph represents that the FH-444 X Tipo-1 and CIM-600 X FH-444 exhibited higher number of monopodial branches (Fig. 1). The analysis of variance (ANOVA) showed significant genetic variation among the cotton genotypes regarding the monopodial branches (Table 1). Significant variability among cotton genotypes for monopodial branches was observed by Chapara et al., (2022) and Kathiravan et al., (2025).

3.2. Number of Sympodial Branches

Cotton plants exhibit a distinctive growth pattern known as sympodial branching. The number of these branches in cotton can change based on genetic factors, environmental conditions, and cultivation practices. This trait is crucial for cotton production as it influences the crop's yield and quality. The mean graphs showed that the Tipo-1 x Tipo-1 showed higher number of sympodial branches among other genotypes (Fig. 2). The ANOVA specified significant genetic variation among the cotton genotypes regarding the total sympodial branches per plant (Table 1). Similar results have been reported by Córdova-Sinarahua et al., (2026), where highly significant differences among genotypes were observed for sympodial branches. Moreover, there was also the influence of environmental conditions on trait expression.

3.3. Number of bolls per plant

The number of bolls in cotton plants is a vital factor that significantly impacts fiber production, crop yield and fiber quality. Bolls, the fruiting structures of the cotton plant, contain the cotton fibers. The mean graph represents that the FH-444 X Tipo-1 and CIM-600 X FH-444 respectively, represented the higher number of bolls per plant (Fig. 3). The ANOVA presented significant genetic variation among the cotton genotypes regarding the number of boll number per plant (Table 1). Sarwar et al., (2021) reported the significant variability among cotton germplasm for number of bolls per plant indicating its importance in selection and breeding programs.

Table 1: The mean square values for various traits in cotton

SOV	MBPP	SBPP	NBPP	PH	BW	GOT	SPB	SCY	LI	SI
Replication	0.1058	0.0513	0.0815	0.0022	0.0578	-0.0106	12.3954	0.0835	0.0049	0.065
Genotype	0.993	7.3551	19.3413	301.9384	0.251	17.4004	3.9542	68.9894	0.2335	0.4383
Error	0.1396	0.1783	0.1141	0.3722	0.0332	0.2639	1.1488	0.0922	0.0533	0.0673

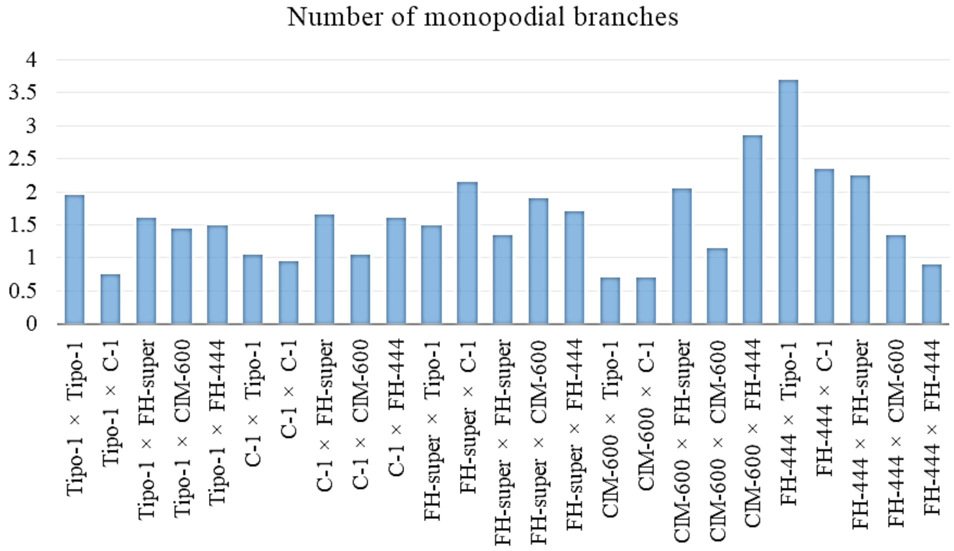


Fig. 1: Means performance of five parents and 25 crosses for monopodial branches

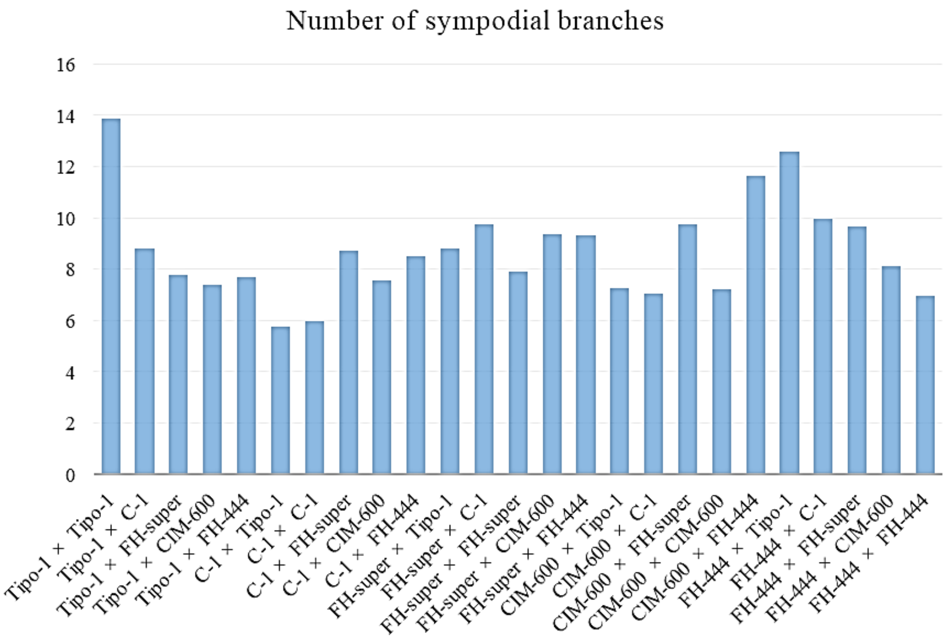
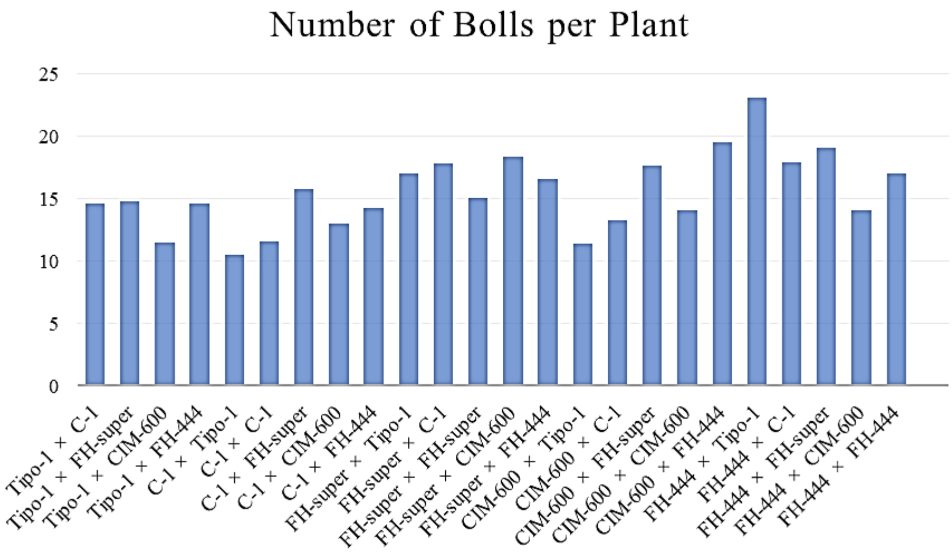


Fig. 2: Means performance of five parents and 25 crosses for sympodial branches



Fig, 3: Means performance of five parents and 25 crosses for number of boll per plant

3.4. Plant Height

The height of cotton plants plays a key role in their growth, development, and ultimate yield. Multiple factors contribute to plant height, including genetic makeup, soil type, water availability, temperature, and nutrient levels. FH-444 X Tipo-1 and Tipo-1 X Tipo-1 had higher plant height as compared to other genotypes (Fig. 4). The ANOVA showed significant genetic variation among the cotton genotypes regarding the height of plant. (Table 1). Similar findings have been reported by Kathiravan et al., (2025) and Sahar et al., (2021), who observed significant differences among cotton genotypes for plant height. The presence of genetic variability suggests that this trait can be effectively utilized in selection and breeding programs for crop improvement.

3.5. Boll Weight

Boll weight stands as a key measure for estimating yield, assessing fiber quality, managing nutrient and water needs, and detecting potential pest and disease challenges in cotton farming. FH-Super X FH-Super and FH-Super X CIM-600 exhibited higher boll weight among genotypes (Fig. 5). The ANOVA presented significant genetic variation between the cotton genotypes regarding the Boll weight (Table 1). Similar findings have been reported by Liaqat et al., (2026) and Perveen et al., (2026), where significant variability for boll weight was observed among cotton genotypes, highlighting its importance in yield improvement and selection in breeding programs.

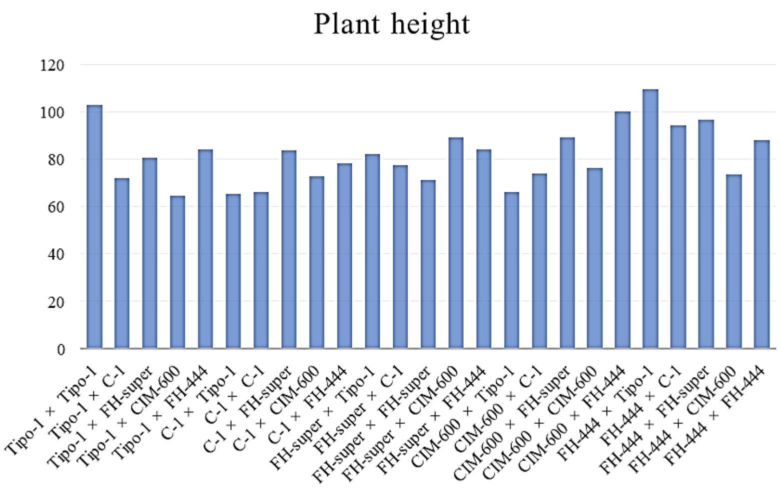


Fig. 4: Means performance of five parents and 25 crosses for Plant height

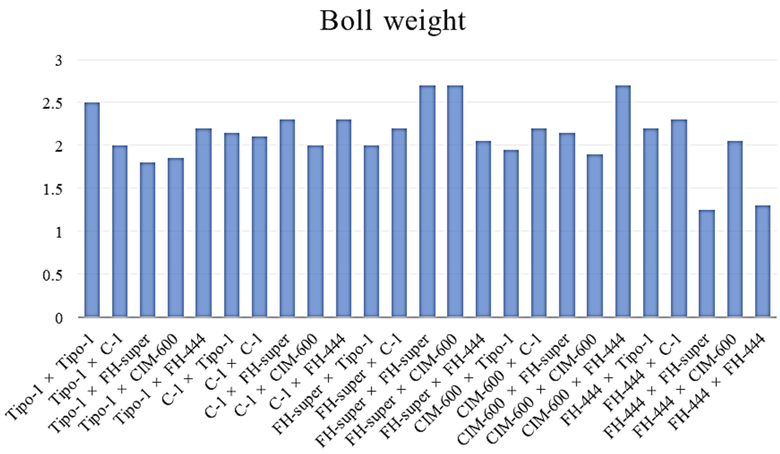


Fig. 5: Means performance of five parents and 25 crosses for boll weight

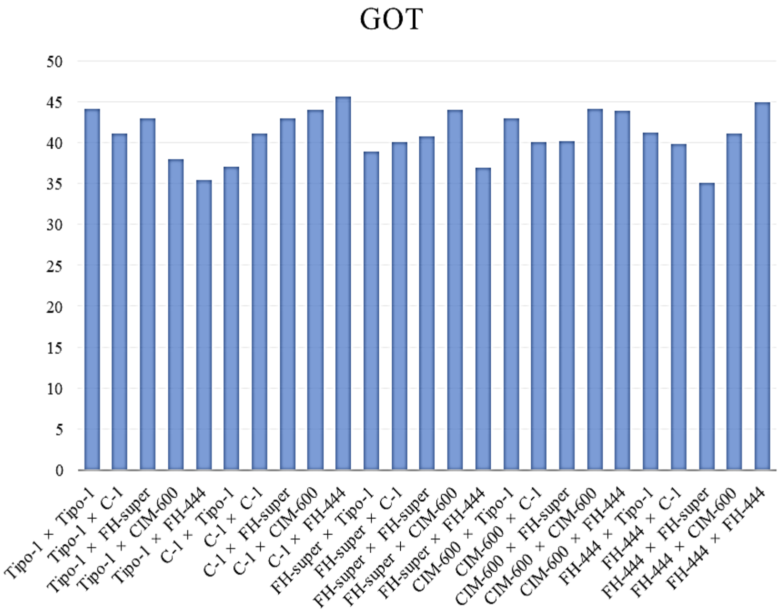


Fig. 6: Means performance of five parents and 25 crosses for GOT

3.6. Ginning out turn%

The ginning turnout percentage holds significant importance in cotton cultivation, offering insights into yield potential, fiber quality, economic value, ginning process efficiency, and downstream processing considerations. By monitoring and optimizing the ginning turnout percentage, farmers can enhance the overall value and profitability of their cotton crop. C-1 X FH-444 and FH-444 X FH-444 exhibited higher ginning out turn percentage (Fig. 6). The ANOVA results specified significant genetic variation between the cotton genotypes regarding the Ginning out turn% (Table 1), as also reported in cotton, where significant variability and heritability for GOT% were observed, indicating the effectiveness of selection in improving this trait (Aralikatti et al., 2025).

3.7. Number of Seeds per Boll

Number of seeds per boll is a crucial trait in cotton cultivation, influencing both yield and quality. Cotton bolls serve as the reproductive structures where seeds develop, and the total seeds number per boll directly impacts overall yield of seed cotton. FH-Super X Tipo-1 and C-1 X FH-Super showed higher number of seed per boll (Fig. 7). The ANOVA results for the number of seeds per boll show significant differences between genotypes, indicating genetic diversity in this trait (Table 1). Similar findings were reported by Chapara et al., (2022) and Aralikatti et al., (2025).

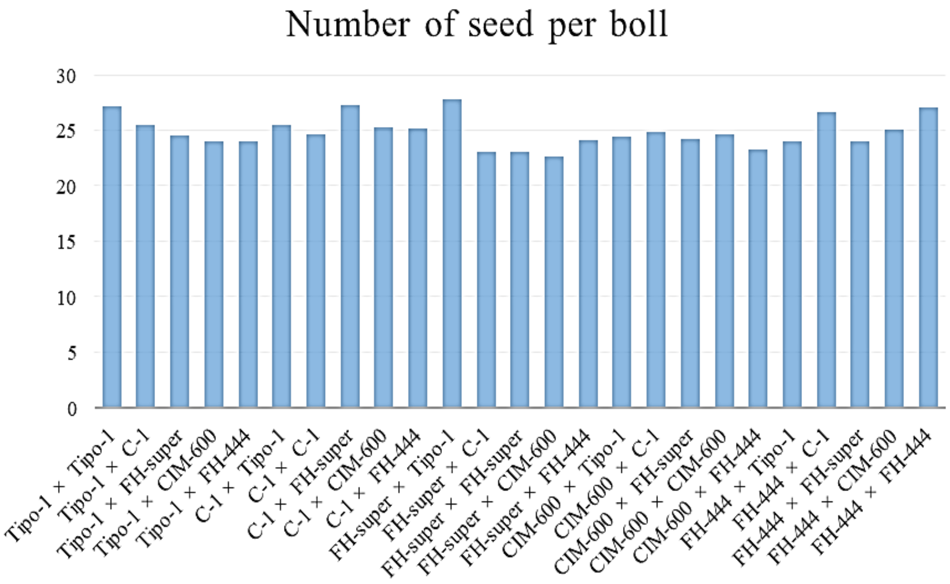


Fig. 7: Means performance of five parents and 25 crosses for number of seed per boll

3.8. Seed Cotton Yield

Seed cotton yield in cotton cultivation refers to the quantity of seed produced per unit area of cultivated cotton plants. It serves as a vital measure of cotton productivity and is commonly expressed in weight units such as kilograms per acre or hectare. FH-444 X Tipo-1 exhibited strong seed cotton yield (Fig. 8). The ANOVA results for the number of seed cotton yield show significant differences among genotypes, indicating genetic diversity in this trait (Table 1). Seed cotton yield is controlled by multiple traits including boll number, boll weight, and sympodial branching. It could be possible that certain crosses show this performance due to the combined effects of these traits. Significant variation among genotypes has also been reported by Perveen et al., (2026), indicating their importance in yield improvement.

3.9. lint Index

The Lint Index helps as a quantitative measure representing the quality of cotton fibers, taking into account factors like length, strength, fineness, and maturity. This metric holds significant importance for cotton buyers and manufacturers, guiding their assessment of the suitability and value of cotton crops for textile production. Tipo-1 X FH-444 showed highest lint index (Fig. 9). The ANOVA results for the lint index show significant variances between genotypes, indicating genetic diversity in this trait (Table 1). Divya et al., (2023) also reported the same results for significant variability among cotton genotypes for the lint index.

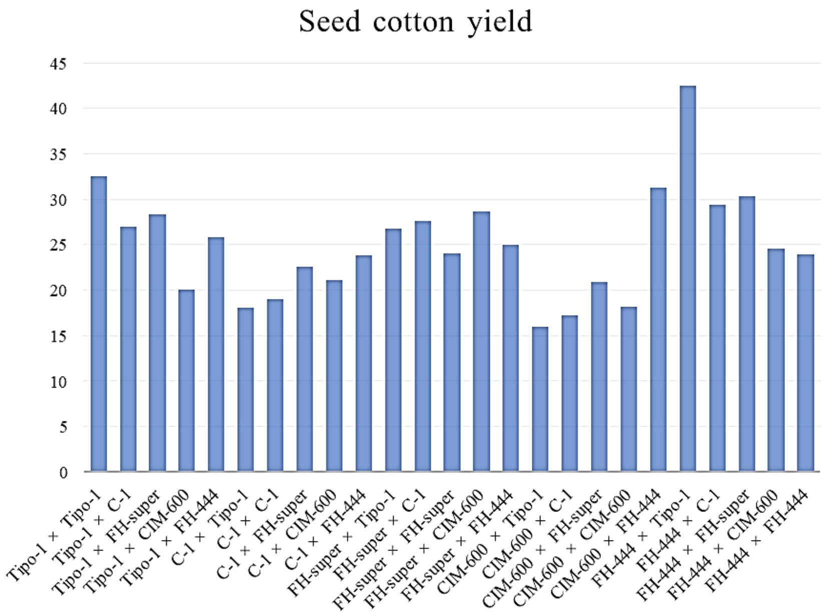


Fig. 8: Means performance of five parents and 25 crosses for number of seed cotton yield

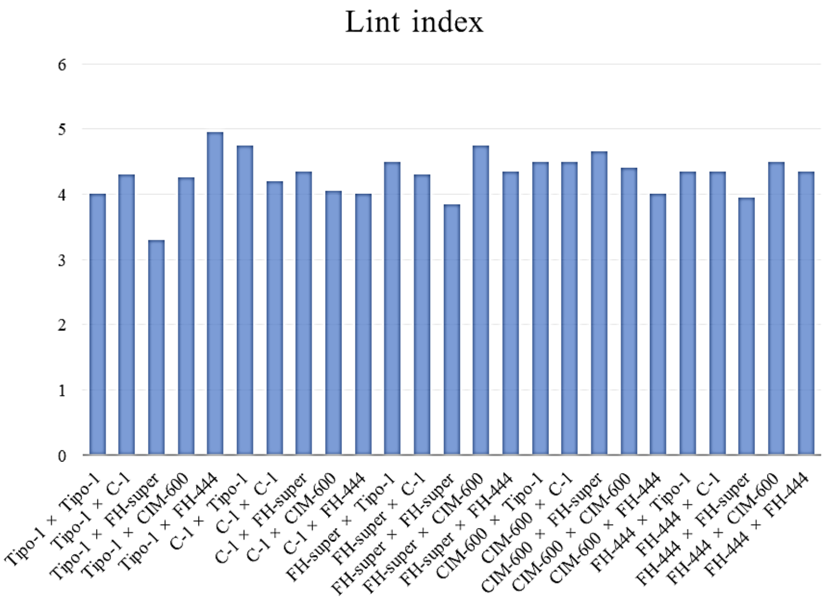


Fig. 9: Means performance of five parents and 25 crosses for lint index

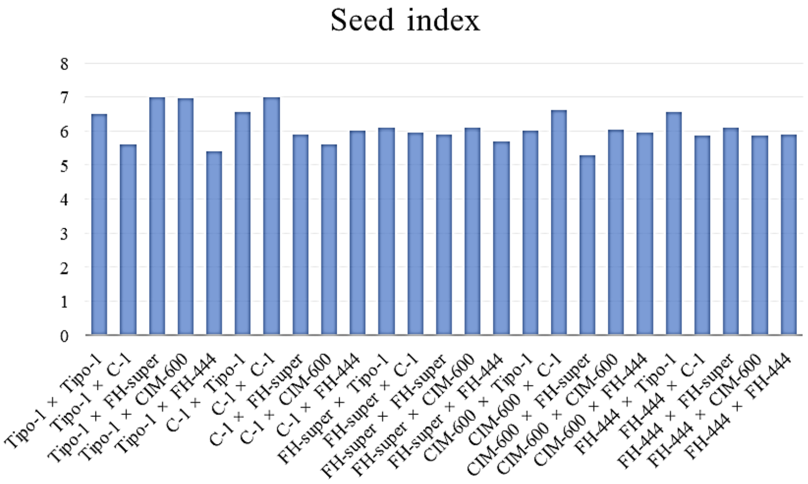


Fig. 10: Means performance of five parents and 25 crosses for number of seed index

3.10. Seed Index

The seed index is an important characteristic considered in cotton production and breeding programs. It provides valuable information about the seed size, which can have implications for germination, seedling vigor, and the potential yield of the cotton crop. Tipo-1 X FH-Super, Tipo-1 X CIM-600 and C-1 X C-1 exhibited higher seed index (Fig. 10). The ANOVA results for the Seed index show significant variances between genotypes, indicating genetic diversity in this trait (Table 1). Moreover, significant variability for seed index has also been reported in cotton germplasm, highlighting its importance in breeding programs (Mawblei et al., 2022).

4. Conclusion

Cotton (*Gossypium hirsutum L.*) is a multipurpose crop that provides inclusive range of benefits for both humans and animals. It is a major source of income and plays a significant role among all the crops. An analysis of variance (ANOVA) was performed on the collected data to ascertain the significance of the genotype-to-genotype differences. There were notable variations between the traits. To estimate genetic variability, we examined all parents and F_1 hybrids. Tipo-1 X FH-444 showed highest lint index, whereas, FH-444 X Tipo-1 exhibited strong seed cotton yield. FH-Super X FH-Super and FH-Super X CIM-600 exhibited higher boll weight among genotypes. These findings suggest that certain genotypes exhibit superior agronomic traits, making them potential candidates for future breeding programs. Understanding the genetic variability among cotton genotypes can aid in selecting superior lines for genetic improvement and hybrid development.

Declarations

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Conflicts of Interest: All authors declare that they have no conflicts of interest.

Data Availability: The data collected for this article are included in the article.

Ethics Statement: No prior study was conducted on live animals/humans; thus, it did not require any ethical approval.

Author's Contributions: AA designed the project and conducted the experiment. SM collected and analyzed the data and wrote the initial draft. Review and editing were performed by AA. All authors approved the final version of the manuscript.

Generative AI Statements: The authors declare that no Gen AI/DeepSeek was used in the writing/creation of this manuscript.

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