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## Assessment of genetic variability and selection potential in $F_2$ segregating populations of upland cotton (*Gossypium hirsutum* L.)

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| ARTICLE INFO                                                                                                                                                                                                                                                                                                                                                                                                                      | ABSTRACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| <p><b>Received:</b><br/>April 22, 2026</p> <p><b>Revised:</b><br/>May 06, 2026</p> <p><b>Accepted:</b><br/>May 20, 2026</p> <p><b>Available Online:</b><br/>June 05, 2026</p> <p><b>Keywords:</b><br/><i>Upland cotton, <math>F_2</math> population, genotypic variance, heritability, genetic advance</i></p> <p><b>Corresponding Author:</b><br/><a href="mailto:balochabdulwahid@yahoo.com">balochabdulwahid@yahoo.com</a></p> | <p>Knowledge of the magnitude of genetic and phenotypic variability present in a crop species is fundamental to designing effective breeding programmes for developing superior cultivars. In this study, eight <math>F_2</math> segregating populations of upland cotton (<i>Gossypium hirsutum</i> L.) was (IUB-2013 <math>\times</math> NIA-95, Chandi-95 <math>\times</math> M-23, NIA-Ufaq <math>\times</math> M-35, NIAB-878 <math>\times</math> Chandi-95, NIA-Noori <math>\times</math> IUB-2013, Sadori <math>\times</math> M-32, Sohni <math>\times</math> NIA-Ufaq, ZAD-1 <math>\times</math> Sadori) along with their twelve respective parents (IUB-2013, NIA-95, Chandi-95, M-23, NIA-Ufaq, M-35, NIAB-878, NIA-Noori, Sadori, M-32, Sohni, ZAD-1), generated from selected intra-specific crosses, were evaluated together with their twelve parental genotypes at the experimental field of the Nuclear Institute of Agriculture (NIA), Tandojam, during the 2025 Kharif season, using a randomized complete block design with three replications. Analysis of variance detected significant differences among genotypes for plant height, sympodial branches plant<sup>-1</sup>, bolls plant<sup>-1</sup>, boll weight, seed cotton yield plant<sup>-1</sup>, ginning outturn percentage, staple length and micronaire, confirming that exploitable genetic variability was present in the breeding material. Among the parents, NIA-Ufaq combined the tallest plant stature, the greatest number of bolls plant<sup>-1</sup> and the highest seed cotton yield plant<sup>-1</sup>, while the <math>F_2</math> crosses NIAB-878 <math>\times</math> Chandi-95 and NIA-Noori <math>\times</math> IUB-2013 recorded the highest seed cotton yield among the segregating populations. Broad-sense heritability estimates varied widely across traits and crosses, ranging from 3.66% (ginning outturn, Chandi-95 <math>\times</math> M-23) to 99.17% (boll weight, Chandi-95 <math>\times</math> M-23), while genetic advance ranged from 0.05 to 70.53 depending on the trait and cross combination considered. Seed cotton yield plant<sup>-1</sup> combined moderate-to-high heritability with substantial genetic advance in several crosses, most notably Chandi-95 <math>\times</math> M-23 and NIA-Ufaq <math>\times</math> M-35, indicating predominance of additive gene action and good scope for direct phenotypic selection in early generations. The crosses Chandi-95 <math>\times</math> M-23, NIA-Ufaq <math>\times</math> M-35, NIAB-878 <math>\times</math> Chandi-95 and NIA-Noori <math>\times</math> IUB-2013 displayed transgressive segregation for seed cotton yield, exceeding both respective parents, and are recommended as promising material for pedigree breeding aimed at developing high-yielding upland cotton genotypes.</p> |

## Introduction

Cotton (*Gossypium hirsutum* L.) is the most widely cultivated source of natural textile fibre in the world, supplying the principal raw material for yarn, fabric and a wide range of industrial products (Mudasir et al., 2021a). In Pakistan, cotton is a key cash crop that underpins the textile sector, generates substantial export earnings and supports the livelihoods of millions of growers as well as workers engaged in ginning, spinning and weaving (Khan et al., 2019; Akbar et al., 2020). Despite its economic importance, cotton productivity in the country has remained largely stagnant over the past few decades, mainly because of climate variability, heat and water stress, and the emergence of insect pests with developed resistance, all of which constrain yield gains and raise production risk (Rana et al., 2018). A parallel decline in fibre-quality attributes such as length, strength and uniformity has further weakened the competitiveness of the crop in international markets, underscoring the need for breeding strategies that simultaneously target yield and fibre quality across diverse environments (Ashraf et al., 2022).

Sustainable genetic improvement of cotton depends on the effective exploitation of heritable variation present in segregating populations. The  $F_2$  generation, produced by selfing  $F_1$  hybrids, displays the greatest recombination of parental alleles and the widest phenotypic diversity of any early generation, making it a logical starting point for quantitative genetic analysis of complex traits such as seed cotton yield, boll weight and fibre quality (Ali et al., 2023). Partitioning of phenotypic variance into its genotypic and environmental components allows the estimation of heritability and expected genetic advance, two parameters that jointly indicate whether a trait is governed mainly by additive gene action and is therefore amenable to direct phenotypic selection, or whether non-additive effects and environmental variation limit the efficiency of simple selection (Singh & Kumar, 2023; Rodriguez et al., 2022). Traits that combine high heritability with high genetic advance are generally considered the most responsive to selection (Alvarez & Torres, 2022), whereas traits with low heritability – frequently fibre-quality components such as fineness and strength – require larger populations, multi-environment testing, or marker-assisted approaches before meaningful genetic gain can be realized (Mehdi & Hasan, 2024).

A substantial body of work on upland cotton has documented wide variability for seed cotton yield, boll number, boll weight and ginning outturn in  $F_2$  and later segregating generations, underscoring the value of early-generation evaluation in breeding programmes (Sharma & Verma, 2021; Li & Zhang, 2022). Such variability also creates the opportunity for transgressive segregation, whereby individual  $F_2$  plants exceed the performance of both parents, providing breeders with novel recombinant types for advancement through pedigree selection (Harris et al., 2019; Polat et al., 2025). Heritability and genetic advance estimates, however, are population- and environment-specific, so locally developed cotton genotypes and their crosses must be independently characterized under the prevailing agro-climatic conditions before these genetic parameters can reliably guide selection decisions (Hameed et al., 2024; Zulfiqar et al., 2025).

## Materials and Methods

### Experimental site

The trial was conducted at the experimental field of the Nuclear Institute of Agriculture (NIA), Tandojam, Sindh, Pakistan, during the Kharif (summer) growing season of 2025. The site is characterized by a semi-arid climate with hot summers, and the soil is moderately fertile and well-drained, conditions well suited to upland cotton cultivation.

### Plant material

Twelve parental genotypes of upland cotton (*Gossypium hirsutum* L.): IUB-2013, NIA-95, Chandi-95, M-23, NIA-Ufaq, M-35, NIAB-878, NIA-Noori, Sadori, M-32, Sohni and ZAD-1, were hybridized in selected combinations and the resulting  $F_1$  plants were self-pollinated to obtain eight  $F_2$  segregating populations: IUB-2013  $\times$  NIA-95, Chandi-95  $\times$  M-23, NIA-Ufaq  $\times$  M-35, NIAB-878  $\times$  Chandi-95, NIA-Noori  $\times$  IUB-2013, Sadori  $\times$  M-32, Sohni  $\times$  NIA-Ufaq, and ZAD-1  $\times$  Sadori. The twelve parents and eight  $F_2$  populations, twenty entries in total, constituted the genetic material evaluated in this study.

### Experimental design and layout

The twenty entries were evaluated in a randomized complete block design (RCBD) with three replications to minimize the effect of field heterogeneity. Each genotype was sown in a two-row plot 10 m long, with 75 cm between rows and 30 cm between plants within a row.

### Data recorded

Data were recorded on five randomly selected, competitive plants per genotype in each replication, and the mean of these observations was used in the statistical analysis. The following traits were assessed: Plant height (cm), Sympodial branches plant<sup>-1</sup>, Bolls plant<sup>-1</sup>, Boll weight (g), Seed index (g), Seed cotton yield plant<sup>-1</sup> (g), Ginning outturn, GOT (%), Staple length (mm), Micronaire (g<sup>-1</sup>).

### Statistical analysis

Analysis of variance (ANOVA) appropriate for the randomized complete block design was performed using R software to test for significant differences among genotypes. For each F<sub>2</sub> population, genotypic, environmental and phenotypic variance components were partitioned, and broad-sense heritability ( $H^2 = \sigma^2_g / \sigma^2_p \times 100$ ) and genetic advance at 5% selection intensity were estimated following the method of Robinson et al. (1949).

where:

$$\begin{aligned} \text{Environmental variance (Ve)} &= \frac{(VP^1 + VP^2)}{3} \\ \text{Genetic variance (Vg)} &= \frac{MS_g - MSe}{3} \\ \text{Phenotypic variance (Vp)} &= Vg + Ve \\ \text{Broad-sense heritability } H^2 &= \frac{Vg}{Vp} \times 100 \end{aligned}$$

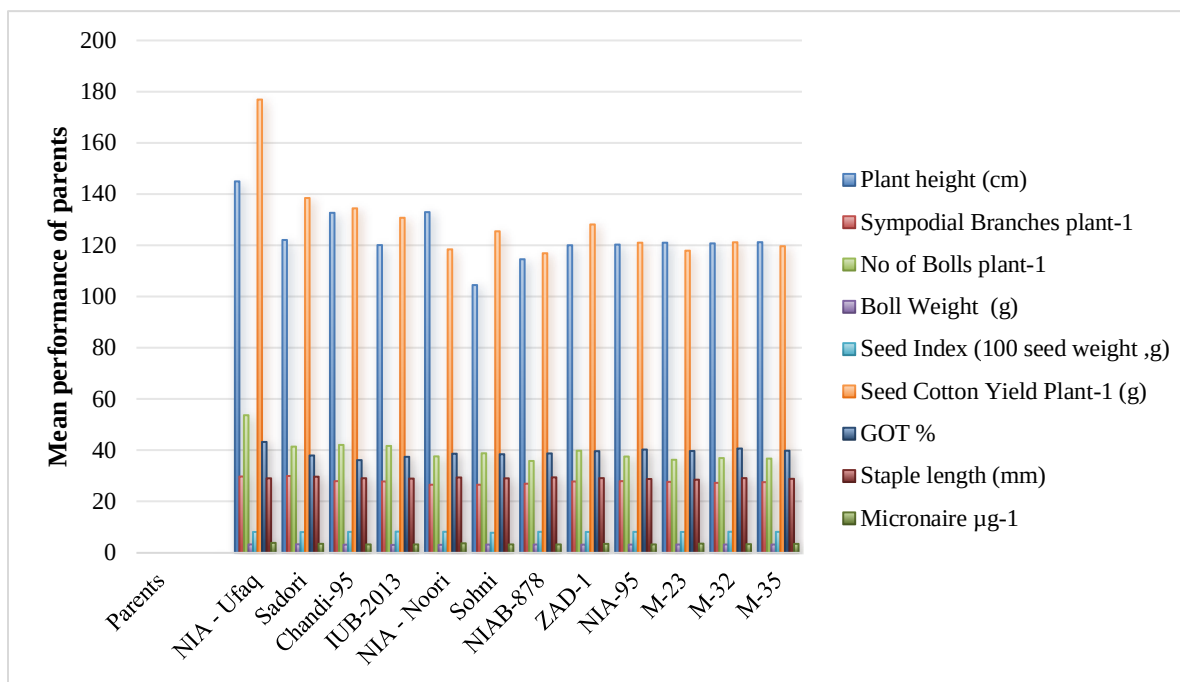
### Results

The mean squares from ANOVA existing in (Table 1) revealed highly significant ( $P < 0.05$ ) differences among the twenty genotypes for plant height, sympodial branches plant<sup>-1</sup>, bolls plant<sup>-1</sup>, boll weight, seed cotton yield plant<sup>-1</sup>, ginning outturn and staple length, and significant ( $P < 0.05$ ) differences for micronaire. Seed index showed a non-significant genotypic mean square overall, although the parents and F<sub>2</sub> progenies sub-groups differed significantly from one another for this trait when examined separately. These results indicate that adequate genetic variability was present among the parents and their F<sub>2</sub> hybrids, justifying further estimation of genetic parameters for each trait.

**Table 1. Mean square from ANOVA for nine morpho-agronomic and fibre-quality traits of cotton**

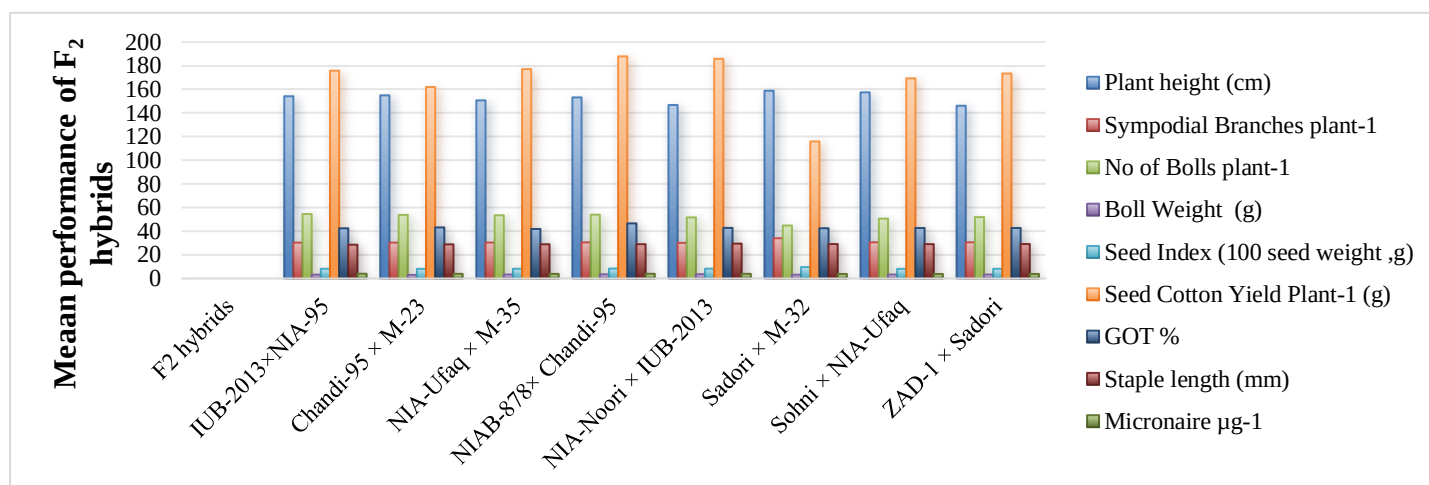
| Source of variance       | D. F | Plant height | Sympodial branches | Bolls plant <sup>-1</sup> | Boll weight | Seed index | Seed cotton yield plant <sup>-1</sup> | GOT (%) | Staple length | Micronaire |
|--------------------------|------|--------------|--------------------|---------------------------|-------------|------------|---------------------------------------|---------|---------------|------------|
| Replications             | 2    | 2.09         | 2.048              | 45.309                    | 0.0039      | 0.10617    | 419.82                                | 0.8301  | 0.00316       | 0.06717    |
| Genotypes                | 19   | 876.99**     | 10.72**            | 160.07**                  | 0.048**     | 0.25 ns    | 2224.03**                             | 19.08** | 0.36**        | 0.19**     |
| Parents                  | 11   | 307.25**     | 3.45**             | 71.05*                    | 0.01*       | 0.29**     | 824.15**                              | 9.70**  | 0.04*         | 0.12**     |
| F <sub>2</sub> progenies | 7    | 64.31**      | 5.06**             | 29.74*                    | 0.10**      | 0.21*      | 1558.65**                             | 6.53**  | 0.82 ns       | 0.02*      |
| Error                    | 38   | 4.458        | 0.4943             | 12.989                    | 0.00252     | 0.21932    | 154.591                               | 1.1834  | 0.01074       | 0.03366    |

\*\* and \* indicate significance at the 1% and 5% probability levels, respectively; ns = non-significant; D.F. = degrees of freedom.



**Figure 1a. Mean performance of twelve parental genotypes for nine yield and fibre-quality traits**

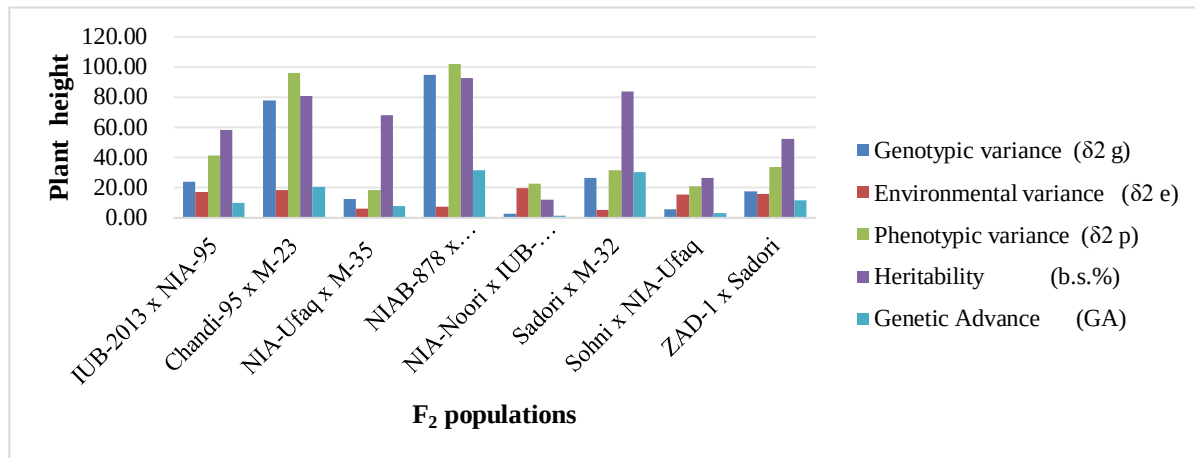
Among the twelve parents (Figure 1a), NIA-Ufaq combined the tallest plant stature (145.00 cm), the highest number of bolls plant<sup>-1</sup> (53.73) and the highest seed cotton yield plant<sup>-1</sup> (176.93 g) with a strong ginning outturn of 43.30%, identifying it as the best-performing parental line overall. Sadori produced the greatest number of sympodial branches plant<sup>-1</sup> (30.00) and the longest staple (29.73 mm) among the parents, while IUB-2013 recorded the heaviest seed index (8.29 g). NIAB-878 had the lowest number of bolls plant<sup>-1</sup> (35.87) and the lowest seed cotton yield (116.95 g), and Chandi-95 the lowest ginning outturn (36.2%) among the twelve parents.



**Figure 1b. Mean performance of eight F<sub>2</sub> populations for nine yield and fibre-quality traits**

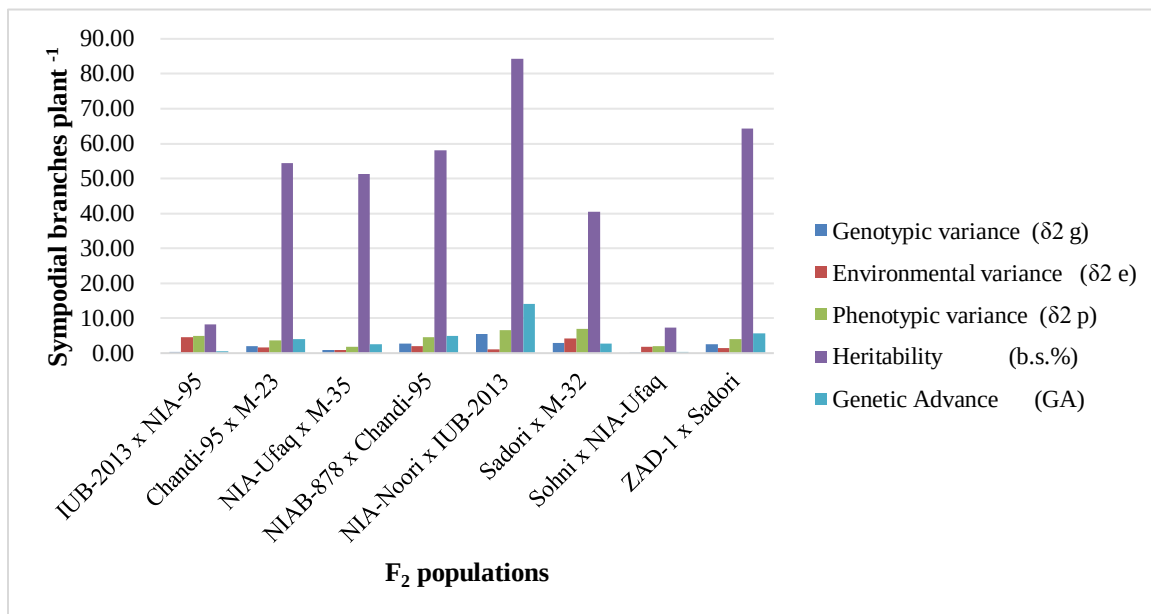
Among the F<sub>2</sub> populations (Figure 1b), Sadori × M-32 attained the greatest plant height (158.87 cm), the highest number of sympodial branches plant<sup>-1</sup> (34.07) and the heaviest seed index (9.67 g), yet recorded the lowest seed cotton yield plant<sup>-1</sup> (116.00 g) and fewest bolls plant<sup>-1</sup> (44.80) among the eight crosses, indicating that vigorous vegetative growth in this combination did not translate into higher yield. In contrast, NIAB-878 × Chandi-95 produced the highest seed cotton yield (187.97 g), the heaviest boll weight (3.48 g) and the best ginning outturn (46.63%), while IUB-2013 × NIA-95 recorded the greatest number of bolls plant<sup>-1</sup>

(54.53) and the highest micronaire (4.00). NIA-Noori  $\times$  IUB-2013 combined a high seed cotton yield (185.93 g) with the longest staple length (29.50 mm) among the crosses, and ZAD-1  $\times$  Sadori showed the shortest plant height (146.20 cm) of the eight  $F_2$  populations.



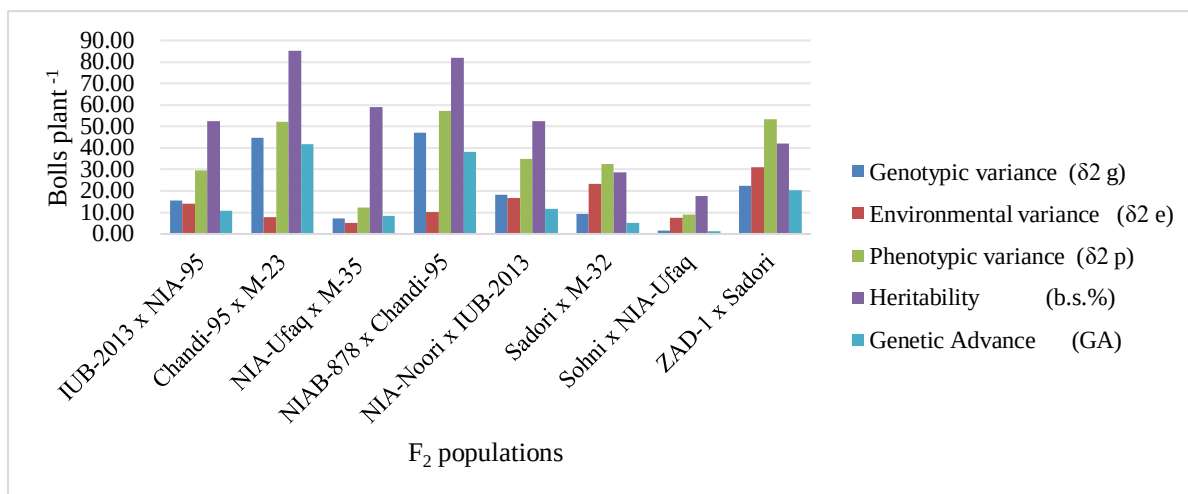
**Figure 2. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for plant height (cm) in eight  $F_2$  populations of cotton**

Genotypic variability for plant height differed widely among the eight  $F_2$  hybrids (Figure 2). NIAB-878  $\times$  Chandi-95 showed the highest genotypic variance (94.67) and the highest broad-sense heritability (92.84%), coupled with the greatest genetic advance (31.40), followed by Sadori  $\times$  M-32 ( $h^2 = 83.80\%$ ,  $GA = 30.32$ ) and Chandi-95  $\times$  M-23 ( $h^2 = 80.83\%$ ,  $GA = 20.60$ ). NIA-Noori  $\times$  IUB-2013 recorded the lowest heritability (11.91%) and genetic advance (1.57), reflecting a comparatively larger environmental contribution to phenotypic variance in this cross.



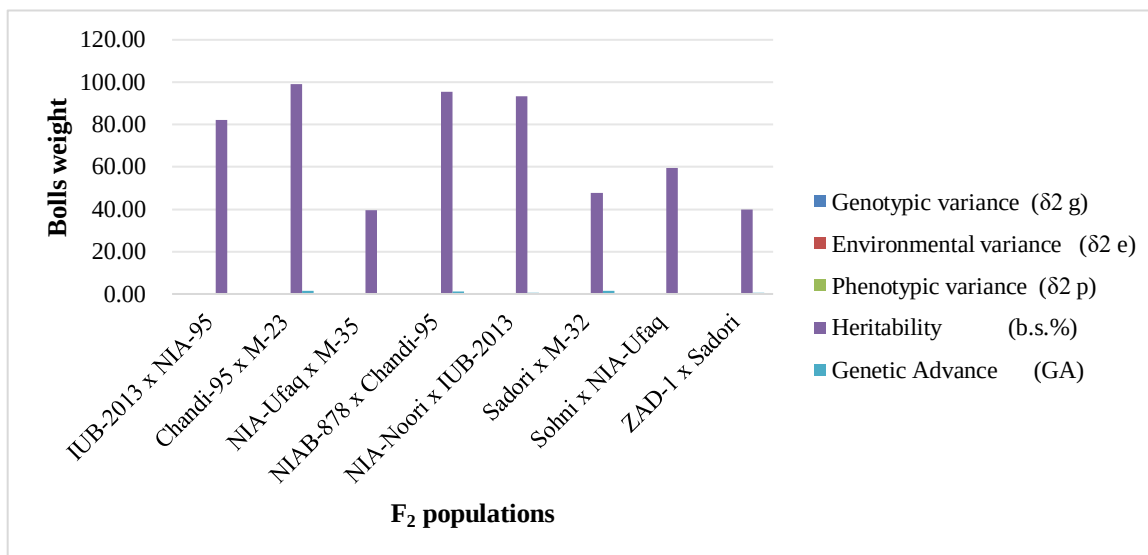
**Figure 3. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for sympodial branches  $\text{plant}^{-1}$  in eight  $F_2$  populations of cotton**

Heritability for sympodial branches  $\text{plant}^{-1}$  ranged from 7.35% (Sohni  $\times$  NIA-Ufaq) to 84.20% (NIA-Noori  $\times$  IUB-2013), with genetic advance ranging correspondingly from 0.27 to 14.15 (Figure 3). The high heritability and genetic advance recorded for NIA-Noori  $\times$  IUB-2013 indicate predominantly additive gene action for this trait in that cross, making it a favourable target for selection.



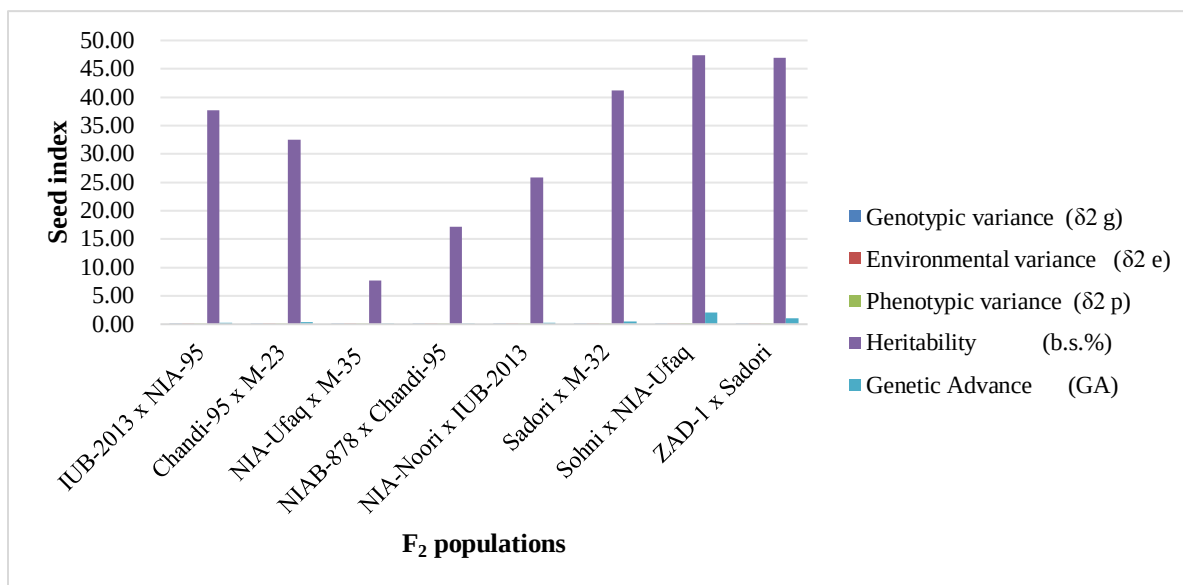
**Figure 4. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for bolls plant<sup>-1</sup> in eight F<sub>2</sub> populations of cotton**

For bolls plant<sup>-1</sup>, heritability varied from 17.77% (Sohni × NIA-Ufaq) to 85.25% (Chandi-95 × M-23), and genetic advance from 1.39 to 41.74 (Figure 4). The combination of high heritability and the largest genetic advance in Chandi-95 × M-23 suggests strong additive genetic control, indicating good potential for improving boll number through direct selection in this cross.



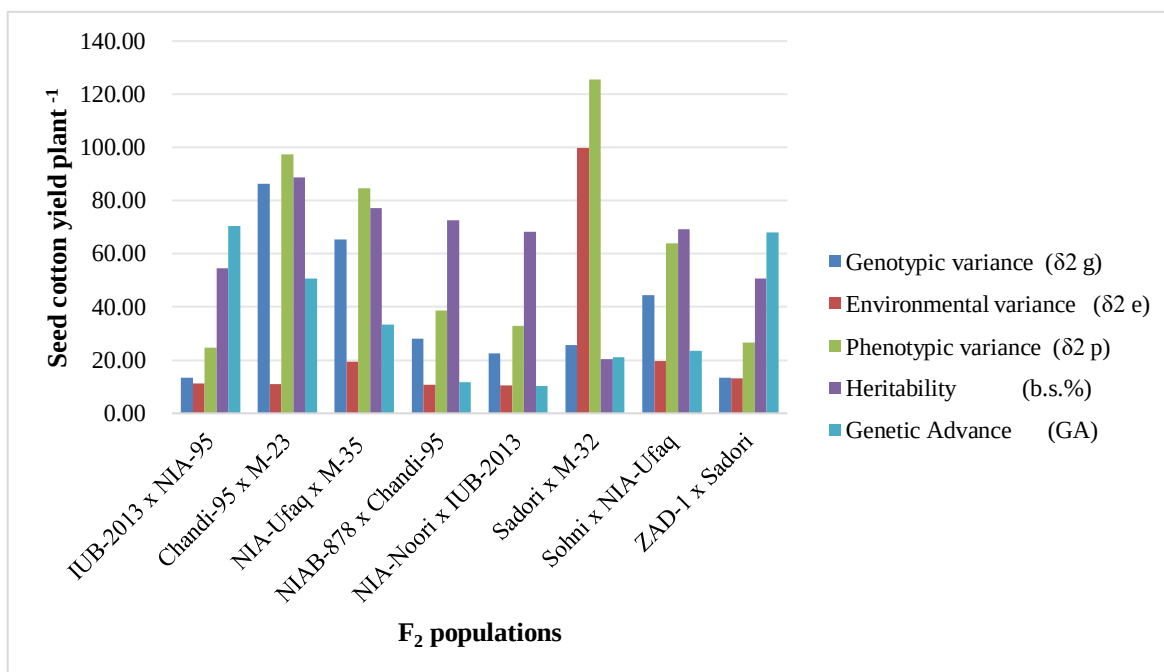
**Figure 5. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for boll weight (g) in eight F<sub>2</sub> populations of cotton**

Boll weight showed heritability ranging from 39.61% (NIA-Ufaq × M-35) to a very high 99.17% (Chandi-95 × M-23), with genetic advance from 0.05 to 1.50 (Figure 5). Although Chandi-95 × M-23 exhibited the highest heritability, its genetic advance (1.41) was comparatively moderate, whereas Sadori × M-32 combined moderate heritability (47.78%) with the largest genetic advance (1.50) recorded for this trait.



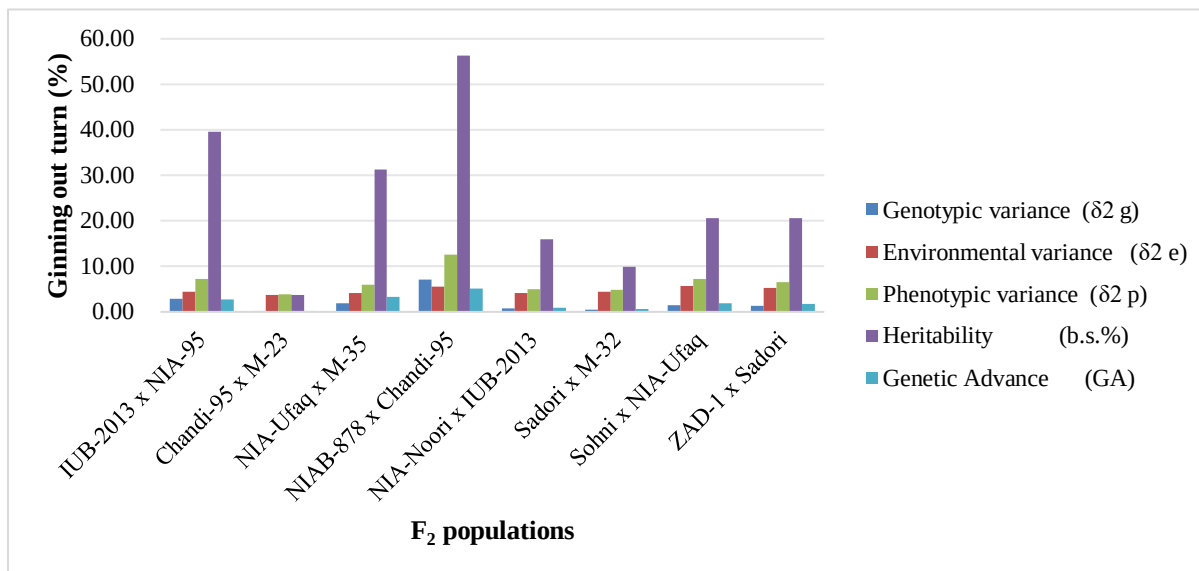
**Figure 6. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for seed index (100-seed weight, g) in eight F<sub>2</sub> populations of cotton**

Heritability for seed index was generally low to moderate, ranging from 7.71% (NIA-Ufaq × M-35) to 47.35% (Sohni × NIA-Ufaq), with genetic advance between 0.03 and 2.08 (Figure 6). The comparatively modest heritability values across most crosses suggest that both additive and non-additive gene effects, together with environmental influence, contribute to the expression of seed size in this material.



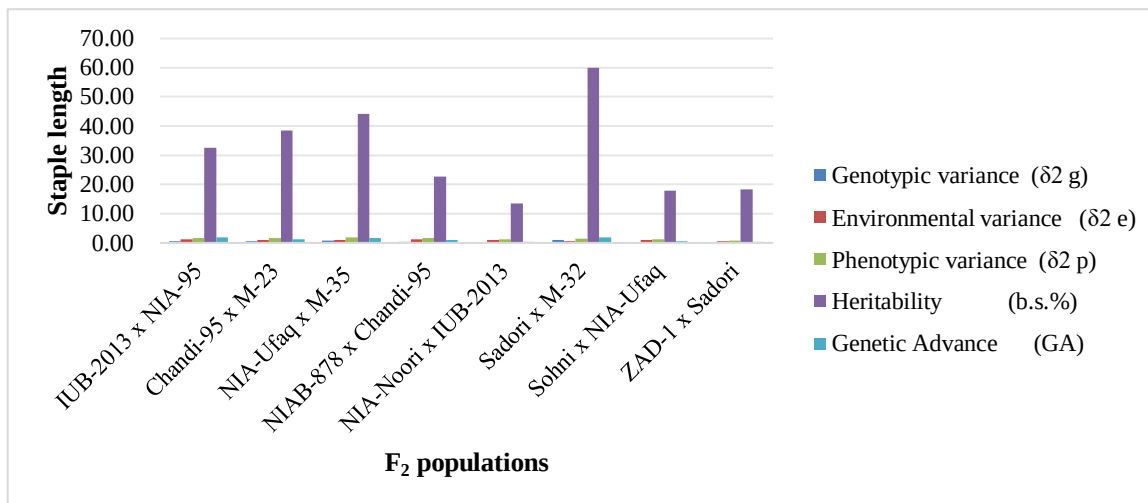
**Figure 7. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for seed cotton yield plant<sup>-1</sup> (g) in eight F<sub>2</sub> populations of cotton**

Seed cotton yield plant<sup>-1</sup> displayed heritability from 20.44% (Sadori × M-32) to 88.65% (Chandi-95 × M-23), with genetic advance ranging from 10.17 to 70.53 (Figure 7). Chandi-95 × M-23 combined high heritability with a high genetic advance (50.63), and IUB-2013 × NIA-95 and ZAD-1 × Sadori likewise showed substantial genetic advance (70.53 and 68.05, respectively) despite only moderate heritability, indicating that selection gains for yield are achievable in several of these crosses.



**Figure 8. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for ginning outturn, got (%) in eight F<sub>2</sub> populations of cotton**

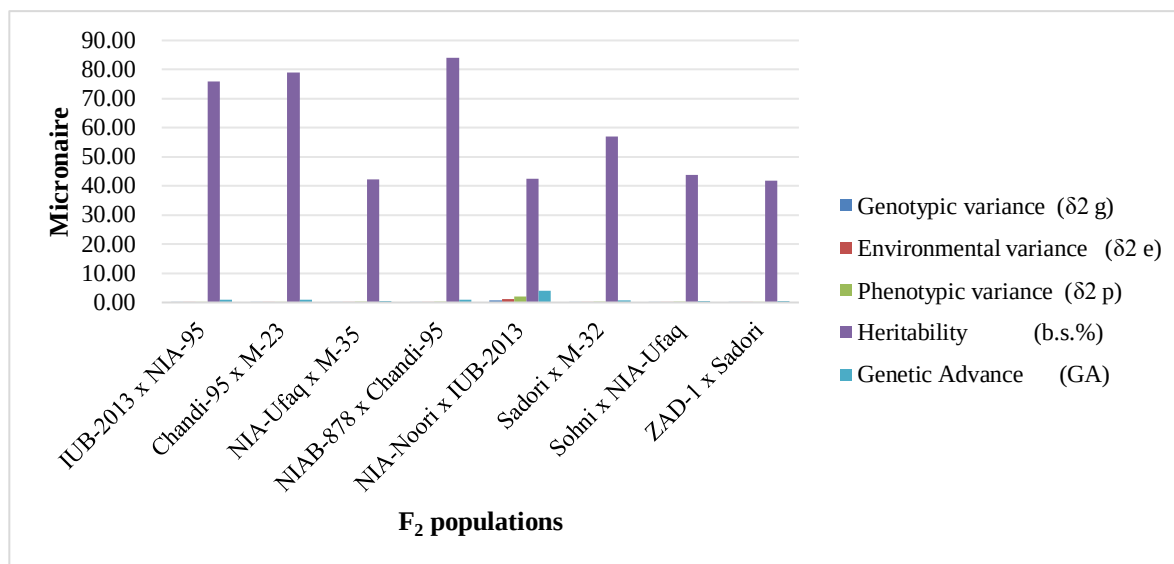
Ginning outturn percentage showed the narrowest heritability range of any trait studied, from 3.66% (Chandi-95 × M-23) to 56.25% (NIAB-878 × Chandi-95), with genetic advance from 0.19 to 5.19 (Figure 8). The low heritability recorded in most crosses points to a relatively strong environmental influence on lint percentage expression in this F<sub>2</sub> material.



**Figure 9. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for staple length (mm) in eight F<sub>2</sub> populations of cotton**

Heritability for staple length ranged from 13.47% (NIA-Noori × IUB-2013) to 59.89% (Sadori × M-32), with genetic advance between 0.38 and 1.93 (Figure 9). The moderate heritability and genetic advance recorded for Sadori × M-32 suggest that fibre length in this cross is influenced by a mix of additive and environmental effects.





**Figure 10. Genotypic variance, environmental variance, phenotypic variance, heritability (broad sense) and genetic advance for micronaire ( $\mu\text{g}^{-1}$ ) in eight F<sub>2</sub> populations of cotton**

Micronaire heritability ranged from 41.94% (ZAD-1 × Sadori) to 83.95% (NIAB-878 × Chandi-95), with genetic advance from 0.43 to 4.03 (Figure 10). NIA-Noori × IUB-2013 recorded the largest genetic advance (4.03) despite only moderate heritability (42.61%), while NIAB-878 × Chandi-95 combined high heritability with a comparatively low genetic advance (1.04), a pattern that points to non-additive gene effects also contributing to micronaire expression in that cross.

## Discussion

The significant genotypic mean squares recorded for almost all traits examined in this study (Table 1) confirm that substantial genetic diversity existed among the parental genotypes and their F<sub>2</sub> hybrids, in agreement with the highly significant differences for morphological characters reported by Kaleri et al. (2025) and the significant variation in yield and fibre traits described by Pavan et al. (2025) and Sipio et al. (2025) in comparable upland cotton material. Such broad-based variability is a prerequisite for any breeding programme, as it provides the raw material from which superior recombinants can be selected.

Plant height, a trait that influences light interception, competitive ability against weeds and ultimately boll-bearing capacity, showed the widest range of heritability (11.91–92.84%) among the traits studied, with the highest heritability and genetic advance recorded in NIAB-878 × Chandi-95. This is consistent with the high heritability and genetic advance for plant height reported by Kadam et al. (2025) and Mawblei et al. (2022), and supports the conclusion of Bhanuchand and Raju (2025) that the trait is governed largely by additive gene action and is therefore amenable to early-generation selection, a pattern also confirmed by Ujjainkar (2024) and Patel et al. (2023).

Sympodial branches, which directly bear the fruiting bolls, showed the highest heritability (84.20%) and the second-highest genetic advance (14.15) in the cross NIA-Noori × IUB-2013, mirroring the strong genetic control reported for this trait by Kathiravan et al. (2025) and Kadam et al. (2025). Similar conclusions were drawn by Patel et al. (2023) and Abro et al. (2021), while Alishah (2021) likewise associated high heritability and genetic advance in sympodial number with predominant additive gene action and a correspondingly favourable response to selection.

Boll number plant<sup>-1</sup>, a primary yield-determining trait directly correlated with seed cotton yield, showed its highest heritability (85.25%) together with the largest genetic advance (41.74) in Chandi-95 × M-23, identifying this combination as particularly responsive to selection. Comparable results have been reported by Abro et al. (2022), Sahar et al. (2021) and Kadam et al. (2025), while Rauf et al. (2024) similarly observed high broad-sense heritability with a strong selection response for boll number, and Sowmya and Patil (2021) attributed such high heritability and genetic advance to the preponderance of additive gene effects controlling this trait.

Boll weight exhibited the highest heritability recorded for any trait in this study (99.17% in Chandi-95  $\times$  M-23), although its genetic advance for that cross was only moderate, whereas Sadori  $\times$  M-32 combined a more modest heritability with the largest genetic advance observed for the trait. Kadam et al. (2025) and Patel et al. (2023) similarly reported high heritability accompanied by significant expected genetic advance for boll weight, and Manan et al. (2022) attributed comparable patterns to additive gene action, consistent with the present findings.

**Seed Index:** Seed index, expressed as the weight of 100 seeds, is a key indicator of seed size and development in cotton. It contributes directly to overall yield potential and fiber quality. Heritability ranged from 7.71% to 47.35%, with Sohni  $\times$  NIA-Ufaq showing moderate heritability (47.35%) but low genetic advance (2.08). Seed index showed comparatively low to moderate heritability across crosses, indicating that both additive and non-additive effects, together with environmental variation, shape seed size in this material; nonetheless, Manan et al. (2022), Kadam et al. (2025) and Rehman et al. (2020) have reported strong heritability and genetic progress for seed index in other cotton populations, suggesting that the trait's genetic control may vary appreciably with genetic background.

Seed cotton yield plant<sup>-1</sup>, the principal economic trait in cotton breeding, displayed moderate-to-high heritability in most crosses and the largest genetic advance values recorded in this study, particularly in IUB-2013  $\times$  NIA-95 and ZAD-1  $\times$  Sadori. This pattern, indicative of predominant additive gene effects and good scope for direct selection, parallels findings by Sri-Subalakshmi et al. (2022), Mawblei et al. (2022) and Meena et al. (2022), while Bhatti et al. (2020) and Sahar et al. (2021) similarly confirmed high heritability with significant genetic advance for yield, and Rauf et al. (2024) emphasized that the combination of high heritability and high genetic advance enhances the prospects for further yield improvement through selection.

Ginning outturn percentage, which reflects lint recovery from seed cotton and is governed by polygenic inheritance, showed the lowest heritability of all traits examined in most crosses, with the exception of NIAB-878  $\times$  Chandi-95, which combined the highest heritability (56.25%) with the largest genetic advance (5.19) for this trait. Rauf et al. (2024) likewise reported high heritability for ginning outturn with limited improvement potential through simple selection, while Rehman et al. (2020) and Ujjainkar (2024) reported high broad-sense heritability for the trait, the latter attributing it to predominant additive gene action.

Staple length, a key determinant of spin-ability and yarn strength, showed its highest heritability (59.89%) in Sadori  $\times$  M-32, a cross also identified as promising for selection in subsequent generations on account of its combined genetic variability and heritability. Rehman et al. (2020) reported a negative association between staple length and fibre strength, highlighting a potential trade-off that breeders must consider, while Siyal et al. (2024) similarly reported high heritability for this fibre trait, supporting direct selection as a viable strategy.

Micronaire, an index of fibre fineness and maturity, displayed its highest heritability (83.95%) but a comparatively low genetic advance (1.04) in NIAB-878  $\times$  Chandi-95, a pattern consistent with the findings of Sipio et al. (2025), who reported high heritability but only low-to-moderate genetic advance for micronaire and recommended biparental mating or diallel selective mating, rather than simple selection, to more effectively exploit the available genetic variability. By contrast, Mahesh et al. (2020) observed both high heritability and high genetic advance over the mean for micronaire, attributing this to additive gene action, which suggests that the relative contribution of additive and non-additive effects to micronaire expression may differ across breeding populations.

## **Conclusion**

Analysis of variance demonstrated significant genetic diversity among the twelve parental genotypes and eight F<sub>2</sub> hybrids of upland cotton for most of the traits studied, confirming that this breeding material holds value for future cotton improvement programmes. Among the parents, NIA-Ufaq exhibited the best overall mean performance, while the F<sub>2</sub> crosses NIAB-878  $\times$  Chandi-95 and NIA-Noori  $\times$  IUB-2013 recorded the highest seed cotton yield plant<sup>-1</sup>, identifying them as valuable genetic resources for cotton breeding. Heritability analysis revealed moderate-to-high heritability for seed cotton yield plant<sup>-1</sup> in most crosses, indicating that this trait is primarily under additive genetic control and that selection for seed yield can be practised effectively in early generations of these populations.

The present findings indicate that the crosses Chandi-95  $\times$  M-23, NIA-Ufaq  $\times$  M-35, NIAB-878  $\times$  Chandi-95 and NIA-Noori  $\times$  IUB-2013 are transgressive segregants that outperformed their respective parents for seed cotton yield. A pedigree breeding approach is therefore recommended for these progenies to develop high-yielding upland cotton genotypes. Given the comparatively low heritability observed for ginning outturn and seed index in most crosses, multi-trait selection indices, replicated multi-environment evaluation, or marker-assisted selection are suggested to complement direct phenotypic selection for these traits.

## Author'S Contribution

MM and AWB conducted the research and analyzed the data; PAS, ZAH, TFA, AMN, and SH, NS, wrote the original draft; PAS, conceptualized, supervised, and reviewed the manuscript.

## Conflict of Interest

The authors declare no conflicts of interest.

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