

GENETIC ANALYSIS OF HERITABILITY AND GENETIC ADVANCE IN F₂ POPULATIONS OF UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.)

Wahid Dino Sipio*, Arif Ali Laghari, Ameer Hussain Jarwar, Chetan Kumar, Nawab Jan Baloch, Sadam Hussain Lodo, Adeel Aslam Perzado and Jan Muhammad Keerio

Cotton Research Institute, Agriculture Research Center, Tandojam, Pakistan

*Corresponding author's email: wahidsipio@hotmail.com

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ABSTRACT

The research was conducted at the Cotton Research Institute (CRI) Tandojam in 2023 using a randomized complete block design with three replications. Nine intra-hirustum F₂ hybrids and six parental lines were evaluated for genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritability estimates (h²b.s), and genetic advance (G.A) for plant stature, sympodial branches plant⁻¹, total bolls plant⁻¹, boll weight, seed cotton yield plant⁻¹, fiber length, seed index, Ginning Outturn, and micronaire value. Analysis showed significant differences ($P < 0.01$) among parents and F₂ progenies for all characters, except for micronaire value in F₂ progenies. The parental lines, Mehran and Nusrat, showed promising performances. Among the F₂ hybrids, Koonj × Bakhtawar showed the maximum plant stature (130.61 cm), Mehran × Bakhtawar had the highest number of sympodial branches (24.53), Mehran × Shahzadi produced the highest total number of bolls (71.53) and seed cotton yield (239.63 g), Mehran × Bakhtawar had the maximum boll weight (3.57 g) and GOT (39.90%), Koonj × Nusrat showed the highest micronaire (4.56 µg/inch), and Koonj × Bakhtawar had the maximum seed index (8.42 g) and fiber length (29.14 mm). Genetic parameters revealed higher heritability with genetic advances in F₂ hybrids: Mehran × Shahzadi for plant stature and sympodial branches; Koonj × Nusrat for total bolls plant⁻¹; Koonj × Bakhtawar for boll weight, seed cotton yield plant⁻¹, and GOT; Sindh-1 × Nusrat for fiber length; Mehran × Bakhtawar for seed index; and Sindh-1 × Shahzadi for micronaire. These progenies can be used in breeding programs to improve the yield and fiber quality of upland cotton.

Keywords: Heritability, Genetic advance, F₂ population. Micronaire value.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) stands as one of the most significant fiber crops globally, extensively cultivated for its dual purpose, fiber production and oil extraction. Referred to as "white gold" due to its high economic value, it plays a vital role in the textile sector and contributes substantially to the socio-economic development of cotton-growing nations (Siyal *et al.*, 2024; Farooq *et al.*, 2023). The crop thrives in tropical and subtropical climates and is a key component of Pakistan's agricultural economy. Pakistan ranks among the top cotton-producing countries, securing the fourth position in global cotton productivity. Beyond its fiber, cottonseed serves as a source of edible oil and as animal feed in the form of cottonseed cake, enhancing its value (Siyal *et al.*, 2024).

Despite its importance, Pakistan's cotton production has faced a downward trend in recent years, influenced by various biotic and abiotic stresses. The production has declined to approximately 9.86 million bales across 2.373 million hectares, reflecting a 17.5% decrease in yield, which in turn caused a 12.74% reduction in cotton ginning output (Anonymous, 2019–20). With the global population on a continuous rise, meeting the increasing demand for raw materials in the textile industry has become crucial. To overcome these challenges and enhance productivity, the application of modern plant breeding techniques becomes imperative (Farooq *et al.*, 2023).

The economy of Pakistan is heavily dependent on its textile industry, with cotton as the central raw material for this sector. Widely used for clothing and various industrial applications, cotton by-products further extend its economic significance (Khan *et al.*, 2015; Hampannavar *et al.*, 2020). American cotton, a tetraploid species, is particularly valued for its fiber quality and is extensively used in textile exports, providing a substantial contribution to the national GDP. Moreover, cottonseed contains vital proteins and oil, serving as raw material for several chemical and food industries (Sahito *et al.*, 2015).

To ensure sustainable cotton production and meet industrial demands, plant breeders continuously explore the genetic potential of existing germplasm. The availability of genetic variability within breeding material is critical for effective selection and cultivar development (Chen *et al.*, 2022) Understanding the nature and magnitude of genetic diversity allows breeders to select suitable parents and employ efficient breeding methods. Quantitative traits, which

are governed by multiple genes, require detailed evaluation of genetic parameters such as heritability and trait correlations to achieve meaningful genetic gain (Tiwari *et al.*, 2019).

Heritability plays a crucial role in predicting the response of traits to selection. It indicates the proportion of observed variation that is genetic and can be transmitted to future generations (Sootaher *et al.*, 2020). However, the coefficient of variation merely reflects the extent of variability and does not distinguish between genetic and environmental components. Therefore, combining heritability with genetic advance offers a clearer picture of the expected improvement under selection pressure. Furthermore, understanding phenotypic and genotypic correlations among traits is essential for selecting yield-contributing characteristics (Nisar *et al.*, 2022).

Genetic variation encompasses the total phenotypic differences observed among plant populations and forms the basis for evolutionary and breeding advancements. Broad-sense heritability, expressed as the ratio of genetic to phenotypic variance, helps breeders evaluate the potential of trait transmission from parents to offspring (Iqbal *et al.*, 2024). Traits governed by additive gene action are particularly useful for selection-based breeding. Previous studies (Baloch *et al.*, 2018) highlighted significant genotypic variation and high heritability for seed cotton yield and related traits, indicating that such characteristics can be improved through hybridization and transgressive selection.

MATERIALS AND METHODS

Nine random F_2 cross combinations along with six parents were grown at Cotton Research Institute, Agriculture Research Centre Tandojam, Sindh so as to estimate heritability and genetic advance in F_2 segregating populations of upland cotton. The experiment was carried out in a randomized complete block design with three replications. Six parents including Sindh-1, Shahzadi, Nusrat, Mehran, Bakhtawar and Koonj were randomly crossed to develop nine F_2 hybrids. At maturity, five plants per genotype and per replication were randomly tagged as index plants for recording the data. The traits studied were plant stature (cm), sympodial branches plant⁻¹, total bolls plant⁻¹, boll weight (g), seed cotton yield plant⁻¹ (g), fiber length (mm), seed index (g), ginning out turn (%), micronaire value ($\mu\text{g}/\text{inch}$). The recorded data was analyzed according to statistical technique developed by Gomez and Gomez (1984) through Statistix 8.1 computer software. The mean values of all genotypes for each trait were statistically compared using the Least Significant Difference (LSD) test at the 5% significance level. Estimates for genetic, environmental, and phenotypic variances, as well as broad-sense heritability (h^2_{bs}) and genetic advance, were calculated following the method described by Baloch *et al.* (2010).

RESULTS

Analysis of variance

The mean squares from analysis of variance for all the traits studied are presented in Table 1. The results obtained revealed that cotton genotypes differed significantly at $P \leq 0.01$ probability level for all traits studied, indicating the existence of considerable genetic variability among the genotypes for traits studied. The mean performance of parents and F_2 hybrids also varied significantly ($P < 0.01$) for all the characters under study. However, micronaire value was non-significant in F_2 hybrids only. The parents vs. F_2 hybrids revealing disparity comparisons between parents and hybrids and were also significant ($P < 0.01$) for sympodial branches plant⁻¹, total bolls plant⁻¹, boll weight and seed cotton yield plant⁻¹, yet non-significant for plant stature, fiber length, seed index, ginning out turn and micronaire value. These results suggested that considerable genetic variability among the parents and their F_2 populations existed; therefore, data needs further evaluation for the estimation of genetic parameters.

Mean performance of parents and their F_2 hybrids

Mean performance of six parents and their nine F_2 hybrids are presented in Table 2. The parental line Bakhtawar produced tallest plants (124.53 cm), while Nusrat recorded the shortest plants measuring 108.53 cm as compared to other parental lines. In case of F_2 progenies, the values of plant stature varied from 108.77 to 130.61 cm, while the tallest plants were observed in F_2 progenies such as Koonj \times Bakhtawar (130.61cm). On the other hand, the shorter plants were observed in cross Sindh-1 \times Nusrat (108.77cm). In parental lines, the sympodial branches plant⁻¹ ranged from 16.27 in Shahzadi to 22.53 in Mehran. Similarly, the F_2 progenies Mehran \times Bakhtawar and Mehran \times Shahzadi produced higher number of sympodial branches plant⁻¹ like 24.53 and 23.80 respectively, while the lowest number of sympodial branches plant⁻¹ in the F_2 populations were recorded by the crosses Sindh-1 \times Shahzadi (17.00) and Sindh-1 \times Bakhtawar (17.93). With regards to total bolls plant⁻¹, cross Mehran \times Shahzadi set highest bolls plant⁻¹ (71.53), followed by the Mehran \times Nusrat (54.07), while parent Koonj

formed lowest number of bolls (24.40) yet highest bolls plant⁻¹ (69.60) was produced by Mehran. While comparing 06 parents, Bakhtawar recorded the maximum boll weight (3.48g) and the minimum by Koonj (3.00g). From F₂ hybrids, Mehran × Bakhtawar produced heavier bolls weighing 3.57g, whereas smaller bolls (3.00g) were obtained from cross Koonj × Shahzadi. With respect to seed cotton yield plant⁻¹ among 15 tested cotton genotypes, the highest seed cotton was produced by F₂ progeny Mehran × Shahzadi (239.63g) and lowest seed cotton yield plant⁻¹ was harvested from parent Koonj (73.20g).

Table 1. Mean squares from analysis of variance of parents and their F₂ intra-hirustum populations for yield and fiber traits

Characters Studied	Source of variation					
	Replications	Genotypes	Parents	F ₂ Hybrids	Parents vs Hybrids	Error
	D.F. = 2	D.F. = 14	D.F. = 5	D.F. = 8	D.F. = 1	D.F. = 28
Plant stature	4.338	150.690**	141.491**	175.025**	2.005 ^{ns}	2.620
Sympodial branches plant ⁻¹	2.891	22.573**	17.141**	19.137**	77.221**	1.689
Total bolls plant ⁻¹	1.19	754.259**	928.901**	725.884**	108.049**	2.916
Boll weight	0.008	0.095**	0.092**	0.088**	0.166**	0.017
Seed cotton yield plant ⁻¹	358.54	8337.02**	10608.0**	7631.93**	2622.84*	361.14
Fiber Length	0.699	1.441**	1.211**	1.671**	0.751 ^{ns}	0.242
Seed index	0.29	1.143**	1.560**	1.025**	0.002 ^{ns}	0.139
Ginning out turn	6.719	10.017**	12.751**	8.659**	7.211 ^{ns}	1.976
Micronaire value	0.014	0.031**	0.042**	0.025 ^{ns}	0.024 ^{ns}	0.011

** , * Significant at 1 and 5 % of probability levels respectively, ns = non-significant

Among the parental lines, the maximum seed cotton yield plant⁻¹ (231.07g) was obtained from Mehran and minimum seed cotton yield plant⁻¹ (73.20g) was produced by Koonj. Among F₂ hybrids, the highest seed cotton yield plant⁻¹ (239.63g) was obtained from cross Mehran × Shahzadi and the lowest (87.38) from Koonj × Nusrat. From fifteen cotton genotypes, including parents and their F₂ progenies assessed in this experiment, the longest fiber length (29.14mm) was measured by F₂ progeny Koonj × Bakhtawar and minimum (26.54mm) by parent Nusrat. Among the parental lines, the maximum fiber length was recorded in Mehran (28.32mm) and minimum by Nusrat (26.54mm). While among F₂ progenies, the maximum fiber length was observed in Koonj × Bakhtawar (29.14mm) and minimum in cross Sindh-1 × Nusrat (26.75mm). In case of seed index, Koonj produced highest among the parental lines (8.34g), however Shahzadi recorded lowest seed index (6.42g). Among F₂ progenies, the cross between Koonj × Bakhtawar gave highest seed index (8.42g), while lowest seed index was determined by Mehran × Shahzadi (6.52g). In case of GOT %, among parental lines, the maximum GOT % was given by Mehran (38.49%), followed by Nusrat (38.15%) and lowest GOT % among the parental lines was given by Bakhtawar (33.32%). From F₂ progenies, the crosses Mehran × Bakhtawar and Mehran × Nusrat have achieved maximum lint percentage of 39.90 and 38.64% respectively. Whereas the lowest GOT % among the F₂ population was recorded in cross Sindh-1 × Bakhtawar (34.83%). With respect to micronaire value, among parental lines, the maximum micronaire value was recorded by Nusrat (4.56µg/inch) followed by Shahzadi (4.44µg/inch) and lowest micronaire value among the parental lines was noted in Bakhtawar (4.21µg/inch).

Heritability estimates

Plant stature

The genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for plant stature are presented in Figure 1. All nine F₂ progenies displayed greater genetic variability which is about equal to phenotypic variances, which resulted in very high heritability estimates for all the crosses and that ranged from 98.19 to 99.80 %. Similarly, F₂ progenies displayed moderate to high amount of genetic advance, which varied from 22.61 to 47.78 %. Among the progenies, Mehran × Nusrat and Koonj × Nusrat, exhibited higher heritability estimates of 99.80 % and 99.72 % with higher amount of genetic gain of 39.48 to 39.45 % respectively against rest of the progenies evaluated.

Table 2. Mean performance of parents and their F₂ intra-hirsutum populations for various yield and fiber traits.

Genotypes (Parents and hybrids)	Plant stature (cm)	Sympodial branches plant ⁻¹	Total bolls plant ⁻¹	Boll weight (g)	Seed cotton yield plant ⁻¹ (g)	Fiber length (mm)	Seed index (g)	GOT (%)	Mic. value (µg/inch)
Parents									
Sindh-1	110.11	16.47	25.00	3.06	76.5	27.23	7.15	36.92	4.29
Shahzadi	115.29	16.27	30.40	3.21	97.65	27.72	6.42	37.35	4.44
Nusrat	108.53	18.33	28.73	3.39	97.39	26.54	7.02	38.15	4.56
Mehran	113.91	22.53	69.60	3.32	231.07	28.32	7.51	38.49	4.37
Bakhtawar	124.53	18.27	26.20	3.48	91.18	27.62	7.93	33.32	4.21
Koonj	121.52	17.60	24.40	3.00	73.20	28.06	8.34	34.31	4.42
F2 Populations									
Sindh-1 × Shahzadi	111.22	17.00	29.13	3.20	93.22	27.90	7.24	37.37	4.30
Sindh-1 × Nusrat	108.77	19.93	31.47	3.44	108.26	26.75	7.31	37.50	4.39
Sindh-1 × Bakhtawar	113.74	17.93	25.20	3.50	88.02	27.40	8.04	34.83	4.33
Mehran × Shahzadi	117.15	23.80	71.53	3.35	239.63	28.90	6.52	37.60	4.47
Mehran × Nusrat	109.61	21.33	54.07	3.38	182.76	27.64	7.14	38.64	4.42
Mehran × Bakhtawar	120.98	24.53	36.47	3.57	130.20	27.67	7.53	39.90	4.30
Koonj × Shahzadi	123.03	21.87	32.60	3.00	97.8	27.83	6.75	35.72	4.43
Koonj × Nusrat	115.52	19.00	26.40	3.31	87.38	27.40	7.10	36.27	4.56
Koonj × Bakhtawar	130.61	20.27	27.60	3.32	91.63	29.14	8.42	35.44	4.28
LSD (5%)	2.27	2.10	2.85	0.19	25.17	0.83	0.61	2.26	0.18

Sympodial branches plant⁻¹

The genetic parameters such as genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for sympodial branches plant⁻¹ are presented in Figure 2. All the nine F₂ progenies displayed greater genetic variability and that was almost at par with phenotypic variances, which resulted in high heritability estimates. However, hybrids like Mehran × Nusrat and Mehran × Bakhtawar, recorded higher heritability estimates of 99.80 to 99.72 % and higher genetic gains of 39.48 and 43.58 % respectively. Results from above crosses suggested that both the progenies from respective crosses can be considered as valuable breeding material for the improvement of said character.

Total bolls plant⁻¹

The genetic parameters like genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for total bolls plant⁻¹ are presented in Figure 3. All the nine F₂ progenies displayed about equal greater genetic variability to their phenotypic variances, which produced higher heritability estimates such heritability ranged from 92.12 to 99.42 % and displaying moderate to higher amount of genetic advances varying from 17.41 to 42.51 %. Cross combinations like Koonj × Nusrat ($h^2 = 99.42$ %) followed by Mehran × Nusrat ($h^2 = 99.22$ %) exhibited higher heritability estimates, alongwith greater genetic gains of 42.51 and 42.42 respectively. The recombinants from these above progenies can be used as suitable breeding material for phenotypic selection in later segregating generations so as to improve the total bolls plant⁻¹, consequently yield.

Boll weight

The genetic parameters such as genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for boll weight are presented in Figure 4. All the nine F₂ progenies displayed almost at par genetic and phenotypic which ended up into higher heritability estimates which ranged from 66.71 % in Sindh-1 \times Nusrat and 96.73 % in Koonj \times Bakhtawar with genetic advance of 0.57 to 0.88 %. However, most of the progenies manifested lower genetic advances. Among the F₂ populations which reflected higher heritability may be exploited for selection in later filial generations and may provide the new gene recombinations to occur which ultimately will result in production of elite germplasm with improved weight boll⁻¹.

Seed cotton yield plant⁻¹

The genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for seed cotton yield plant⁻¹ are presented in Figure 5. All the nine F₂ progenies displayed about equal amount of genetic and phenotypic variances, which resulted in higher heritability estimates in all crosses that ranged from 88.59 % with genetic advances of 60.21 to 79.58 %. Among all the F₂ populations, the crosses Koonj \times Bakhtawar, Koonj \times Nusrat and Mehran \times Bakhtawar calculated higher heritability of 98.02 %, 97.66 % and 97.49 % with genetic gains of 79.58, 92.10 and 103.41 % respectively, considered as high heritability estimates with higher amount of genetic advances. These results revealed that the selection of recombinants in subsequent subsequent filial generations of above crosses would be very effective for the improvement of seed cotton yield plant⁻¹.

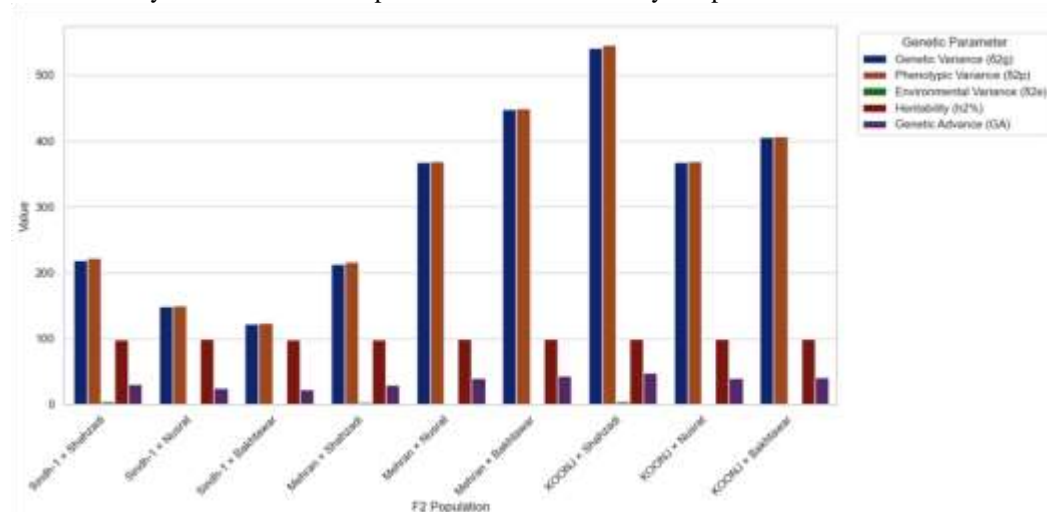


Fig. 1. Estimates of heritability and genetic advance for plant stature in nine F₂ upland cotton populations.

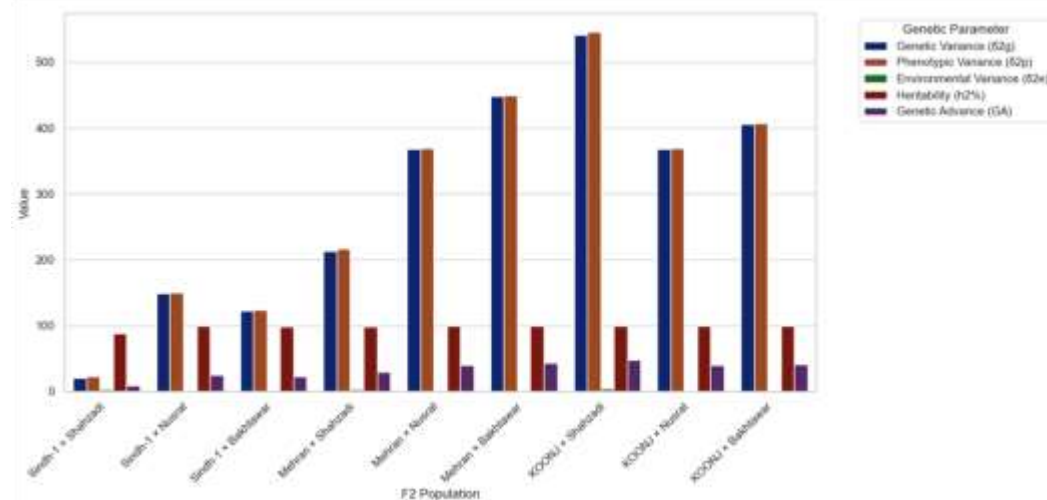


Fig. 2. Heritability estimates and genetic advance for sympodial branches plant⁻¹ in nine F₂ upland cotton populations.

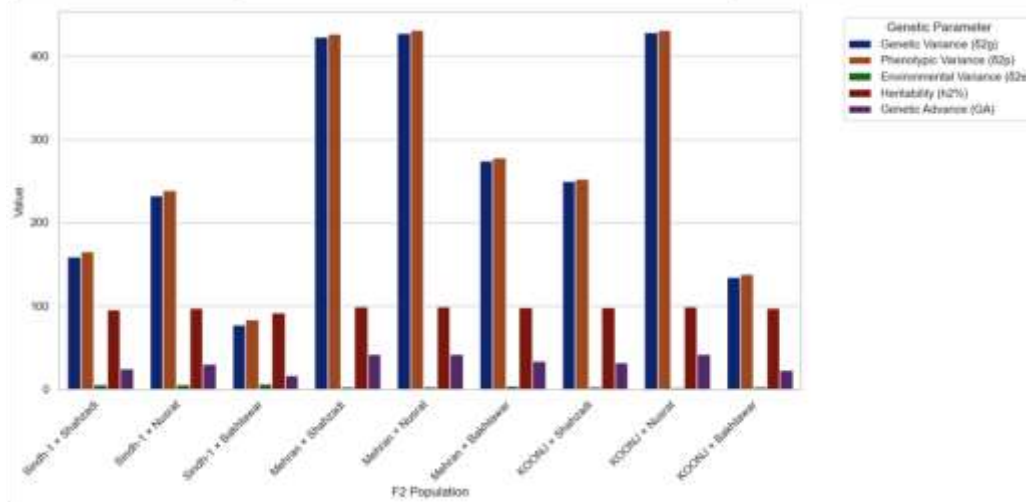


Fig. 3. Heritability estimates and genetic advance for total bolls plant in nine F₂ upland cotton populations.

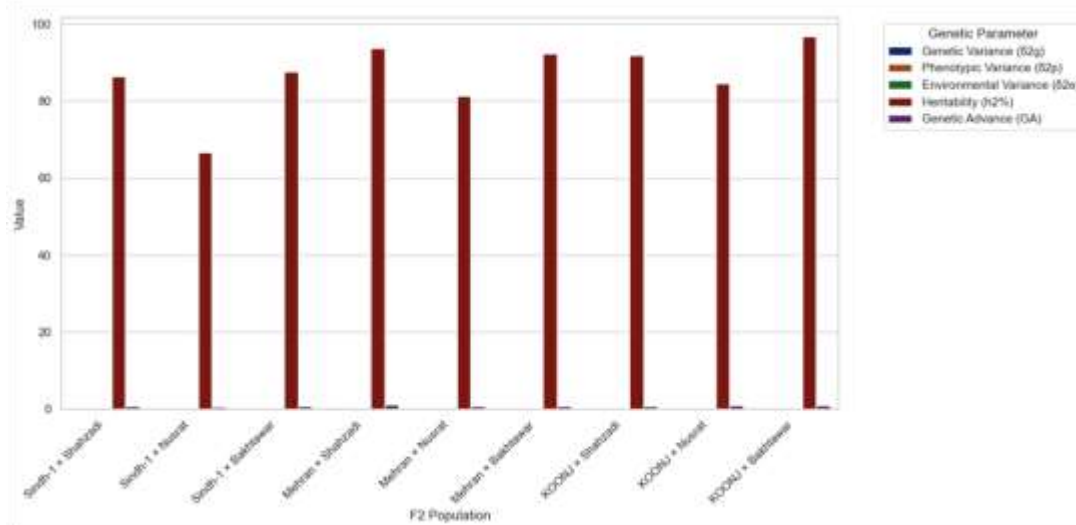


Fig. 4. Heritability estimates and genetic advance for boll weight in nine F₂ upland cotton populations.

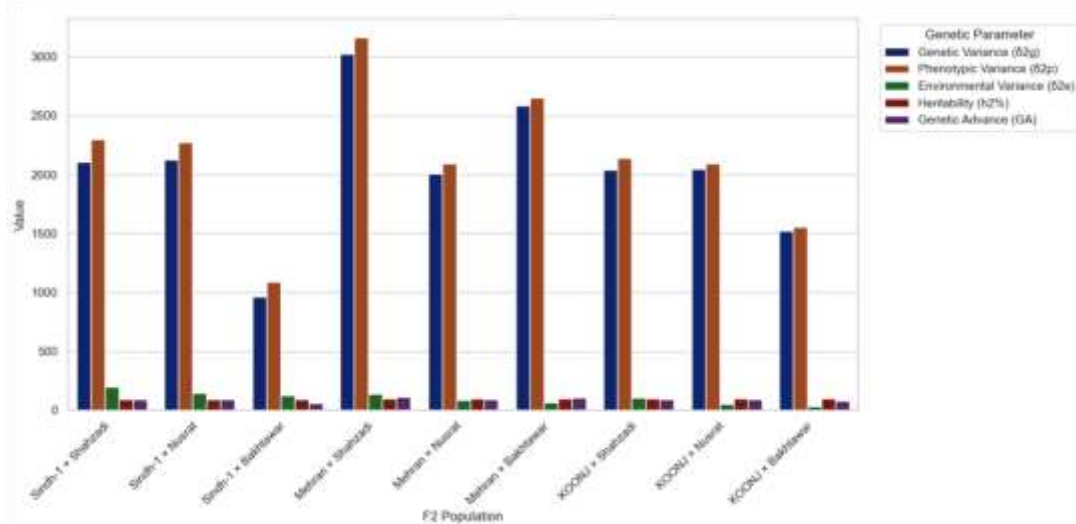


Fig. 5. Heritability estimates and genetic advance for seed cotton yield plant⁻¹ in nine F₂ upland cotton populations.

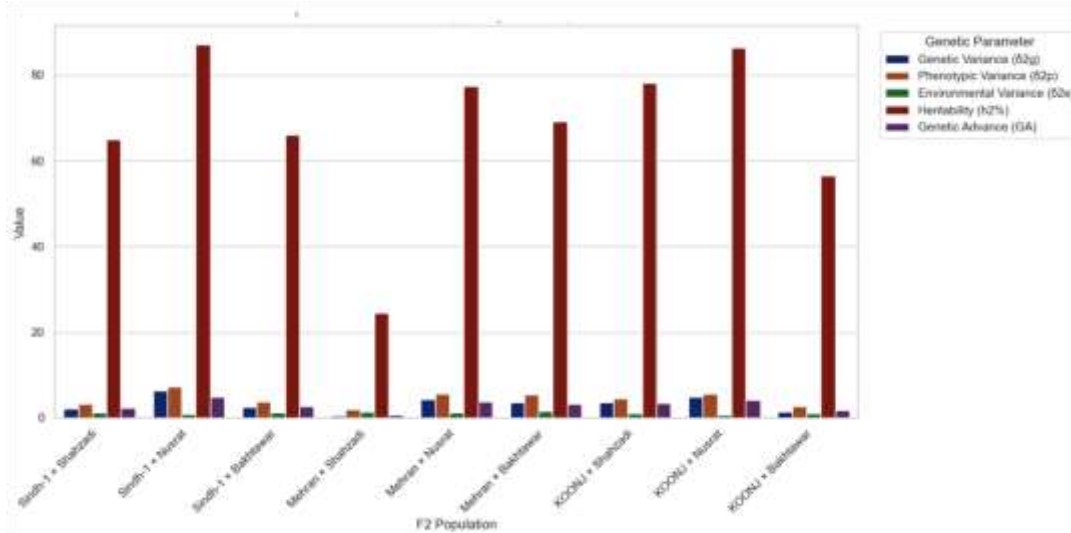


Fig. 6. Heritability estimates and genetic advance for fiber length in nine F₂ upland cotton populations.

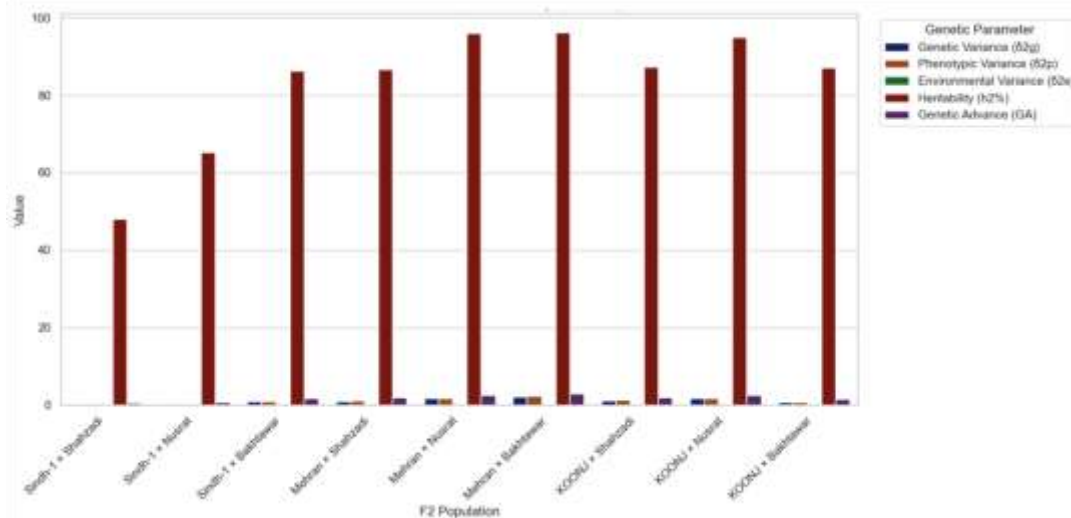


Fig. 7. Heritability estimates and genetic advance for seed index in nine F₂ upland cotton populations.

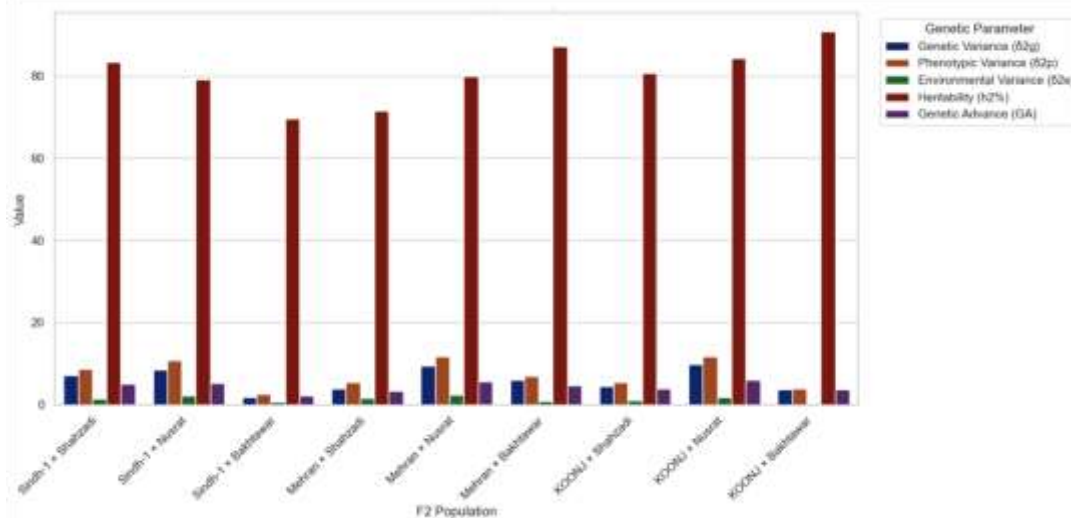


Fig. 8. Heritability estimates and genetic advance for GOT % in nine F₂ upland cotton populations.

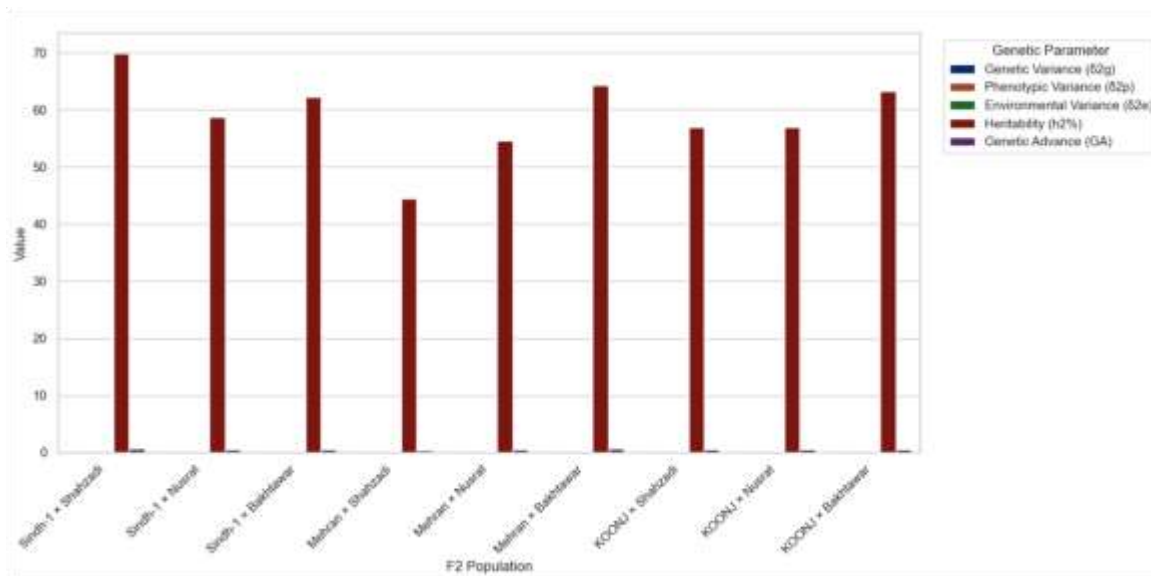


Fig. 9. Heritability estimates and genetic advance for micronaire value in nine F₂ upland cotton populations.

Fiber Length

The genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for fiber length are presented in Figure 6. All nine F₂ progenies displayed nearly equal genotypic and phenotypic variances, except Mehran × Shahzadi showed greater phenotypic variances than genotypic variability which resulted in low heritability estimates of 24.58 %. Similarly, F₂ progenies displayed lower to fair amount of genetic advance that varied from 0.72 to 4.83 %. Among the progenies, Sindh-1 × Nusrat, however exhibited maximum heritability estimates of 87.10 % with fair amount of genetic advance (4.83 %).

Seed index (100 seed weight)

The genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with and genetic advance for seed index (100-seed weight) are presented in Figure 7. Almost all the nine F₂ progenies displayed about equal genotypic and phenotypic variability that caused low, moderate and high heritability estimates which ranged from 48.15 % to 96.14 %. Whereas genetic gains varied from very low to fair, this ranged from 0.62 to 2.99 %. Mehran × Bakhtawar, however, exhibited highest heritability estimates of 96.14 % with fair amount of genetic advance 2.99 % being the potential F₂ population.

Ginning out turn (%)

The genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for GOT % are presented in Figure 8. All nine F₂ progenies displayed at par genetic and phenotypic variability which resulted into higher heritability estimates in all the crosses. The heritability ranged from 69.67 to 90.76 % coupled with genetic advance which varied from 2.30 to 3.76 %. Among the progenies, Koonj × Bakhtawar, Mehran × Bakhtawar and Koonj × Nusrat, however, exhibited higher heritability estimates and genetic advance of $h^2 = 90.76$ %, $G.A = 3.76$ %, $h^2 = 87.15$ % $G.A = 4.73$ and $h^2 = 84.37$ % $G.A = 5.98$ respectively. These results suggested that the segregating populations from above crosses can be subsequently selected and evaluated for higher GOT %.

Micronaire value ($\mu\text{g}/\text{inch}$)

The genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance for micronaire value ($\mu\text{g}/\text{inch}$) are presented in Figure 9. Some F₂ progenies displayed greater genetic variability than their phenotypic variances, which resulted in low, moderate and higher heritability estimates that varied from 44.40 % to 69.84 %. Similarly, F₂ progenies displayed fair amount of genetic advance which ranged from 0.36 to 0.68 %. Among the progenies, cross Sindh-1 ×

Shahzadi however exhibited higher heritability estimates of 69.84 % and genetic gain of 0.68 % being the potential population.

DISCUSSION

The analysis of variance and mean performance of six parents and their nine F₂ progenies are given in Tables 1 and 2, respectively. The genotype's degrees of freedom were split into parents, hybrids and parents vs. F₂ hybrids. The objective of current research was to estimate genetic variance, broad sense heritability and genetic advance at 20 % selection pressure in F₂ populations of upland cotton (*Gossypium hirsutum* L.). The mean squares from the analysis of variance summarized in Table 1, indicated that genotypes differed significantly at $P \leq 0.01$ probability level for all the traits studied. The mean performance of the parents also differed significantly for all the characters. Similarly, the F₂ hybrids also differed significantly for all the traits studied except micronaire value which was non-significant. Baloch *et al.*, (2018) and Siyal *et al.*, (2024) worked with F₂ populations alongwith their respective parents and observed significant differences among the genotypes for studied traits. Alkudusi *et al.* (2013) and Farooq *et al.*, (2023) reported that genotypes varied significantly for all the studied characters. The results of each character are discussed in the following paragraphs.

Plant stature is an important characteristic which makes crop plants compete specifically with weeds. The cotton breeders believe that varieties with medium height are desirable for obtaining higher seed cotton yields. Moreover, this character influences the fruiting bodies greatly. The mean performance of plant stature is presented in Table 2 which pointed out that the parental line Bakhtawar produced tallest plants of 124.53 cm, whereas Nusrat recorded shortest plants measuring 108.53 cm as compared to other parental lines. While among the F₂ progenies, plant stature varied from 108.77 to 130.61cm. Progenies from the cross Koonj \times Bakhtawar gave taller plants (130.61cm). On the other hand, the shorter plants were recorded by the cross Sindh-1 \times Nusrat (108.77 cm). Results regarding genetic parameters presented in Table 3 suggested that the progenies Mehran \times Nusrat and Koonj \times Nusrat, exhibited higher heritability estimates of 99.80 % and 99.72 % with greater amount of genetic gains of 39.48 to 39.45 respectively. These results suggested that recombinants from both the progenies can be used as useful segregating material for selection in subsequent generations so as to improve plant height. Soomro *et al.*, (2010) estimated higher heritability with notable genetic gains for plant stature and significant genetic and phenotypic variances as well. Ranganatha *et al.* (2013) studied genetic variability, heritability estimates and genetic advance and revealed high broad sense heritability and genetic gains for plant stature.

Sympodial branches are known as fruiting branches on which the bolls are set in cotton plant, thus these branches play crucial role in increasing seed cotton yield. Researchers and plant breeders suggested that sympodial branches provide a good criterion for selecting high yielding varieties. The mean performance shown in Table 2 indicated that among the parents, maximum sympodial branches plant⁻¹ (22.53) was produced by Mehran. Similarly, the F₂ progenies Mehran \times Bakhtawar and Mehran \times Shahzadi produced maximum sympodial branches plant⁻¹ (24.53 to 23.80) respectively. Results regarding genetic parameters presented in Figure 2 demonstrated that the progenies expressed higher heritability estimates in all the crosses, yet hybrids like Mehran \times Nusrat and Mehran \times Bakhtawar, exhibited higher heritability estimates of 99.80 to 99.72 %, coupled with higher genetic gains of 39.48 and 43.58 % respectively. The present research is further supported by the findings of Aziz *et al.* (2014); they stated that sympodial branches plant⁻¹ presented higher heritability (bs) associated with sufficient genetic advance in F₃ generations of upland cotton (*Gossypium hirsutum* L.)

Total bolls plant⁻¹ is regarded as an essential economic trait in cotton crop which has direct impact on seed cotton yield plant⁻¹. Thus, brings significant improvement in this trait, eventually causes increase the seed cotton yield. With regard to mean performance, progeny Mehran \times Shahzadi set highest total bolls plant⁻¹ (71.53), followed by Mehran \times Nusrat (54.07), while parent Mehran produced maximum (69.60) total bolls plant⁻¹. Figure 3 presents results concerning genetic parameters, which revealed that all of the progenies manifested about equal genetic and phenotypic variances resulting in higher heritability estimates. Among the progenies, combinations like Koonj \times Nusrat ($h^2 = 99.42$ %) followed by Mehran \times Nusrat ($h^2 = 99.22$ %) exhibited higher heritability estimates, alongwith greater genetic gains of 42.51 and 42.42. The recombinants from these above progenies can be used as suitable breeding material for phenotypic selection in later filial generations to improve total bolls plant⁻¹. Similar to our results, Yazied *et al.* (2014) also reported high estimates of heritability in broad sense were observed for total bolls plant⁻¹ in two populations and increased from F₂ to F₃ generations. Zeng and Pettigrew (2015) also observed high heritability estimates in F₂ populations for total bolls plant⁻¹.

Boll weight plays a fundamental role in increasing seed cotton yield plant⁻¹ because as the boll weight increases, the yield also increases. Bolls are in various sizes such as large, medium and small. Results in Table 2 presented the mean performance of genotypes and the variety Bakhtawar weighed the heaviest bolls (3.48g) and the minimum boll

weight (3.00g) was recorded in Koonj. In F_2 hybrids, Mehran \times Bakhtawar gave bigger bolls weighing 3.57g while smaller bolls were observed in cross Koonj \times Shahzadi (3.00g). Results in Figure 4 present the results regarding the genetic parameters viz genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance of nine F_2 progenies. In general, genetic variances were at par with phenotypic for majority of the populations in boll weight. Thus, F_2 populations expressed high heritability estimates in all crosses, which ranged from $h^2 = 66.71\%$ in Sindh-1 \times Nusrat to $h^2 = 96.73\%$ in Koonj \times Bakhtawar with very low genetic advance of 0.57 to 0.88% respectively. The F_2 populations which reflected higher heritability may be exploited for selecting desirable plants in lateral filial generations and may provide new gene recombination which ultimately may result in production of elite germplasm with improved boll weight. With agreement to our findings, Raza *et al.* (2016) reported moderate to higher heritability for all the characters including boll weight.

The seed cotton yield depends on number of total bolls plant, number of seeds boll⁻¹, boll weight etc. The yield is most important character in any crop breeding programmes. It is one of the main goals of plant breeders to increase cotton yield, hence breeders divert high attention to enhance yield because it will not only improve the socio-economic conditions of farmers but also the country. Results in Table 2 showed that for mean performances, the parental line Mehran gave maximum seed cotton yield plant⁻¹ (231.07g) and minimum yield (73.20g) was obtained from Koonj. Among F_2 hybrids, the highest seed cotton yield plant⁻¹ (239.63g) was obtained from cross Mehran \times Shahzadi and the lowest (87.38g) yield from cross Koonj \times Nusrat. Figure 5 demonstrate that the genetic parameters viz. genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance of nine F_2 progenies showed at par genetic and phenotypic variability. All the nine F_2 progenies displayed almost similar amount of genetic and phenotypic variability which resulted in high heritability estimates for all the crosses that ranged from 88.59 to 98.02 %, with genetic advance of 60.21 to 79.58 % which were considered as high genetic gain. Among all the F_2 populations, the crosses Koonj \times Bakhtawar, Koonj \times Nusrat and Mehran \times Bakhtawar manifested heritability estimates of 98.02 %, 97.66 % and 97.49 % with genetic gains of 79.58, 92.10 and 103.41, considered as high heritability estimates with higher amount of genetic advances, which revealed that the selection of recombinants in subsequent generation of above crosses may be very effective for the improvement of seed cotton yield plant⁻¹. Analogous to our findings, Aziz *et al.* (2014) Raza *et al.* (2016) and Reddy and Reddy (2016) also estimated higher heritability for seed cotton yield plant⁻¹.

Fiber length is regarded as key quality characteristic in cotton and is also called as staple length. It is valuable for textile mills. Results in Table 2 indicated that among the parental lines, the maximum fiber length was recorded by Mehran (28.32mm) and minimum by Nusrat (26.54mm). While among F_2 progenies, the maximum fiber length was measured by Koonj \times Bakhtawar (29.14mm) and minimum was given by Sindh-1 \times Nusrat (26.75mm). The results from genetic parameters indicated that majority of the F_2 progenies expressed almost equal genetic and phenotypic variances, which resulted in low to higher heritability ranging from 24.58 to 87.10 %. Higher heritability estimates were associated with sufficient amount of genetic advances estimated by the progenies Sindh-1 \times Nusrat ($h^2 = 87.10\%$, G. A= 4.83), followed by Koonj \times Nusrat ($h^2 = 86.46\%$, G.A = 4.25) respectively. It is very clear from these results in Figure 6 that progenies which displayed greater genetic variability, higher heritability estimates associated with fair amount of genetic advances may be subjected to selection in further segregating generations to improve this trait. Our results are in consonance with those of Khan *et al.*, (2015) who reported moderate to higher heritability estimates in broad sense for Fiber length in F_1 and F_2 generations of intra-hirustum hybrids. Malagouda *et al.* (2014) and Yazied *et al.* (2014) also observed moderate to higher heritability estimates alongwith moderate to better genetic advance for the said character.

Seed index is an additional important yield parameter in cotton crop. Results presented in Table 2 revealed that Koonj (8.34g) produced highest seed index among the parental lines, while Shahzadi recorded lowest seed index (6.42g). The cross between Koonj \times Bakhtawar recorded highest seed index weighing 8.42g, while lowest seed index was calculated by Mehran \times Shahzadi (6.52g) among F_2 progenies. The results of genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance of nine F_2 progenies presented in Figure 7 showed greater amount of both genetic and phenotypic variability which resulted in moderate to higher heritability estimates ranging from 48.15 to 96.14 %. While all F_2 progenies displayed lower to fair genetic gains ranging from 0.62 to 2.99%. The F_2 progenies from crosses like Mehran \times Bakhtawar, Mehran \times Nusrat and Koonj \times Nusrat expressed maximum heritability estimates of 96.14, 95.94 and 94.99%, along with considerable amount of genetic gains i.e., 2.99, 2.63 and 2.61%, respectively. On basis of above results, selection can be effective for segregants to improve seed index. Raza *et al.* (2016) and Reddy and Reddy (2016) worked on subsequent generations of different intra-hirustum cross combinations and observed moderate to higher heritability estimates in yield contributing traits besides seed index. Results of these researchers are also in consonance with our findings.

Ginning out turn percentage refers to as the proportion of lint from the total seed cotton sample and also denoted as lint percentage. It is a complex trait, which is controlled by polygenes. Lint weight has direct bearing with ginning out turn ratio. Selection for higher ginning out turn % often increases in the production unit⁻¹ area. Based on mean performance, parental line producing maximum GOT % was noted as Mehran (38.49%) followed by Nusrat (38.15%) and lowest GOT % among the parental lines was observed in Bakhtawar (33.32%). While from F₂ progenies, the crosses Mehran × Bakhtawar and Mehran × Nusrat gained maximum lint percentage of 39.90 and 38.64% respectively. Whereas the lowest GOT % among the F₂ population was recorded in cross Sindh-1 × Bakhtawar (34.83%). The results for genetic parameters such as genetic variance (δ^2g), phenotypic variance (δ^2p), environmental variance (δ^2e), heritable estimates in the broad sense (h^2b) along with genetic advance of nine F₂ progenies are depicted in Figure 8. High heritability estimates but low amount of genetic gains were noted among the progenies that varied from $h^2 = 69.67\%$, G.A = 2.30 to $h^2 = 90.76\%$, G.A = 3.76. The crosses Koonj × Bakhtawar, Mehran × Bakhtawar and Koonj × Nusrat exhibited higher heritability estimates of $h^2 = 90.76\%$, G.A = 3.76; $h^2 = 87.15\%$, G.A = 4.73 and $h^2 = 84.37\%$, G.A = 5.98 respectively. The results suggested that segregating populations from above crosses can be subsequently selected and evaluated for GOT %. Our results are line with those of Baloch *et al.* (2010), who also found high heritability percentage for lint %.

Micronaire value is measure of fiber fineness and is related to maturity. Fiber fineness affects yarn appearance, yarn uniformity and yarn strength. With respect to micronaire value among parental lines, the maximum micronaire value was recorded by Nusrat (4.56 μ g/inch) followed by Shahzadi (4.44 μ g/inch) and lowest micronaire value among the parental lines was noted in Bakhtawar (4.21 μ g/inch). From F₂ progenies, the crosses Koonj × Nusrat and Mehran × Shahzadi recorded maximum micronaire value of 4.56 and 4.47 μ g/inch respectively. Whereas the lowest micronaire value among the F₂ population was recorded by cross Koonj × Bakhtawar (4.28 μ g/inch). Results regarding genetic parameters and heritable estimates in the broad sense (h^2b) along with genetic advance of nine F₂ progenies revealed in the Figure 9 indicated moderate to higher heritability percentage which ranged from 44.40 to 69.84 % coupled with low genetic progress. Cross Sindh-1 × Shahzadi exhibited high heritability estimates among all the F₂ hybrids, whereas Mehran × Shahzadi recorded as the progenies with minimum percentage of heritability (44.40 %).

Conclusions

The analysis of variance expressed significant difference ($P \leq 0.01$) among parents and F₂ hybrids for all the characters except micronaire value which was non-significant in F₂ hybrids. The outcome of present research suggested that based on average performance, the parental lines Mehran and Nusrat exposed promising performance for a range of characters. Whereas, among the progenies, the F₂ hybrids, Koonj × Bakhtawar revealed desirable plant stature, longer Fiber length and higher seed index; Mehran × Bakhtawar formed higher number of sympodial branches plant⁻¹, bigger bolls and ginned maximum GOT %; higher total bolls plant⁻¹ and more seed cotton yield plant⁻¹ were recorded by Mehran × Shahzadi, and highest micronaire value by Koonj × Bakhtawar. The genetic parameters revealed that among F₂ hybrids, higher heritability estimates associated with more genetic advances for plant stature and sympodial branches plant⁻¹ were recorded by Mehran × Nusrat; for total bolls plant⁻¹ by Koonj × Nusrat; for boll weight, seed cotton yield plant⁻¹ and GOT % by Koonj × Bakhtawar; for Fiber length by Sindh-1 × Nusrat; for seed index by Mehran × Bakhtawar; and micronaire value by Sindh-1 × Shahzadi. Results thus suggested that these progenies are promising populations and can further be exploited in various breeding programs to improve yield and fiber quality traits in upland cotton.

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