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Combining Ability Analysis of Yield and Its Component Traits in Upland Cotton (*Gossypium hirsutum* L.) Using a Diallel Mating Design

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Abstract

Cotton (*Gossypium hirsutum* L.) is a valuable fiber crop that is of great economic importance. The genetic basis of the yield-related traits was investigated in this study in a full diallel mating design that involved four parental genotypes (AGC-2, MNH-998, RH-647 and Super Gold) and their twelve F1 hybrids. Characteristics such as plant height, monopodial and sympodial branches, bolls per plant, boll weight, lint percentage and seed cotton yield were considered. ANOVA indicated that there was a significant genetic variation across genotypes. The integration of the ability analysis revealed that not only general combining ability (GCA) but also specific combining ability (SCA) played a significant role with non-additive gene action dominating the majority of traits. Some crosses such as AGC-2 × RH-647, AGC-2 × MNH-998 and MNH-998 × RH-647 had high SCA effects and heterotic potential. The existence of important reciprocal effects (RE) indicated the importance of maternal influence. These results indicate that cross breeding and using heterosis is an effective method in enhancing cotton production and fiber-related characteristics.

Keywords: Diallel Analysis, Dominant, Non-Additive, Combining Ability, Reciprocal Effects, Heterosis

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Introduction

Gossypium hirsutum L. is a vital fiber crop that is grown across the world and has wide application in the textile sector (1). The crop is also crucial in supplying raw materials in the textile production industry and sustaining millions of farmers and industrial employees around the world (2). In the 2025-26 season, the world cotton produced about 26 million tons, with China, India, Brazil and United States as the largest producers (3,4). As of 2025, Pakistan was able to produce approximately 1.15-1.20 tons of cotton and was one of the top cottons producing countries (5).

Cotton is an important aspect of the industrial and agricultural economy in Pakistan (6). The cotton-related textile sector plays a significant role in terms of gross domestic product (GDP), job creation and foreign exchange income (7). Cotton is believed to be the workhorse of the textile industry and a source of valuable revenue to the rural communities (8). Hence, enhancing cotton productivity and the quality of the fiber is one of the main goals of plant breeding programs (9).

Many traditional breeding methods such as hybridization, mutation breeding, mass selection and pedigree selection have been adopted in the development of better cotton varieties (10,11). Nevertheless, yield related characteristics in cotton are complex quantitative characteristics that are regulated by multiple genes and affected by environmental factors (12,13). Consequently, genetic information of these traits is crucial to successful selection and breeding.

The diallel analysis is an effective genetic method to examine the inheritance of the quantitative traits and approximate gene action (14,15,16). It allows the assessment of various parental lines by crossing systematically and gives information on genetic variability and combining ability (17). GCA is an indicator of the overall impact of genes and shows the performance of the average genotype; SCA is a non-additive gene effect which includes dominance and epistasis (18). Recognition of parents of high GCA and crosses of high SCA improves breeding efficiency and leads to generation of better hybrids (19,20).

The diallel mating system is especially beneficial among the various mating designs, which allows estimation of GCA and

SCA, gene action and heterosis simultaneously. Unlike the line x tester design, which only gives relatively limited genetic information, diallel analysis provides a more detailed insight on the effects of additive and non-additive genotype and reciprocal (maternal) effects.

Consequently, a diallel mating design was used to determine the estimates of combining ability, gene action and heterosis of key yield-relevant traits in upland cotton in the current study. These were: (i) to determine GCA and SCA of yield-related traits; (ii) the nature of gene action governing these traits; and (iii) the best parental lines and promising hybrid mixtures to improve cotton.

Materials and Methods

The experiment was carried out in the research site of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, in 2024-2025. Parental lines were four genetically different upland cotton (*Gossypium hirsutum* L.) genotypes, i.e., AGC-2, MNH-998, RH-647 and Super Gold. These were genotypes that varied in key agronomic and fiber characteristics.

The parental plants were cultivated in earthen pots (30 x 30 cm) in the greenhouse. The soil was duly ready, and its pH and the soil were tested to make sure that it was suitable to grow cotton. An optimal number of fertilizers was used to supply the necessary nutrients. Seeds were delinted, washed well and sown in October 2024. The ideal light and temperature conditions were upheld to guarantee good germination and growth of the plants.

A full diallel mating design (4 × 4), comprising of both direct and reciprocal crosses, was used. Hand emasculation and controlled pollination during the flowering stage were used to perform hybridization. Precautions were observed to prevent any contamination of pollen, and enough crosses were done to get sufficient F1 hybrid seed. The total number of crosses in a full diallel mating design (including reciprocals) was calculated using the formula: $n(n - 1)$; where n represents the number of parental genotypes.

The parental combinations were designated as: P_1 = AGC-2, P_2 = MNH-998, P_3 = RH-647, P_4 = Super Gold. The direct and reciprocal crosses were developed.

The parental lines and F_1 hybrids were evaluated under field conditions using a randomized complete block design (RCBD) with two replications. All genotypes were planted in 1-in-10 rows with a spacing of 30 cm between the plants and 75 cm between the rows. The growing season was carried out under normal agronomic practices. At each replication, five random guarded plants were observed and their data collected on the following traits:

Monopodial branches

Monopodial branches are branches of the vegetation originating in the main stem. At maturity, the count of the monopodial branches per plant was counted and the average was obtained.

Sympodial branches

Sympodial branches are fruit bearing branches which grow on the upper part of the plant. The number of sympodial branches per plant was recorded and averaged.

Plant height (cm)

At the maturity stage, the height of the stem was determined in centimeters with the base of the plant as the reference point. The average height of five plants was used for statistical analysis.

Bolls per plant

The number of bolls per plant was counted by adding up all pickings and the average amount of bolls per plant was determined.

Lint percentage (%)

Lint percentage was determined using a single roller electric gin. It was calculated using the following formula:

Lint percentage = (Weight of lint) / (Weight of seed cotton) × 100

Seed cotton yield (g)

Seed cotton was harvested from mature bolls at each picking. The total yield per plant was recorded in grams using an electronic balance and the average yield per genotype was calculated.

Statistical Analysis

The data were collected and analyzed using the method of analysis of variance (ANOVA) as outlined by Steel et al. (1997), to establish the level of significance of the difference in genotypes. Method II, Model I of Griffing was used to estimate GCA, SCA and RE through diallel analysis (21). These parameters were employed to establish the type of gene action that controls the traits under study.

Results and Discussion

The ability analysis and genetic variability need to be combined to effectively use the genetic potential in cotton breeding programs. The data about GCA and SCA gives an idea about the essence of the gene action that determines the quantitative and morphological characters. In the current experiment, the characteristics such as height of plants, monopodial branches, sympodial branches, bolls per plant, boll weight, lint percentage and seed cotton yield were compared between parental genotypes and F_1 hybrids. Analysis of variance (ANOVA) was utilized in analyzing the data in accordance with procedure outlined by Steel et al. (1997).

ANOVA results indicated that there was a high significance of the differences in genotypes in all traits studied and thus showed the existence of substantial genetic variability. Such variability can be critical in the successful selection and development of hybrids in cotton breeding projects. Additional diallel analysis further separated the genetic variance into additive and non-additive genetic components, which are essential to determining better parents (via GCA) and promising crosses (via SCA). The relative size of GCA and SCA variances gives an indication on the kind of breeding strategies to use, either selecting additive effects or breeding on heterosis (non-additive effects).

Plant height (cm)

The plant height analysis of variance showed that there was a significant difference between the genotypes, which means that there was a lot of genetic variation in plant height. This variability is significant in enhancement of the plant architecture by breeding programs. The combining ability analysis (Table 1) revealed that GCA, SCA and RE were all

significant indicating that there are additive and non-additive gene interactions in the inheritance of plant height.

The GCA effects of the parental genotypes are shown in figure 1. The maximum positive GCA value was recorded at MNH-998 (6.700), AGC-2 (0.696) which implies that they have good additive genes and can be regarded as good general combiners of plant height. Conversely, RH-647 (-2.867) and Super Gold (-4.529) had negative GCA values, implying that they contribute less to the enhancement of the plant height. The high additive gene effects in MNH-998 and AGC-2 are indicative that these parents can be successfully used in breeding programs that are based on selections (20,22).

The SCA effects of direct crosses (Figure 2) showed that AGC-2 $\times$ RH-647 (6.333) and AGC-2 $\times$ MNH-998 (5.733) had the highest positive values, indicating that there was a strong non-additive interaction between the two genes in these combinations. Conversely, MNH-998 $\times$ RH-647 (-7.154) and AGC-2 $\times$ Super Gold (-6.987) showed negative SCA effects. The fact that high SCA effects have been observed in some crosses underscores the significance of dominance and epistatic interactions between genes in regulating the height of plants. As such, the crosses may be used in hybrid breeding to increase the growth of plants by heterosis (13,22).

The effects on crosses in both directions were also significantly different (Figure 2 and Figure 3) meaning that maternal or cytoplasmic factors affect plant height. Super Gold $\times$ AGC-2 (5.300) registered the maximum positive reciprocal effect and Super Gold $\times$ RH-647 (-4.067) registered the least positive reciprocal effect. These results suggest that the direction of crossing plays an important role and should be considered in breeding strategies (22). These findings were further supported by variance component analysis. Table 1 indicates that SCA variance (58.5982) exceeded GCA variance (27.2591), which means that non-additive gene action is the predominant one in the inheritance of plant height. Reciprocal variance (18.9152) was not as big as SCA variance, but it was significant, which proves the existence of maternal effects. Most of the non-additive gene action is an indication that hybrid breeding and heterosis exploitation is more effective as compared to simple selection to enhance the plant height and overall cotton productivity (23,24).

Monopodial branches

ANOVA showed that monopodial branches differed significantly across the 4×4 diallel set of genotypes, so there was adequate genetic variation in the trait. The combining ability test (Table 1) revealed that the combining abilities of SCA and RE were significant, but not GCA, which indicated that the monopodial branch inheritance is mostly regulated by the non-additive gene action and not the additive effect (25).

The GCA effects of the genotypes of parents are shown in figure 1. Super Gold exhibited the highest positive GCA value (0.125), followed by MNH-998 (0.083) and AGC-2 (0.042), while RH-647 showed a neutral effect (0.000). Compared to Super Gold, there was a relatively greater GCA effect, but the general non-significance and relatively small

amount of GCA variance indicates that there is little additive genetic control on this trait. Thus, it is more effective in combination with hybrids than selection-based breeding.

Significant differences in SCA effects (Figure 2) among crosses were observed. The greatest positive SCA interactions were in AGC-2 $\times$ Super Gold (0.292), AGC-2 $\times$ RH-647 (0.250) and MNH-998 $\times$ RH-647 (0.125) suggesting that there are strong non-additive gene interactions that affect monopodial branching. Conversely, MNH-998 $\times$ Super Gold (-0.333) and AGC-2 $\times$ MNH-998 (-0.167) showed negative SCA effects. These findings imply that there are particular hybrid combinations which can be used to enhance plant architecture via heterosis, which indirectly leads to yield potential. Prior studies have also reported the role of non-additive action of genes in cotton (19,26).

The cross effects were reciprocal with different crosses showing different effects, which implies there are maternal or cytoplasmic inheritance effects. The greatest positive reciprocal effect was found between MNH-998 $\times$ AGC-2 (0.167) and the least effect was found between RH-647 $\times$ MNH-998 (-0.500). These results indicate that the orientation of crossing has a strong impact on monopodial branch expression and hence caution should be taken in terms of the selection of female parents when it comes to breeding programs (13,27).

These findings were further supported by variance component analysis whereby, SCA variance (7.86325) was greater than the GCA variance (-2.76356). There was also reciprocal variance (4.53703) which contributed to the trait variation which showed that there are maternal effects. Altogether, a major part of non-additive gene action implies that breeding based on heterosis, and development of hybrids are more appropriate approaches than mere selection to enhance the monopodial branches in upland cotton (16,23,25).

Sympodial branches

Full diallel ANOVA revealed that genotypic differences for sympodial branches were highly significant among parents and hybrids, indicating substantial genetic variability for this trait. This confirms the presence of considerable exploitable genetic variation for improving sympodial branching through breeding approaches. The combining ability analysis (Table 1) showed that GCA, SCA and RE were significant, indicating that both additive and non-additive gene actions are involved in trait inheritance.

GCA effects (Figure 1) indicated that MNH-998 (1.083) and RH-647 (1.000) exhibited positive and relatively higher values, suggesting the presence of favorable additive alleles for increased sympodial branching. Conversely, AGC-2 (-1.292) and Super Gold (-0.792) showed negative GCA effects, indicating lower additive genetic contribution. These results identify MNH-998 and RH-647 as superior general combiners for improving reproductive branching and indirectly enhancing yield potential in cotton. The importance of additive gene action in yield-related traits has

also been reported in previous studies (28,29).

SCA effects varied significantly among crosses. Positive SCA effects were recorded in AGC-2 $\times$ MNH-998 (2.000), AGC-2 $\times$ Super Gold (0.875) and MNH-998 $\times$ RH-647 (0.375), indicating favorable non-additive gene interactions. However, MNH-998 $\times$ Super Gold (-2.333) and RH-647 $\times$ Super Gold (-0.083) showed negative SCA effects (Figure 2). These findings suggest that specific hybrid combinations can be exploited to enhance plant architecture and yield potential through heterosis, rather than relying solely on selection. Similar observations have been reported in cotton breeding studies (30,31,32).

RE also showed variation among crosses, indicating the influence of maternal or cytoplasmic inheritance. Super Gold $\times$ AGC-2 (3.667), Super Gold $\times$ MNH-998 (2.167) and RH-647 $\times$ AGC-2 (1.667) exhibited the highest positive RE, while MNH-998 $\times$ AGC-2 (-3.000) and RH-647 $\times$ MNH-998 (-0.667) showed negative values (Figure 3). This indicates that the direction of crossing significantly influences sympodial branch expression, highlighting the importance of selecting appropriate female parents in breeding programs. Similar maternal effects in cotton have been reported previously (32,33).

Variance component analysis further showed that SCA variance (2.84641) and dominance variance (2.84641) were higher than GCA variance (0.91605) and additive variance (1.8321) (Table 1). This clearly indicates the predominance of non-additive gene action in controlling sympodial branches. Therefore, heterosis breeding and hybrid development are more effective than simple selection for improving plant architecture and yield potential in upland cotton (34). Both additive and non-additive gene effects contribute to this trait and crosses AGC-2 $\times$ MNH-998 and AGC-2 $\times$ Super Gold are promising for future breeding programs aimed at improving yield-related architecture.

Bolls per plant

ANOVA of the number of bolls per plant in the 4 $\times$ 4 diallel cross resulted in highly significant differences, showing a large genetic variation between parents and the combinations of parents. This supports the fact that boll number is a very heritable and selectable character and can be effectively enhanced with proper breeding measures. The combining ability analysis (Table 1) showed that there was a significant GCA, SCA and RE which indicated that there are both additive and non-additive actions of genes in the inheritance of this trait. The results of GCA (Figure 1) showed that RH-647 (0.723) and AGC-2 (0.390) had positive and more favorable values, which demonstrates that there were favorable additive alleles to a greater number of bolls. On the other hand, MNH-998 (-0.635) and Super Gold (-0.477) exhibited negative GCA effects, indicating that additive

genetic potential of this trait is less. These findings name RH-647 and AGC-2 as the best general combiners and possible parental lines that can be used to enhance boll production and the overall yield in cotton. Previous studies have also indicated the significance of additive gene action in yield-related traits (32,35,36).

The effects of SCA were significantly different between crosses. The maximum positive SCA effects were seen in AGC-2 $\times$ MNH-998 (4.544), AGC-2 $\times$ RH-647 (3.619) and RH-647 $\times$ Super Gold (2.052) indicating that there are strong non-additive gene interactions which affect the number of bolls. In contrast, AGC-2 $\times$ Super Gold (-3.981) and MNH-998 $\times$ RH-647 (-0.990) showed negative SCA effects (Figure 2). The findings indicate that there are certain cross combinations that can be utilized to produce heterosis breeding to enhance boll production and better yield performance in cotton. Earlier studies have shown similar results (36,37).

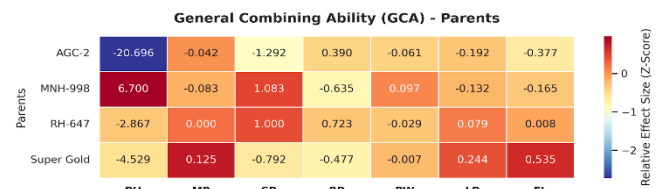


Figure 1: Genetic Effect of General Combining Ability (GCA) of Various Parameters in Upland Cotton (*Gossypium hirsutum* L.)

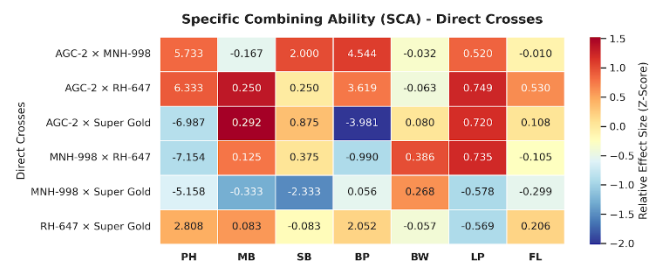


Figure 2: Genetic Effect of Specific Combining Ability (SCA) of Various Parameters in Upland Cotton (*Gossypium hirsutum* L.)

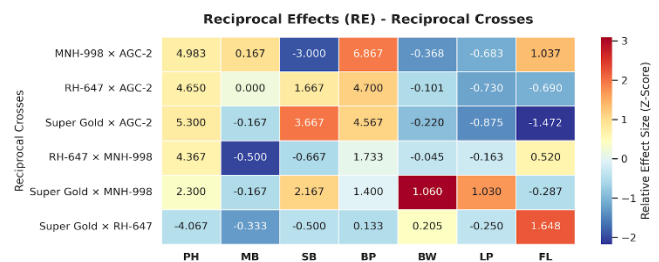


Figure 3: Genetic Effect of Reciprocal Effects (RE) for Various Parameters in Upland Cotton (*Gossypium hirsutum* L.)

There was also significant variation in the same between crosses which showed RE, suggesting that maternal or cytoplasmic genetic effects have occurred. RE were found to be greatest in MNH-998 x AGC-2 (6.867), then RH-647 x AGC-2 (4.700) and Super Gold x AGC-2 (4.567), which implies that the direction of crossing has a significant impact on the expression of boll numbers. On the other hand, a lesser reciprocating effect was recorded in Super Gold x MNH-998 (1.400) and Super Gold x RH-647 (0.133) (Figure 3). These findings affirm that female parental selection has a significant role to play in ensuring the number of bolls are maximized in cotton hybrids. Previous researchers have reported similar maternal effects in cotton (11,38).

Variance component analysis also showed that SCA variance (16.68094) was more than GCA variance (-2.74446) indicating that non-additive gene action dominated. This supports the fact that the additive effects of this trait are of little importance in the current material although additive variance was negative. The influence of the maternal effects was also confirmed by the fact that the reciprocal variance (15.63734) was also significant. On the whole, the findings suggest that the action of dominance genes and cytoplasmic influences are significant in boll number inheritance. Thus, hybrid breeding and heterosis breeding would be superior to mere selection methods. The cross combinations AGC-2 x MNH-998 and AGC-2 x RH-647 have a potential to be used in the future breeding programs to improve the cotton yield potential (7,17).

Weight of the boll

The Analysis of variance indicated significant differences between the genotypes in boll weight, which showed that the genetic variability in boll weight was large. This substantiates that boll weight is a major yield factor that has good potential to be improved by breeding. Combining ability analysis (Table 1) revealed that GCA, SCA and RE were significant and therefore there are both additive and non-additive gene effects in the inheritance of boll weight.

The estimated components of variance (Table 1) showed that SCA variance ($\delta^2D = 9.93275$) was significantly greater than GCA variance ($\delta^2A = -2.97487$) but the reciprocal variance (0.22320) was relatively low. This is a clear indication that in control of boll weight in upland cotton, non-additive gene action, especially dominance effects, are predominant. These results indicate that heterosis breeding is an effective tool that can be applied to enhance boll weight and productivity (39,40).

GCA effects (Figure 1) revealed that MNH-998 had the highest positive value (0.097) which means that MNH-998 has positive additive alleles to improve boll weight. Super Gold did not significantly affect GCA (-0.007), but AGC-2 (-0.061) and RH-647 (-0.029) did, indicating that they did

not add significantly. The high GCA effect of MNH-998 makes it an attractive parent in breeding programs to enhance boll weight and yield potential in cotton breeding programs (36,41).

Effects of SCA differed among crosses. The most positive SCA effect was found in MNH-998 x RH-647 (0.386), then MNH-998 x Super Gold (0.268) indicating substantial non-additive gene interactions and good hybrid performance. Conversely, RH-647 x Super Gold (-0.057) and AGC-2 x RH-647 (-0.063) exhibited negative SCA effects, implying that the combination of these two hybrids is poor with respect to this trait. This implies that there are certain cross combinations that can be used to breed through heterosis to increase boll weight and yield performance in cotton (42,43). Crosses also exhibited significant variation in RE suggesting that there was a maternal or cytoplasmic effect. The highest reciprocal effect was observed in Super Gold x MNH-998 (1.060), followed by Super Gold x RH-647 (0.205), whereas MNH-998 x AGC-2 (-0.368) and Super Gold x AGC-2 (-0.220) showed negative effects (Figure 3). These findings suggest that crossing direction has a huge impact on the boll weight expression and the right choice of female parents may be used to improve yield performance in cotton hybrids.

The prevalence of non-additive gene action and observable reciprocal interactions indicates that hybrid breeding and exploitation of heterosis is more successful than mere additive selection to enhance boll weight and productivity in upland cotton. The same results existed in previous diallel experiments on traits related to yield in cotton (18,44).

Lint percentage

The ANOVA showed that there were significant genotypic differences ($P < 0.05$) between the four parents and the twelve F1 crosses in lint percentage, which indicated that there is a lot of genetic variation in the experimental material. This proves that the percentage of lint is a genetic characteristic and can be genetically enhanced by breeding. The diallel combining ability analysis (Table 1) resulted in significant mean squares of GCA, SCA and RE, which show that the inheritance of this trait involves both additive and non-additive actions of genes.

Variance component analysis (Table 1) indicated that SCA variance (1.04019) surpassed GCA variance (-0.32548) whereas RE (0.45298) fell short of SCA variance. This shows that non-additive gene action, especially dominance effects have been predominant in the control of the lint percentage. Thus, breeding heterosis and hybrid development are likely to be more efficient measures to enhance this trait. This has been observed in previous diallel studies in cotton (45,46).

The GCA effects (Figure 1) indicated that Super Gold (0.244) and RH-647 (0.079) had positive values implying

that they had favorable additive alleles to enhance lint percentage. AGC-2 (-0.192) and MNH-998 (-0.132) had a negative GCA effect, which implies that they are additively less influential as genetic factors. The excellent performance of Super Gold and RH-647 indicates that these genotypes can be successfully applied as general combiners in lint percentage improvement programs (45,47).

There was a significant variation of SCA effects across crosses. The positive SCA effects were highest in AGC-2 × RH-647 (0.749), MNH-998 × RH-647 (0.735) and AGC-2 × Super Gold (0.720) which showed strong non-additive gene interactions. On the other hand, MNH-998 × Super Gold (-0.578) and RH-647 × Super Gold (-0.569) exhibited negative SCA effects (Figure 2), which indicates the poor performance of this trait as a hybrid. The results show that there are certain cross combinations that can be adopted in the breeding of heterosis to increase the percentage of lint and total fiber yield. The same results have been observed in cotton genetic studies (29,48).

There was also considerable variation in the RE across crosses, suggesting that there was a maternal or cytoplasmic inheritance. Super Gold × MNH-998 (1.030) had the highest positive reciprocal effect, but the negative RE were observed in Super Gold × AGC-2 (-0.875) and RH-647 × AGC-2 (-0.730) (Figure 3). Such findings indicate that the crossing direction is a significant factor in the expression of lint percent and that great care should be taken to select female parents to enhance the performance of hybrids. Major maternal effects have been observed in breeding cotton (26,37,49). This is a dominant type of gene action with

considerable degree of RE, which implies that dominance and epistatic interactions play a significant role in the inheritance of lint percentage. Hence, mixed breeding and harnessing of heterosis is more efficient than plainly chosen methods to enhance lint percentage and other associated yield characteristics in upland cotton.

Yield of the cotton seed

ANOVA of the 4 × 4 diallel experiment showed that there were highly significant differences among the four parents and the twelve F1 crosses meaning that the seed cotton yield is highly variable. This supports the fact that yield is a very dynamic and a choice able character in the current genetic material. This combining ability analysis also revealed extremely significant GCA, SCA and RE that suggest that additive and non-additive action of genes are both involved in the inheritance of this trait.

Variance component analysis (Table 1) showed that the SCA variance (464.056) was significantly greater than GCA variance (-116.147), which shows that the non-additive component of gene action, especially dominance effects, played a greater role in determining seed cotton yield. This implies that hybrid vigor contributes significantly to the expression of yield in the genotypes in this study. SCA variance was smaller than reciprocal variance (270.486), which was smaller than additive variance, which means that maternal or cytoplasmic effects had an impact on yield performance. These results indicate that heterosis breeding is a good approach to enhancing seed cotton yield and productivity, which is in line with other diallel investigations in upland cotton (50,51).

Table 1. Summary of Combining Ability Analysis, Variance Components and Predominant Gene Action for Yield and Yield-Related Traits in Upland Cotton (*Gossypium hirsutum* L.)

Trait	MS (GCA)	MS (SCA)	F (GCA)	F (SCA)	σ^2_{GCA}	σ^2_{SCA}	σ^2_A	σ^2_D	σ^2_A/σ^2_D	Predominant Gene Action
Plant height	197.58	95.872	303.94**	147.48**	27.259	58.598	27.259	58.598	0.47	Non-additive
Monopodial Branches	6.481	0.185	1.13NS	3.23**	-1.382	7.863	-2.764	7.863	-	Non-additive
Sympodial Branches	11.917	4.944	37.36**	315.50**	0.916	2.846	1.832	2.846	0.35	Non-additive
Bolls per Plant	3.483	27.524	8.35**	69.96**	-2.744	16.681	-5.489	16.681	0.64	Non-additive
Boll Weight	3.757	0.169	4.96**	22.30**	-1.487	9.933	-2.975	9.933	-	Non-additive
Lint Percentage	0.324	1.756	4.92**	26.66**	0.163	1.040	0.325	1.040	0.33	Non-additive
Seed Cotton Yield	232.91	755.50	165.09**	535.53**	-58.1	464.06	-116.15	464.057	0.30	Non-additive
									0.31	Non-additive
									0.25	

MS = Mean Square; GCA = General Combining Ability; SCA = Specific Combining Ability; σ^2_A = Additive Variance; σ^2_D = Dominance Variance; NS = Non-significant; ** = Significant at $P \leq 0.01$. Predominant gene action was determined based on the relative magnitude of additive and dominance variance components.

Table 2. Standard Error for General Combining Ability (GCA), Specific Combining Ability (SCA) and Reciprocal Effects (RE) for Agronomic Traits in Upland Cotton (*Gossypium hirsutum* L.)

	Plant height	Monopodial Branches	Sympodial Branches	Bolls per Plant	Boll Weight	Lint Percentage	Seed Cotton Yield
SE (GCA)	0.2466	0.0734	0.1729	0.1978	0.0267	0.0786	0.1031
SE (SCA)	0.4507	0.1339	0.3157	0.3611	0.0487	0.1434	0.1882
SE (RE)	0.5700	0.1694	0.3994	0.4568	0.0616	0.1815	0.2382

SE = Standard error

Table 1 (GCA effects) revealed that the AGC-2 (4.292) and MNH-998 (3.410) had positive values, which means that they have good additive alleles and can be used as good general combine to increase the yield. The opposite is true of RH-647 (-0.135) and Super Gold (-7.567), which exhibited negative GCA effects indicating reduced additive genetic contribution to yield traits.

Effects of SCA differed across crosses. The best positive SCA interactions were found in MNH-998 x RH-647 (21.526), AGC-2 x MNH-998 (12.851) and AGC-2 x RH-647 (8.332), indicating high non-additive interactions between genes and excellent hybrid performance. On the other hand, relatively low or negative SCA effects were observed in Super Gold x AGC-2 (-3.947) and MNH-998 x Super Gold (0.746), among others (Figure 2). These findings show that there are certain crosses that can be utilized well to achieve heterosis breeding to increase seed cotton yield.

RE was also very cross-breed different, thus suggesting the impact of maternal or cytoplasmic inheritance. The highest positive RE were recorded in MNH-998 x AGC-2 (22.592) and RH-647 x AGC-2 (20.802), whereas Super Gold x RH-647 (-6.598) showed a negative effect (Figure 3). These results indicate that the orientation of crossing has a significant effect on the yield and that selection of female parents should be careful in order to obtain maximum hybrid performance. The same effect of maternal inheritance on yield traits in cotton has been previously reported (34,51,52). The prevalence of the non-additive gene action and the strong RE implies that dominance and maternal effects have a significant role in the inheritance of seed cotton yield. Thus, compared to the simple selection techniques, the hybrid breeding and exploitation of heterosis are more efficient in enhancing yield in upland cotton.

Conclusion

The current research investigated the genetic architecture of the breeding system of the upland cotton based on the 4 x 4 diallel mating design which showed that there was great genetic variation across the parental lines and their F1 hybrids in all the investigated breeding traits, including plant height, monopodial and sym pod branches, bolls per

plant, boll weight, lint percentage and seed cotton yield. This affirms that there is a lot of exploitable genetic variation to improve cotton. The integration of ability analysis showed that there were additive (GCA) and non-additive (SCA) genes effects in the trait inheritance process, but SCA effects were usually stronger, especially with yield-related traits, which pointed to the fact that non-additive gene action dominated and the effect of heterosis in cotton breeding was important. The importance of RE also indicated the impact of maternal or cytoplasmic inheritance. Parents MNH-998, AGC-2 and RH-647 had greater effects on GCA, which makes them potential breeding program candidates, whereas crosses, like AGC-2 x RH-647, AGC-2 x MNH-998 and MNH-998 x RH-647, had better effects on SCA and can therefore be used to The results indicate that hybrid breeding and exploitation of heterosis outperforms selection that is based on additive effects alone in enhancing yield and its associated traits in cotton and this can offer valuable information in the use of better parents and cross combinations in future cotton improvement programs.

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