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Original Research Article

DECIPHERING THE GENETIC CODES: GENE ACTION AND COMBINING ABILITY IN GOSSYPIUM HIRSUTUM L. AND THEIR IMPACT ON PLANT TRAITS

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Abstract: *Cotton, scientifically known as Gossypium, is a crucial agricultural and economic commodity, widely used for its soft, durable fibers in the textile industry. This study conducted a comprehensive 5x5 full diallel analysis on five cotton genotypes: FH-114, FH-207, CRS-456, MNH-992, and KAHKASHAN. The primary focus was to investigate the combining ability effects and gene action contributions for various plant traits. Key traits examined included plant height, the number of direct and indirect fruit-bearing branches, the first fruiting branch's position, yield, and related characteristics. Data gathered for these traits underwent thorough statistical analysis. The F-values derived from this statistical evaluation revealed significant variation across all examined parameters in the F1 generations. Results observed from the complete diallel mating design indicate that the collected data for all parameters were enough for Griffing's approach (1956). Combining ability analysis for all parameters presented the maximum differences for GCA and SCA effects. Less contribution of the GCA variance determines that the traits such as the height of plant, indirect fruit bearing branches, weight of individual boll, seed cotton yield of the individual plant, lint index seed index, percentage of lint, number of bolls on a single plant and first fruiting branch is governed by non-additive type of gene action because the value of GCA/SCA ratio is less than one which indicates that hybrids are more vigorous for all parameter under study. Still, the greater contribution of GCA variance indicates that the traits such as direct fruit bearing branches are largely controlled by dominant gene action because the value of GCA/SCA is greater than one.*

Keywords: Cotton, Gene Action, Combining Ability

Introduction

Many nations throughout the world cultivate cotton. It serves as both a food and a fibre crop. It also offers cotton seed cake, utilized as animal feed fiber. Cotton helps a country's industrial, economic, and agricultural development. It is a significant fiber and oil seed crop in many tropical regions worldwide. It is a perennial plant with an erratic growth pattern. Cotton seeds are the primary source of natural fiber and are also used to obtain edible oil. Low-quality oil is utilized while creating lubricants and soap. For cattle feed, the remaining seed cake is a valuable source of protein. The importance of the cotton crop is growing in the economies of many nations, including Pakistan. The genetic makeup of cotton has been improved via significant work by researchers and cotton breeders. Due to its importance on a global scale, this crop is primarily farmed for its fibre value and is known as "white gold." (Shakeel et al., 2012). In Pakistan, cotton farming provides a living for about 1.5 million people (Hussain et al., 2010). Pakistan's cotton seed production is lower than that of certain other nations. The complex quality of cotton output results from the expression of several component qualities. It is a quantitative trait governed by numerous genes and is difficult to alter. Therefore, it should be important that genetic variety exists within species to create new genotypes. Executing a breeding program implies a breeding scheme (Azhar et al., 2005; Khalid et al., 2022; Khalid and Amjad, 2018, 2019). Various breeding strategies are utilized to get the required traits, such as polyploidization, hybridization selection of better parent, and introduction of foreign material with more diversity (Shaukat l et al,. 2013). Selection is the best strategy for evaluating parents with robust variation, which leads to achieving a breeding program. Diallel analysis is being used for the evaluation of combining ability and hybrid vigor. A tool like combining ability is also best for selecting better-performing parents to create hybrid vigor (Usama et al., 2022; Umar et al., 2022; Hussain et al., 2023; Abbas et al., 2023ab;). It is also utilized to evaluate best-performing crosses from the parental stock. Combining ability also indicates that when the value of GCA is greater than the character utilized for when a diverse parent was crossed, the F1 produced if this F1 performed better than the best parent, called heterosis (Roupakias et al., 1998).

Methodology

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The current study was performed to analyze how the different quantitative parameters of Gossypium hirsutum L are governed by the pattern of combining ability and by the action of genes at the experimental designing area of research at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the years 2019-2020. Five Cotton varieties were nominated as FH-114, FH207. MNH-992, CRS-456, and KAHKASHAN were grown in earthen pots placed 30 × 30 cm apart in a greenhouse in October 2016. Possible controlled environmental conditions (Temperature, light) were provided for the plants' better germination and vegetative growth. At the time of flowering, all these five Parental Lines differing in their characters were crossed in all possible combinations by following the diallel mating design to develop plant material. All the necessary precautionary measures were applied during the cross-combination to control the foreign contamination of required genetic material.

The resulting F0 seeds of twenty hybrids and five parent genotypes were collected and then grown under RCBD design with 3 repeats in the normal field condition. All three repeats consisted of 20 F1 hybrids and five parental lines. Each entry is grown with 10 plants on a single row. Plant to Plant and Row to Row Distances were maintained at 30cm and 75cm, respectively. All plant protection measures and required agronomic practices were applied at the time of need for healthy crop growth from sowing to harvesting. When the crop matured, data from each row randomly of 5 plants for the following traits was calculated: Plant height, sympodial branches per plant, no. of bolls on each plant, Boll weight, Seed Index, Lint index, Seed cotton yield, and ginning out per turn percentage. Recorded data from various plant characters related to yield and fiber quality, which were studied, was proceeded for further analysis of variance by applying the technique (Steel et al., 1997) to find out the significant genetic variation between the cotton lines utilized in the current study for various parameters. To check the SCA and GCA effects of parents and their crosses, the data was subjected to combining ability analysis of full diallel analysis using the Griffing's approach model II, method I (Griffing's 1956).

Results

From the analysis of variance for plant height, a significant variation exists between the cotton genotype for various combined ability effects such as SAC, GCA, and RE. Table 2 represented that in the 5×5 full diallel analysis, the genotype FH-114 (2.2073) and FH-207 (1.6097) showed the greater value of GCA for plant height while the genotype MNH- 992 (-2.0183) and CRS-456 (-1.4667) showed the minimum value of GCA for plant height. The table 2 also indicates that when the value of SCA is greater than the plant height is governed by the dominant type of gene action, which is valuable for selecting a better-yielding genotype (Kiani et al., 2007). Table 1 represents that in the cross of CRS-456×MNH-992 the higher value for SCA was noted as (3.4820) with significant variation for plant height, while in other crosses of FH-207×MNH-992 and FH-114×CRS-456 with respective values of minimum SCA are (-5.5376) and (-5.5103). The cross combination with a greater value of SCA for plant height can be utilized for further selection of good-yielding cultivars and may also be involved in heterosis breeding (Yong-Jun et al., 2006).In reverse cross combination of CRS-456×FH-207 and MNH-992×CRS-456 greater values were noted for RE as (10.2650) and (6.2550) respectively for plant height while the cross of Kahkashan×FH-207 presented minimum value for RE for height of the plant. All other crosses were found to have no variation in plant height. The cross combination with more value of RE showing the maternal effects can be utilized for the yield enhancement of cotton (Azhar et al. 2005). From table 1 we can analyze that the higher value of SCA (19.2936) and dominant variance for crosses (19.2936) is shown while the lower value of GCA (2.8067) and additive variance (5.6134) is shown. From the table 1, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for yield improvement in cotton. Because of less value of reciprocal variance than SCA variance were (15.06) and (19.2936) respectively, indicating that there is an anon-additive type of gene action. The exact results were determined by Kiani et al. (2007) and Rauf et al. (2005)..

Table 1: Combining ability of 5 x 5 diallel Analysis of plant height in upland cotton (Gossypium hirsutum L).

SOV	D.F	SS	MS	F. Value	Variance(δ2)	Genetic effects
GCA	4	137.83	34.459	5.3910**	2.8067	δ2A=5.6134
SCA	10	256.85	25.685	4.0184**	19.2936	δ2D=19.2936
RCA	10	365.25	36.525	5.7143**	15.06	
Error	24	306.81	6.3920			

* = Significant **= Highly Significant. N.S = Non-Significant

Table 2: Genetic effects of parents and crosses for plant height in upland cotton (Gossypium hirsutum L).

Parents	GCA
FH-114	2.2073 **
FH-207	1.6097 *
CRS-456	-1.4667 *
MNH-992	-2.0183 **
Kahkashan	-0.3320 ns
S.E. (gi - gj)	0.7151

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Direct Crosses	SCA
FH-114×FH-207	2.6367 ns
FH-114×CRS-456	-5.5103 **
FH-114×MNH-992	0.7414 ns
FH-114×Kahkashan	-1.7983 ns
FH-207×CRS-456	2.2840 ns
FH-207×MNH-992	-5.5376 **
FH-207×Kahkashan	-1.5223 ns
CRS-456×MNH-992	3.4820 *
CRS-456×Kahkashan	2.9457 ns
MNH-992×Kahkashan	2.9290 ns
S.E. (sij – sik)	2.0226
Indirect crosses	RCA
FH-207×FH-114	2.0217 ns
CRS-456×FH-114	-2.1317 ns
CRS-456×FH-207	10.2650 **
MNH-992×FH-114	1.1617 ns
MNH-992×FH-207	-0.5050 ns
MNH-992×CRS-456	6.2550 **
Kahkashan×FH-114	0.8167 ns
Kahkashan×FH-207	-4.7450 *
Kahkashan×CRS-456	0.3050 ns
Kahkashan×MNH-992	2.1500 ns
S.E. (rij – rkl)	1.4742

From the analysis of variance, it was observed that for sympodial branches, the 5×5 full diallel analysis represents the significant variation for GCA and RCA value while non-significant for SCA for five cotton genotypes. Table 3 presented the higher value of GCA from the 5×5 full diallel analysis for genotypes Kahkashan (0.8999) and MNH-992 (0.4052) gradually, but on the other side, the genotypes FH-114 (-0.6695) and FH-207 (-0.7191) respectively lower value for the GCA for the number of Sympodial branches. So, the genotypes with higher values of GCA for sympodial branches are governed by the additive type of gene action and can be further utilized to improve high-yielding genotypes (Azhar et al. 2005). Recorded values for Sympodial branches in Table 3 for crosses CRS-456×MNH-992, MNH-992×Kahkashan and CRS- 456×Kahkashan are 0.3791, 0.2678, and 0.2411, respectively have the greater value of SCA while the crosses of FH- 207×MNH-992, FH-114×CRS-456 and FH-114×FH-207 as -0.8832, -0.5479 and -0.4202 respectively have the lowest value for the SCA. A greater value of SCA indicates that the non-additive type of action governs the trait, but most of the crosses have very low values of SCA and are observed as poor specific combiners Saravanan et al. (2010). In many of the reverse crosses, the value for the RE noted in table 3 is higher for sympodial branches in crosses of MNH-992×FH-207 and MNH-992×CRS-456 as 2.3033 and 1.4683 respectively. Still, less for the crosses of MNH-992×FH-114 and CRS-456×FH-207 noted as -2.1283 and -1.3000 respectively. Few of them show a smaller value of RE and are evaluated as poor combiners. Table 4 shows that the higher value of SCA (-0.1198) and dominant variance for crosses (-0.1198) is shown while the lower value of GCA 0.4033 and additive variance of 0.8066 is shown. From Table 4, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for yield improvement through sympodial branches in cotton. Because of the lower value of reciprocal variance than SCA, the variance was 1.3232 and (- 0.1198, respectively), indicating an additive type of gene action. Significant variation in Sympodial branches on a single plant was because of the general combining ability observed by Memon et al. (2014) and the reciprocal combining ability by Islam (2014). Patel et al. (2014) and Memon et al. (2016) observed a non-additive type of gene effect.

Table 3: Various genetic effects of parents and crosses for number of sympodial branches in upland cotton (Gossypium hirsutum L).

Parents	**GCA**
FH-114	-0.6695 *
FH-207	-0.7191 **
CRS-456	0.0835 ns

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MNH-992	0.4052 ns
Kahkashan	0.8999 **
S.E. (gi - gj)	0.2580
Direct Crosses	SCA
FH-114×FH-207	-0.4202 ns
FH-114×CRS-456	-0.5479 ns
FH-114×MNH-992	0.0788 ns
FH-114×Kahkashan	-0.0675 ns
FH-207×CRS-456	-0.3332 ns
FH-207×MNH-992	-0.8832 ns
FH-207×Kahkashan	0.0271 ns
CRS-456×MNH-992	0.3791 ns
CRS-456×Kahkashan	0.2411 ns
MNH-992×Kahkashan	0.2678 ns
S.E. (sij – sik)	0.7299
Indirect crosses	RCA
FH-207×FH-114	1.1500 ns
CRS-456×FH-114	0.9850 ns
CRS-456×FH-207	-1.3000 *
MNH-992×FH-114	-2.1283 **
MNH-992×FH-207	2.3033 **
MNH-992×CRS-456	1.4683 *
Kahkashan×FH-114	0.0900 ns
Kahkashan×FH-207	-0.3900 ns
Kahkashan×CRS-456	0.2600 ns
Kahkashan×MNH-992	-1.0917 ns
S.E. (rij – rkl)	0.6451

Table 4: Combining ability of 5 x 5 diallel Analysis of number of sympodial branches of Gossypium hirsutum L.

SOV	**D.F**	**SS**	**MS**	**F Value)**	**Variance(δ2)**	**Genetic effects**
GCA	4	19.4602	4.8650	5.8451**	0.4033	δ2A=0.8066
SCA	10	7.1253	0.7125	0.8561n.s	-0.1198	δ2D=0.1198
RCA	10	34.7868	3.4787	4.1795**	1.3232	
Error	24		0.8323			

* = Significant **= Highly Significant N.S = non-significant

The analysis of variance for the Number of Bolls on individual plants illustrated that a significant variation exists between the genotype of cotton for various combining ability effects such as SAC, GCA, and RE. Table 5 represents that in the 5×5 full diallel analysis, the genotype KAHKASHAN (1.9750) showed the greater value of GCA for the Number of Bolls on the individual plant while the genotype FH-207 (-2.0033) and showed the minimum value of GCA for Number of Bolls on the individual plant. The table also indicates that when the value of SCA is greater than the trait, the number of bolls is governed by the dominant type of gene action, which valuable for the selection of a better is the genotype for a greater number of bolls (Kiani et al., 2007). Table 5 represents that the cross of CRS-456×Kahkashan and FH-114×FH-207 shows the higher value for SCA noted as (5.5967) and (2.3580), respectively, with significant variation for the Number of Bolls on the individual plants while in other crosses of FH-114×MNH-992and FH-114×Kahkashan with respective values of minimum SCA are (-4.1150) and (-2.2487). The cross combination with a greater value of SCA for the number of bolls can be utilized for further selection of good-yielding cultivars. It may also involved in heterosis breeding (Rauf et al., 2005).In reverse cross combination of FH-207×FH-114, MNH- 992×FH-114, CRS-456×FH-114, Kahkashan×MNH-992, MNH-992×FH-207, and Kahkashan×CRS-456 the greater values were noted for RE as 5.6417, 4.6833, 4.5817,4.4650, 3.3933 and 2.9900respectively for boll numbers while the cross of Kahkashan×FH-114 (-2.2600) presented minimum value for RE for the number of boll on the individual plant. All other crosses were found to have no variation for boll numbers. The cross combination with more value of RE showing the maternal effects can be utilized for the yield enhancement of cotton (Azhar et al. 2005). From table 6, we can see that the higher value of SCA (19.3310) and dominant variance for crosses (19.3310) is shown, while the lower value of GCA (1.8735) and additive variance (3.747) is shown. From Table 6, the greater value for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for yield improvement in cotton. Because of less value of reciprocal variance than SCA variance were 11.3859 and 19.3310, respectively, indicating that there is non-additive type of gene action. The exact results were determined by Murtaza et al. (2005) and Singh et al. (2010).

Table 5: Various genetic effects of parents and crosses for number of bolls per plant upland cotton (Gossypium hirsutum L.).

Parents	**GCA**
FH-114	-0.5163 ns
FH-207	-2.0033 **
CRS-456	0.1683 ns
MNH-992	0.3763 ns
Kahkashan	1.9750 **
S.E. (gi - gj)	0.4140
Direct Crosses	SCA
FH-114×FH-207	2.3580 **
FH-114×CRS-456	-0.6903 ns
FH-114×MNH-992	-4.1150 **
FH-114×Kahkashan	-2.2487 *
FH-207×CRS-456	-1.6583 ns
FH-207×MNH-992	-1.5347 ns
FH-207×Kahkashan	-1.3683 ns
CRS-456×MNH-992	-1.3080 ns
CRS-456×Kahkashan	5.5967 **
MNH-992×Kahkashan	0.5637 ns
S.E. (sij – sik)	1.1709 0.8534
Indirect crosses	RCA
FH-207×FH-114	5.6417 **
CRS-456×FH-114	4.5817 **
CRS-456×FH-207	0.3117 ns
MNH-992×FH-114	4.6833 **
MNH-992×FH-207	3.3933 **
MNH-992×CRS-456	-1.4550 ns
Kahkashan×FH-114	-2.2600 *
Kahkashan×FH-207	-1.4500 ns
Kahkashan×CRS-456	2.9900 **
Kahkashan×MNH-992	4.4650 **
S.E. (rij – rkl)	1.0349

Table 6: Combining ability of 5 x 5 diallel Analysis of number of bolls per plant in upland cotton Gossypium hirsutum L.

SOV	**D.F**	**SS**	**MS**	**F Value)**	**Variance(δ2)**	**Genetic effects**
GCA	4	83.5080	20.8770	9.7464**	1.8735	δ2A=3.747
SCA	10	214.7302	21.4730	10.0247**	19.3310	δ2D=19.3310
RCA	10	249.1380	24.9138	11.6310**	11.3859	
Error	24		2.1420			

* = Significant **= Highly Significant N.S = Non Significant

From the analysis of variance for seed cotton yield of individual plants, a significant variation exists between the cotton genotype for various combined ability effects such as SAC, GCA, and RE. Table 7 shows that in the 5×5 full

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diallel analysis, the genotype CRS-456 (1.3180) showed the greater value of GCA for seed cotton yield of the individual plant while the genotype MNH-992 (-1.6320) and FH-114 (-0.8087) showed the minimum value of GCA for seed cotton yield of the individual plant. Table also states that when the value of SCA is greater than the seed cotton yield, it is governed by the dominant type of gene action, which is valuable for selecting a high-yielding genotype (Chincanc et al. 2007). Table 7 represents that in the cross of CRS-456×MNH-992, FH-207×Kahkashan, and FH-114×Kahkashan the higher value for SCA noted as 5.0020, 3.2653 and 1.7753 with significant variation for seed cotton yield while in other crosses of FH- 207×CRS-456, FH-114×MNH-992 and FH-114×FH-207with respective values of minimum SCA are-4.1313, -3.6047 and - 1.9880. The cross combination with a greater value of SCA for individual seed cotton yield can be utilized for further selection of good-yielding cultivars. It may also involved in heterosis breeding (Yong-Jun et al., 2006).In reverse cross combination of MNH-992×CRS-456, MNH-992×FH-207, MNH-992×FH-114 and Kahkashan×CRS-456greater values were noted for RE as 4.3500, 3.2333,3.0333and 2.4500 respectively for seed cotton yield while the cross ofCRS-456×FH-114 and FH-207×FH-114 as-5.1000 and -2.7833 presented minimum value for RE for cotton yield. All other crosses were found to have no variation in cotton yield. The cross combination with more value of RE showing the maternal effects can be utilized for the yield enhancement of cotton (Azhar et al. 2005). From Table 8, we can see that the higher value of SCA (19.5108) and dominant variance for crosses (19.5108) is shown, while the lower value of GCA (1.2319) and additive variance (2.4638) is shown. From Table 8, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for yield improvement in cotton. Because of less value of reciprocal variance than SCA variance were 7.4239 and 19.5108, respectively, which indicates that there is non-additive type of gene action. Exact results were determined by Kiani et al. (2007) and Anisa et al. (2005).

Table 7: Various genetic effects of parents and crosses for yield of seed cotton of Gossypium hirsutum L

Parents	GCA
FH-114	-0.8087 *
FH-207	0.5347 ns
CRS-456	1.3180 **
MNH-992	-1.6320 **
Kahkashan	0.5880 ns
S.E. (gi - gj)	0.3893
Direct Crosses	SCA
FH-114×FH-207	-1.9880 *
FH-114×CRS-456	1.5787 ns
FH-114×MNH-992	-3.6047 **
FH-114×Kahkashan	1.7753 *
FH-207×CRS-456	-4.1313 **
FH-207×MNH-992	0.5687 ns
FH-207×Kahkashan	3.2653 **
CRS-456×MNH-992	5.0020 **
CRS-456×Kahkashan	-0.0680 ns
MNH-992×Kahkashan	1.0153 ns
S.E. (sij – sik)	1.1011 0.8025
Indirect crosses	RCA
FH-207×FH-114	-2.7833 **
CRS-456×FH-114	-5.1000 **
CRS-456×FH-207	0.6667 ns
MNH-992×FH-114	3.0333 **
MNH-992×FH-207	3.2333 **
MNH-992×CRS-456	4.3500 **
Kahkashan×FH-114	-1.9333 ns
Kahkashan×FH-207	0.1333 ns
Kahkashan×CRS-456	2.4500 *
Kahkashan×MNH-992	1.0833 ns
S.E. (rij – rkl)	0.9732

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Table 8: Combining ability of 5 x 5 diallel Analysis of seed cotton in American cotton (Gossypium hirsutum L.).

SOV	D.F	SS	MS	F Value)	Variance(δ2)	Genetic effects
GCA	4	56.8538	14.2134	7.5032**	1.2319	δ2A=2.4638
SCA	10	214.0512	21.4051	11.2996**	19.5108	δ2D=19.5108
RCA	10	167.4222	16.7422	8.8381**	7.4239	
Error	24		1.8943			

* = Significant **= Highly Significant N.S = Non Significant

From the analysis of variance for individual boll weight, a significant variation exists between the cotton genotype for various combined ability effects such as SAC, GCA, and RE. Table 9 represented that in the 5×5 full diallel analysis, the genotype FH-114 (0.2058) showed the greater value of GCA for individual boll weight of individual plants while the genotype FH-207 (-0.1145) showed the minimum value of GCA for individual boll weight. Table also indicates that when the value of SCA is greater than the boll weight, it is governed by the dominant type of gene action, which is valuable for selecting a better-yielding genotype with more boll weight (Kiani et al., 2007). Table 9 represents that in the cross of FH-114×FH-207the higher value for SCA was noted as 0.2469 with significant variation for individual boll weight while in other crosses of FH-207×MNH-992with respective values of minimum SCA are-0.3208. The cross combination with a greater value of SCA for boll weight can be utilized for further selection of good-yielding cultivars and may also involved in heterosis breeding (Yong-Jun et al., 2006). In the reverse cross, a combination ofKahkashan×FH-114and MNH-992×FH-207 greater values are noted for RE as 0.3933 and 0.3150, respectively, for individual boll weight while all other crosses were found to have no variation for boll weight. The cross combination with more value of RE showing the maternal effects can be utilized for the yield enhancement of cotton (Azhar et al. 2005). From Table 10 it has been found that the higher value of SCA (0.0317) and dominant variance for crosses (0.0317) is shown while the low value of GCA (0.0118) and additive variance (0.0236) is shown. From Table 10, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for yield improvement in cotton. Because of less value of reciprocal variance than SCA variance was 0.0155 and 0.0317respectively, which indicates that there is non-additive type of gene action. Exact results were determined by Ahmad et al. (2000).

Table 9: Various genetic effects of parents and crosses for Boll weight in upland cotton (Gossypium hirsutum L.).

Parents	GCA
FH-114	0.2058 **
FH-207	-0.1145 *
CRS-456	0.0188 ns
MNH-992	-0.0782 ns
Kahkashan	-0.0319 ns
S.E. (gi - gj)	0.0558
Direct Crosses	SCA
FH-114×FH-207	0.2469 *
FH-114×CRS-456	-0.2048 ns
FH-114×MNH-992	0.0539 ns
FH-114×Kahkashan	0.1709 ns
FH-207×CRS-456	-0.0745 ns
FH-207×MNH-992	-0.3208 **
FH-207×Kahkashan	0.0212 ns
CRS-456×MNH-992	0.1909 ns
CRS-456×Kahkashan	-0.0555 ns
MNH-992×Kahkashan	-0.0618 ns
S.E. (sij – sik)	0.1580 0.1151
Indirect crosses	RCA
FH-207×FH-114	-0.0600 ns
CRS-456×FH-114	0.0717 ns
CRS-456×FH-207	-0.0267 ns
MNH-992×FH-114	0.0467 ns

[Citation: Khan, Z., Gul, N., Mehboob, A., Amjad, S., Munir, T., Hammad, M., sardar, H., Akbar, F., Saqib, M., Mahmood, K. (2023). Deciphering the genetic codes: gene action and combining ability in *Gossypium Hirsutum* l. And their impact on plant traits. *Biol. Clin. Sci. Res. J.,* **2023***: 569*. doi: https://doi.org/10.54112/bcsrj.v2023i1.569]

MNH-992×FH-207	0.3150 *
MNH-992×CRS-456	-0.0150 ns
Kahkashan×FH-114	0.3933 **
Kahkashan×FH-207	-0.0167 ns
Kahkashan×CRS-456	0.2500 ns
Kahkashan×MNH-992	0.1467 ns
S.E. (rij – rkl)	0.1396

Table 10: Combining ability of 5 x 5 diallel Analysis of boll weight in upland cotton (Gossypium hirsutum L.).

SOV	D.F	SS	MS	F Value)	Variance(δ2)	Genetic effects
GCA	4	0.6296	0. 7415	4.0374*	0.0118	δ2A=0.0236
SCA	10	0.7071	0.0707	1.8139ns	0.0317	δ2D=0.0317
RCA	10	0.7001	0.0700	1.7961ns	0.0155	
Error	24		0.0390			

* = Significant **= Highly Significant N.S = Non Significan.

From the analysis of variance for seed cotton yield of individual plants significant variation exists between the cotton genotype for various combining ability effects such as SAC, GCA, and RE. Table 11 represented that in the 5×5 full diallel analysis, the genotype FH-207 (0.1329) showed the greater value of GCA for lint index while all other genotypes had no variation for GCA of lint index. Table also shows that when the value of SCA is greater than the lint index is governed by the dominant type of gene action, which is valuable for selecting better-yielding genotype with a good lint index (Imran et al., 2012). Table 11 represents that in the cross of FH-114×FH-207 and CRS-456×Kahkashan the higher value for SCA was noted as 0.3601 and 0.2047with significant variation for lint index while in other crosses MNH-992×Kahkashan with respective values of minimum SCA are-0.2139. The cross combination with a greater value of SCA for lint index can be utilized for further selection of good-yielding cultivars and may also involved in heterosis breeding (Kaliyaperumal et al., 2010). In reverse cross combination of Kahkashan×FH-207, Kahkashan×MNH-992and CRS-456×FH-114 greater values are noted for RE as 0.3017,0.4750 and 0.2717 respectively for lint index while the cross of Kahkashan×CRS-456and FH-207×FH-114as-0.4883 and -0.2650 presented minimum value for RE for lint index. All other crosses were found to have no variation for lint index. The cross combination with more value of RE showing the maternal effects can be utilized for the better genotypes for lint index (Mukhtar et al. 2000). table 12 indicates that the higher value of SCA (0.0498) and dominant variance for crosses (0.0498) is shown while the lower value of GCA (0.0040) and additive variance is (0.0080) is shown. From Table 12, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding to improve lint quality in cotton. Because of less value of reciprocal variance than SCA variance were 0.0080 and 0.0498, respectively, which indicates that there is non-additive type of gene action. The exact like results were determined by Kiani et al. (2007), Azhar et al. (2005), and Rauf et al. (2005).

Table 11: Various genetic effects of parents and crosses for lint index in upland cotton (Gossypium hirsutum L.).

Parents	GCA
FH-114	-0.0224 ns
FH-207	0.1329 **
CRS-456	0.0049 ns
MNH-992	-0.0631 ns
Kahkashan	-0.0524 ns
S.E. (gi - gj)	0.0424
Direct Crosses	SCA
FH-114×FH-207	0.3601 **
FH-114×CRS-456	-0.0019 ns
FH-114×MNH-992	-0.0673 ns
FH-114×Kahkashan	-0.1579 ns
FH-207×CRS-456	-0.1606 ns
FH-207×MNH-992	0.0507 ns
FH-207×Kahkashan	-0.0866 ns
CRS-456×MNH-992	0.0221 ns
CRS-456×Kahkashan	0.2047 *

[Citation: Khan, Z., Gul, N., Mehboob, A., Amjad, S., Munir, T., Hammad, M., sardar, H., Akbar, F., Saqib, M., Mahmood, K. (2023). Deciphering the genetic codes: gene action and combining ability in *Gossypium Hirsutum* l. And their impact on plant traits. *Biol. Clin. Sci. Res. J.,* **2023***: 569*. doi: https://doi.org/10.54112/bcsrj.v2023i1.569]

MNH-992×Kahkashan	-0.2139 *
S.E. (sij – sik)	0.1199 0.0874
Indirect crosses	RCA
FH-207×FH-114	-0.2650 *
CRS-456×FH-114	0.2717 *
CRS-456×FH-207	0.0017 ns
MNH-992×FH-114	0.0783 ns
MNH-992×FH-207	0.0717 ns
MNH-992×CRS-456	0.1350 ns
Kahkashan×FH-114	-0.0950 ns
Kahkashan×CRS-456	-0.4883 **
Kahkashan×MNH-992	0.4750 **
S.E. (rij – rkl)	0.1059
Kahkashan×FH-207	0.3017 **

Table 12: Combining ability of 5 x 5 diallel Analysis of lint index in upland cotton (Gossypium hirsutum L.).

SOV	D.F	SS	MS	F Value)	Variance(δ2)	Genetic effects
GCA	4	0.2491	0.0623	2.7744*	0.0040	δ2A=0.0080
SCA	10	0.7227	0.0723	3.2197**	0.0498	δ2D=0.0498
RCA	10	1.4753	0.1475	6.5722**	0.0625	
Error	24		0.0224			

* = Significant **= Highly Significant N.S = Non Significant

From the analysis of variance for seed, a significant variation exists between the genotype of cotton for various combining ability effects such as SAC, GCA, and RE. Table 13 represented that in the 5×5 full diallel analysis, the genotype CRS-456 (0.1541) showed the greater value of GCA for seed index while all other genotypes had no variation for GCA of seed index. Table 3 also indicates that when the value of SCA is greater than the seed index, it is governed by the dominant type of gene action, which is valuable for selecting a better genotype for the seed index (Kiani et al., 2007). Table 13 represents that in the cross of CRS-456×MNH-992, FH-114×CRS-456, FH-207×Kahkashanand FH-114×FH-207the higher value for SCA noted as 0.7489, 0.6186, 0.6109 and 0.5099 with significant variation for seed index while in other crosses of FH-207×CRS-456 and MNH-992×Kahkashan with respective values of minimum SCA are-0.6504 and -0.4431. The cross combination with a greater value of SCA for seed index can be utilized for further selection of good cultivars and may also involved in heterosis breeding (Nadeem et al., 2006). In reverse cross combination of MNH-992×FH-207, Kahkashan×FH-114, Kahkashan×CRS-456, and CRS-456×FH-207greater values were noted for RE as 0.9133, 0.7733, 0.6017 and 0.3733respectively for seed index while the cross ofKahkashan×FH-207, MNH-992×FH-114and FH-207×FH-114 as -0.7117, -0.4383 and -0.3817 presented minimum value for RE for seed index. All other crosses were found to have no variation in the yield of the seed index. The cross combination with more value of RE showing the maternal effects can be utilized to the index (Mukhtar et al. 2000). table 14 indicates that the higher value of SCA (0.5650) and dominant variance for crosses (0.5650) is shown, while the low value of GCA (0.0024) and additive variance (0.0048) is shown. From Table 14, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for the seed index improvement in cotton. Because of less value of reciprocal variance than SCA variance were 0.25 and 0.5650, respectively, which indicates that there is non-additive type of gene action. Exact like that result was determined by Kiani et al. (2007), Azhar et al. (2005), and Muthu et al. (2005).

Table 13: Various genetic effects of parents and crosses for seed index in upland cotton (Gossypium hirsutum L.).

Parents	GCA
FH-114	-0.0346 ns
FH-207	0.0094 ns
CRS-456	0.1541 *
MNH-992	-0.0216 ns
Kahkashan	-0.1073 ns
S.E. (gi - gj)	0.0742
Direct Crosses	SCA

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FH-114×FH-207	0.5099 **
FH-114×CRS-456	0.6186 **
FH-114×MNH-992	0.1459 ns
FH-114×Kahkashan	-0.1701 ns
FH-207×CRS-456	-0.6504 **
FH-207×MNH-992	-0.1581 ns
FH-207×Kahkashan	0.6109 **
CRS-456×MNH-992	0.7489 **
CRS-456×Kahkashan	-0.2121 ns
MNH-992×Kahkashan	-0.4431 **
S.E. (sij – sik)	0.2098 0.1529
Indirect crosses	RCA
FH-207×FH-114	-0.3817 *
CRS-456×FH-114	-0.1817 ns
CRS-456×FH-207	0.3733 *
MNH-992×FH-114	-0.4383 *
MNH-992×FH-207	0.9133 **
MNH-992×CRS-456	-0.1367 ns
Kahkashan×FH-114	0.7733 **
Kahkashan×FH-207	-0.7117 **
Kahkashan×CRS-456	0.6017 **
Kahkashan×MNH-992	0.1517 ns
S.E. (rij – rkl)	0.1854

Table 14: Combining ability of 5 x 5 diallel Analysis of Seed index in upland cotton (Gossypium hirsutum L.).

SOV	D.F	SS	MS	F Value)	Variance(δ2)	Genetic effects
GCA	4	0.3699	0.0925	1.3448ns	0.0024	δ2A=0.0048
SCA	10	6.3372	0.6337	9.2153**	0.5650	δ2D=0.5650
RCA	10	5.7051	0.5705	8.2962**	0.25	
Error	24		0.0688			

* = Significant **= Highly Significant N.S = Non Significant

From the analysis of variance for the first fruiting branch, a significant variation exists between the cotton genotype for various combined ability effects such as SAC, GCA, and RE. The table 15 shows that in the 5×5 full diallel analysis, the genotype MNH-992 (0.3246) showed the greater value of GCA for the first fruiting branch while all other genotypes were found to have no variation for GCA of the first fruiting branch. Table also indicates that when the value of SCA is greater than the first fruiting branch, it is governed by the dominant type of gene action, which is valuable for the selection of a better genotype with an earlier first fruiting branch (Kaliyaperumal et al., 2010). Table 15 represents that in the cross of CRS-456×MNH-992and FH-207×CRS-456the higher value for SCA noted as 0.8191 and 0.7527 with significant variation for first fruiting branch yield, while in other crosses of CRS-456×Kahkashan and FH-207×MNH-992with respective values of minimum SCA are-1.8933 and -1.0476. The cross combination with the greater -ve value of SCA for first fruiting branch can be utilized for further selection of good-yielding cultivars and may also involved in heterosis breeding (Basel et al., 2011).

In reverse cross combination of Kahkashan×CRS-456greater values are noted for RE as 1.1600 for the first fruiting branch while the cross ofCRS-456×FH-207and Kahkashan×FH-114as -0.8217 and -0.8117 presented minimum value for RE for first fruiting branch. All other crosses were found to have no variation for the first fruiting branch. The cross combination with more value of RE showing the maternal effects can be utilized for the yield enhancement of cotton (Amein et al. 2013). The table 16 indicates that the higher value of SCA (1.3785) and dominant variance for crosses (1.3785) is shown, while the lower value of GCA (0.0201) and additive variance (0.0402) is shown. From Table 16, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for the earlier first fruiting branches. Because of less value of reciprocal variance than SCA variance were 0.2682 and 1.3785, respectively, which indicates that there is non-additive type of gene action. The exact results were determined by Kiani et al. (2007) and Azhar et al. (2005).

[Citation: Khan, Z., Gul, N., Mehboob, A., Amjad, S., Munir, T., Hammad, M., sardar, H., Akbar, F., Saqib, M., Mahmood, K. (2023). Deciphering the genetic codes: gene action and combining ability in *Gossypium Hirsutum* l. And their impact on plant traits. *Biol. Clin. Sci. Res. J.,* **2023***: 569*. doi: https://doi.org/10.54112/bcsrj.v2023i1.569]

Table 15: Various genetic effects of parents and crosses for first fruiting branch in upland cotton (Gossypium hirsutum L.).

Parents	**GCA**
FH-114	-0.2884 ns
FH-207	0.0543 ns
CRS-456	0.0293 ns
MNH-992	0.3246 *
Kahkashan	-0.1197 ns
S.E. (gi - gj)	0.1588
Direct Crosses	SCA
FH-114×FH-207	0.5037 ns
FH-114×CRS-456	-0.0596 ns
FH-114×MNH-992	0.4617 ns
FH-114×Kahkashan	-0.1323 ns
FH-207×CRS-456	0.7527 *
FH-207×MNH-992	-1.0476 **
FH-207×Kahkashan	0.0567 ns
CRS-456×MNH-992	0.8191 *
CRS-456×Kahkashan	-1.8933 **
MNH-992×Kahkashan	0.6097 ns
S.E. (sij – sik)	0.4491 0.3273
Indirect crosses	RCA
FH-207×FH-114	0.6700 ns
CRS-456×FH-114	-0.6650 ns
CRS-456×FH-207	-0.8217 *
MNH-992×FH-114	-0.1600 ns
MNH-992×FH-207	0.4400 ns
MNH-992×CRS-456	-0.2783 ns
Kahkashan×FH-114	-0.8117 *
Kahkashan×FH-207	-0.3900 ns
Kahkashan×CRS-456	1.1600 **
Kahkashan×MNH-992	0.4883 ns
S.E. (rij – rkl)	0.3970

Table 16: Combining ability of 5 x 5 diallel Analysis of First fruiting branch in upland cotton (Gossypium hirsutum L.).

SOV	**D.F**	**SS**	**MS**	**F Value**	**Variance(δ2)**	**Genetic effects**
GCA	4	2.0664	0.5166	1.6392ns	0.0201	δ2A=0.0402
SCA	10	16.9368	1.6937	5.3743**	1.3785	δ2D=1.3785
RCA	10	8.5158	0.8516	2.7022*	0.2682	
Error	24		0.3151			

* = Significant **= Highly Significant N.S = Non-Significant

From the analysis of variance for lint percentage, a significant variation exists between the cotton genotype for various combining ability effects such as SAC, GCA, and RE. Table 17 represents that in the 5×5 full diallel analysis, the genotype MNH-992 (1.8291) showed the greater value of GCA for lint percentage while the genotype CRS-456 (-0.9734) and Kahkashan (-0.8599) showed the minimum value of GCA for lint percentage. Table also shows that

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when the value of SCA is greater than the Lint percentage, it is governed by the dominant type of gene action, which is valuable for selecting a better genotype with lint percentage. (Amein et al., 2013). Table 17 represents that in the cross of CRS-456×Kahkashan and FH-114×CRS-456the higher value for SCA was noted as 1.0246 and 0.9477 with significant variation for lint percentage while in other crosses of MNH-992×Kahkashan and FH-207×MNH-992with respective values of minimum SCA are-2.4207 and -1.1001. The cross combination with a greater +ve value of SCA for lint percentage can be utilized for further selection of good-yielding cultivars and may also involved in heterosis breeding (Base et al., 2011). In reverse cross combination of MNH-992×FH-207and MNH-992×CRS-456greater values were noted for RE as 0.9867 and 0.9750 for lint percentage while the cross ofKahkashan×FH-207as -1.0067 presented minimum value for RE for lint percentage. All other crosses were found to have no variation for the first fruiting branch. The cross combination with more value of RE showing the maternal effects can be utilized to enhance lint percentage (Azhar et al. 2005). Table 18 indicates that the higher value of SCA (3.7468) and dominant variance for crosses (3.7468) is shown, while the lower value of GCA (1.2262) and additive variance (2.4524) is shown. From Table 18, greater values for SCA and dominance variance determine that these genotypes can be utilized in hybrid breeding for the lint percentage. Because of less value of reciprocal variance than SCA variance were 0.2604 and 3.7468, respectively, which indicates that there is non additive type of gene action. Amein et al. (2013) and Azhar et al. (2005) determined similar results.

Table 17: Various genetic effects of parents and crosses of GOT in upland cotton (Gossypium hirsutum L.)

Parents	**GCA**
FH-114	-0.1130 ns
FH-207	0.1173 ns
CRS-456	-0.9734 **
MNH-992	1.8291 **
Kahkashan	-0.8599 **
S.E. (gi - gj)	0.1750
Direct Crosses	SCA
FH-114×FH-207	-0.3296 ns
FH-114×CRS-456	0.9477 *
FH-114×MNH-992	-0.3681 ns
FH-114×Kahkashan	0.6493 ns
FH-207×CRS-456	0.1107 ns
FH-207×MNH-992	-1.1001 **
FH-207×Kahkashan	0.1589 ns
CRS-456×MNH-992	0.0323 ns
CRS-456×Kahkashan	1.0246 **
MNH-992×Kahkashan	-2.4207 **
S.E. (sij – sik)	0.4951 0.3609
Indirect crosses	RCA
FH-207×FH-114	-0.5467 ns
CRS-456×FH-114	-0.0900 ns
CRS-456×FH-207	0.4267 ns
MNH-992×FH-114	0.8583 ns
MNH-992×FH-207	0.9867 *
MNH-992×CRS-456	0.9750 *
Kahkashan×FH-114	0.4650 ns
Kahkashan×FH-207	-1.0067 *
Kahkashan×CRS-456	0.0200 ns
Kahkashan×MNH-992	-0.3738 ns
S.E. (rij – rkl)	0.4376

Table 18: Combining ability of 5 x 5 diallel Analysis of GOT in upland cotton (Gossypium hirsutum L.).

SOV	**D.F**	**SS**	**MS**	**F Value)**	**Variance(δ2)**	**Genetic effects**
GCA	4	50.5811	12.6453	33.0181**	1.2262	δ2A=2.4524
SCA	10	41.2981	4.1298	10.7834**	3.7468	δ2D=3.7468
RCA	10	9.0393	0.9039	2.3602*	0.2604	
Error	24		0.3830			

* = Significant **= Highly Significant N.S = Non Significant

[Citation: Khan, Z., Gul, N., Mehboob, A., Amjad, S., Munir, T., Hammad, M., sardar, H., Akbar, F., Saqib, M., Mahmood, K. (2023). Deciphering the genetic codes: gene action and combining ability in *Gossypium Hirsutum* l. And their impact on plant traits. *Biol. Clin. Sci. Res. J.*, **2023***: 569*. doi: https://doi.org/10.54112/bcsrj.v2023i1.569]

A significant variation has existed among all the parental genotypes that were studied currently at (p=0.5) for almost all parameters such as the height of the plant, direct fruit-bearing branches, number of boll, weight of boll, lint index and percentage of lint for GCA except than the seed index and monopodial branches as elaborated in table 4.14. While in the case of the direct crosses traits, except for the direct and indirect fruit-bearing branches and weight of the boll, all other parameters were found to have maximum variation among them. In the case of reciprocal crosses excluding the indirect fruit-bearing branches and weight of the boll, all characters were determined as significant, which is elaborated on in Table 14. Calculated combining ability in American cotton for various parameters and their mean square value as well as genetic variance for every parameter indicates the maximum variation at (p=0.5) as visible in tables (4.11, 4.12, and 4.13), which promoted us to use Grilling's approach (1956) for the determination of part or sharing of variance from the parental genotypes due the causes of SCA, GCA and RE and their inheritance pattern for various parameter under study in American cotton. Calculated data from the experiment determine the maximum variation is present due to the cause of GCA. Variation observed by the cause of SCA is smaller than that of GCA for a parameter such as the height of the plant, direct fruit-bearing branches, number of the boll, the weight of boll, lint index and percentage of lint which represented in table 4.14. It is estimated that the sharing of reciprocal and general combining ability effects is more than that of SCA for parameter plant height, sympodial branches, number of bolls, and seed index, while the SCA effects were indicated more for seed cotton yield, lint index got and first fruiting branch than the reciprocal and general combining ability effects from table 14. From the result, table 4.14 investigated that the parameter plant height, monopodial branches, boll per plant, seed cotton yield, and its related traits were highly governed by the non-additive type of gene action because the value of GCA/SCA ratio is less than one, which indicates that hybrids are more vigorous for all parameter under study. Similar results for additive non additive gene action were observed earlier for such parameters by Amein et al. (2013) and Ali et al. (2017).

Declarations

Data Availability statement

All data generated or analyzed during the study are included in the manuscript.

Ethics approval and consent to participate

Approved by the department Concerned.

Consent for publication

Approved

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Conflict of interest

The authors declared absence of conflict of interest.

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