

Assessment of Combining Ability Impact on F1 Generation for Different Quantitative Traits in BT and Non-BT Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

General and specific combining ability are one of the important plant breeding tools used to compare performances of lines in F1 population across growth and yield contributing traits. The experiment was carried out in 2014 under the agro-ecological condition of Tandojam, Sindh Pakistan based on a randomized complete block design with four replications. Six parents and their crosses (nine hybrids), in which three female parents as lines (Bt-008, IR-1525, and neelam-131) and three male parents as testers (NIA Sadori, NIA Ufaq and NIA Perkh) were evaluated in the study. In F1 generation, the mean squares for combining ability for targeted characteristics displayed highly significant ($p < 0.01$) general combining ability effects in lines for all traits except lint index. But in the case of testers, the GCA effects were significant for sympodial branches plant-1, seed index, and seed cotton yield plant-1 and highly significant only for monopodial branches plant-1, ginning outturn%, staple length. While, mean squares values for the interaction of line x tester revealed highly significant specific combining ability effects for plant height, monopodial branches plant-1, boll weight, and GOT%. The two parents Neelam-131 and NIA Ufaq manifested higher general combining ability effects and were good general combiners for yield and yield components and can make a potential material for varietal seed development. For yield contributing characters, crosses IR-1525 × NIA Ufaq and IR-1525 × Perkh showed significant SCA effects among the rest of the crosses. From this study, it is suggested that crosses exhibiting greater SCA value and parents indicating good GCA value must be chosen for enhancement of a specific trait.

Keywords: BT cotton, General combining ability, hybrids, non-BT cotton, specific combining ability

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INTRODUCTION

Cotton (*Gossypium hirsutum* L.) crop possess a central place in the economy of Pakistan and is the main contributor in the provision of raw material for textile industry. Cotton made products are the significant contribution in Pakistan's export as well as the export of lint as raw material. The input of cotton as value-added in agriculture and GDP is 7.0% and 1.5%. The cultivated area under cotton crop during 2019-20 was 2.517 million hectares with production of 9.148 million bales (GoP, 2020). Presently, the efforts for further improvement in cotton crop are underway to bring genetic improvement both quantitatively and qualitatively to meet the escalating needs of today. There is an association between seed cotton yield and its components and these components are genetically linked with each other that might be developmental or genetically controlled (Adams and Grafius, 1971; Bing Tang, 1992; Nidagundi et al., 2012).

Plant breeders perform different crosses to investigate genetic variations, the extent of heritability and the kinds of gene involved in controlling the variations. Further, the segregation and non-segregation of variations compared among generations (Kearsey and Pooni, 1996). In addition to that the breeders are interested in identification of genotypes which are superior in performance in light of progeny performance. The selection of appropriate lines based on the better mean performance is affected by combining ability. Because the combining ability depends on the gene action controlling the trait to be improved. In any mapping population, mean line can be controlled by either additive or dominant gene effects. Actually, it is the mating design that describes the GCA estimation for a specific line (Acquaah, 2012; Zhang et al., 2015). Thus, theoretically, GCA measures the differences between maternal groups. Conversely, the better performance of hybrids is studied by SCA (specific combining ability) (Madić et al., 2014). The specific trait studied in hybrids through SCA is controlled by the non-additive gene (Acquaah, 2012; Klykov et al., 2018). A successful plant breeding program based on the estimation of combining ability which driven by genes actions (Panhwar et al., 2008)

Various mating designs have been described and compared in many research investigations (Kearsey and Pooni, 1996; Hallauer et al., 2010; Acquaah, 2012). The most prominently used designs are six included BIP (biparental progenies), polycross, topcross, North Carolina (I, III, III), Diallels (I, II, III, IV) and Line x tester design. North Carolina Design II is a factorial mating pattern in which two groups of parents are involved as male and female group providing equal mating opportunity for every member of a group to other member of opposite group. This design is applied for the evaluation of inbred lines for the study of GCA and SCA. Design II is often tested for those plants having both male and female flowers. In this design blocking is developed to permit equally matings chances subjected to two male and female groups to ensure unit integrity (Acquaah, 2012).

Combining ability analysis is indispensable for parents' identification to develop superior lines or hybrids. During the development of hybrid from those genotypes based on its better performance, would not necessarily be enough for establishing progenies of preferred traits. It is therefore, necessary to identify promising lines based on crosses using appropriate mating design. The study of both general specific is indispensable for choosing parents and hybrids which give highest improvement in the character under consideration and also provide information on the nature of genetic variation present in material under study. Combining ability is most widely used biometrical genetical approach in plant breeding. Success of development of high yielding and widely adapted hybrids depends on the specific combining ability of parental crosses (Patil et al., 2011; Kumar et al., 2013). Keeping in view the importance of above mentioned analysis, this study was aimed to investigate the combining ability analysis as GCA and SCA of parents and hybrids in cotton.

MATERIALS AND METHODS

This study was conducted at the experimental field of Nuclear Institute of Agriculture, Tandojam to assess the genetic variations among cotton genotypes for

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determining the general and specific combining ability and selection parameters for quantitative and qualitative traits in F1 hybrids of *Gossypium hirsutum* L. The experiment was based on randomized complete block design with four replications. Six cultivars and their crosses were investigated using North Carolina design II mating in which three lines of Bt-008, IR-1525 and neelam-131 as female parents and three testers such as NIA Sadori, NIA Ufaq and NIA Perkh were used during F1 crosses.

Parents and their crosses

Lines

P1 = Bt-008

P2 = IR-1525

P3 = Neelam-131

Testers

P4 = NIA Sadori

P5 = NIA Ufaq

P6 = NIA Perkh

Crosses or F1 hybrids

Bt-008 × NIA Sadori

Bt-008 × NIA Ufaq

Bt-008 × NIA Perkh

IR-1525 × NIA Sadori

IR-1525 × NIA Ufaq

IR-1525 × NIA Perkh

Neelam-131 × NIA Sadori

Neelam-131 × NIA Ufaq

Neelam-131 × NIA Perkh

The seeds of parents and their F1 hybrids were obtained from the Nuclear Institute of Agriculture and sown @ 30 kg ha⁻¹ through the ridge method while maintaining a 75 cm distance between rows. At the time of land preparation, all recommended phosphorus of 75 kg ha⁻¹ and 1/3 of recommended nitrogen (125 kg ha⁻¹) were applied. Whereas, the 2/3 nitrogen was equally splitted into 3 doses and applied at first irrigation, flowering and boll setting. For maintaining the proper plant distancing of 30 cm thinning of seedlings were carried out before first irrigation. The agronomic practices like weed eradication, pesticides spray and hoeing were performed during the entire crop production.

Traits studied: In this study 10 different characters of cotton cultivars and their crosses were investigated which were included plant height (cm), monopodial branches plant-1, sympodial branches plant-1, bolls plant-1, boll weight (g), seed index (g), lint index (g), GOT (%), staple length (mm) and seed cotton yield plant-1 (g).

Ten plants were randomly selected in each replicated plot for recording the data pertaining to quantitative characteristics. Plant height was noted from ground surface to the tip of plant with help of measuring tape. The branches originating at the base of main stem are the monopodial branches which were counted in each plant and then averaged. While, sympodial branches are the fruit bearing branches which were recorded in ten plants in each plot and then its mean was calculated. Similarly, numbers of bolls plant-1 were noted in ten plants while in case of boll weight (g), 10 bolls were randomly selected in each plant and picked at maturity and then individual boll was weighted and then worked out their average boll weight per plant. For seed index (g), three samples of 100-seeds each were taken at random from each index plant and weighed in grams and finally average was calculated and recorded as seed index. Likewise, lint index is the weight of lint in grams obtained from one hundred seeds. While, staple length (mm) was measured by tuft method through averaging of three samples from individual plant. For ginning outturn (G.O.T.) % or lint percentage, clean and dry sample of seedcotton plant-1 was weighed and then ginned on single roller electric gin.

The lint obtained from each plant was weighed and G.O.T. % worked out by dividing lint weight by total seed cotton weight in terms of percentage.

$$\text{Ginning outturn percentage} = \frac{\text{weight of lint plant}^{-1} (\text{g})}{\text{Weight of seedcotton plant}^{-1} (\text{g})} \times 100$$

Combining ability: Combining ability effects were estimated using Griffing (1956) method-I, model-II and were computed as follows.

General combining ability (GCA) effects

$$\text{GCA} = \frac{1}{2n} \sum (Y_{i.} + Y_{.i}) - \frac{2}{n^2} Y_{2..}$$

Where.

n = Number of parents/varieties.

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Y_i = Total of mean values of F2's resulting from crossing jth lines with ith lines.

$Y_{.i}$ = Total of mean values of F2's resulting from crossing ith lines with jth lines.

$Y_{2..}$ = Grand total of all the mean values in a diallel table.

Specific combining ability (SCA) effects

$$SCA = \frac{1}{2} (Y_{ij} + Y_{ji}) - \frac{1}{2n} (Y_i + Y_{.i} + Y_j + Y_{.j}) + \frac{1}{n^2} Y_{2..}$$

Where,

Y_{ij} = Mean values of the F2 resulting from crossing the ith and jth lines.

Y_{ji} = Mean values for the F2 resulting from crossing the jth and ith inbreds.

Y_i = Total of mean values of F2's resulted from crossing jth line with ith varieties.

$Y_{.i}$ = Reciprocal values of Y_i .

Y_j = Total of mean values of F2's resulted from crossing ith line with jth varieties.

$Y_{.j}$ = Reciprocal Values F2's of Y_j

$Y_{2..}$ = Grand total of the observations

RESULTS AND DISCUSSION

In hybridization technique, the selection of best performing parents is vital for successful breeding program. It is prerequisite to exploit the gene action that existed in the population based on the information pertaining to combining ability and genetic variability affecting yield and yield contributing characteristics. In both cross and self-pollinated plants, the assessment of breeding value of parents depends on the estimation of GCA and SCA (Griffing 1956; Kempthorne, 1956) The data regarding yield and yield contributing factors reflecting the analysis of variance under the influence of combining ability is shown in Table 1. The GCA values of lines were found statistically highly significant ($p \leq 0.01$) for the quantitative trait included plant height, sympodial branches plant-1, monopodial branches plant-1, bolls plant-1, boll weight, seed index, GOT%, and staple length. Whereas, other traits like sympodial branches plant-1, seed index, and seedcotton yield plant-1 manifested significant differences for GCA values.

However, the lint index expressed statistically at par differences for GCA values. In case of testers, monopodial

branches plant-1, GOT% and staple length revealed highly significant variations in GCA values. In addition, the GCA for sympodial branches plant-1 and seed index indicated significant differences. The remaining parameters of GCA for testers revealed nonsignificant differences. However, specific combining ability (SCA) for plant height, monopodial branches plant-1, boll weight plant-1, and GOT% varied significantly. While, rest of the parameters showed statistically at par differences for SCA.

Plant height: The highest significant positive GCA effects were observed in parent NIA Sadori (6.74) followed by 2.84 in parent Bt-008 and genotype IR-1525 had minimum (1.28) positive GCA effects (Table 2). The former entries therefore could confer more additive genes for tallness in the parents. Parent Neelam-131 had the highest negative GCA effects (-4.12) followed by NIA Perkh (-3.92) which is indicative of shorter plant height (Table 2). Five crosses displayed positive SCA effects and remaining four had negative SCA effects. Maximum (10.68) positive SCA effects were calculated for the cross IR-1525 x NIA Perkh followed by 9.06 SCA effect for cross Neelam-131 x NIA Ufaq and minimum positive SCA effect of 4.74 was observed in cross Bt-008 x NIA Sadori. However, the maximum (-18.57) negative SCA effects were exhibited by the cross Neelam-131 x NIA Perkh (Table 3).

Number of sympodial branches plant-1: Three parents such as Bt-008, IR-1525 and NIA Perkh exhibited negative values whereas Neelam-131, NIA Saodori and NIA Ufaq showed positive GCA effects for sympodial branches plant-1. NIA Sadori revealed highest positive (2.207) GCA effects, while NIA Perkh gave highest negative GCA effects (-4.07) (Table 2). Among them, the positive SCA effect was noted for five crosses, where IR-1525 x NIA Sadori manifested greater positive SCA effects (1.414). The maximum negative SCA effects (-0.1.836) were demonstrated by the cross Neelam-131 x NIA Sadori (Table 3).

Number of monopodial branches plant-1: Four cultivars Bt-008, IR-1525, NIA Sadori and NIA Perkh displayed significant positive GCA effects (Table 2) whereas parents such as Neelam-131 and NIA Ufaq manifested negative



GCA effects for monopodial branches plant-1, among them NIA Ufaq gave maximum negative GCA effects (-0.302). Six crosses exhibited significant positive SCA effects for this character, the highest positive SCA effects (0.368) were observed in the cross Neelam-131 x NIA Perkh and that maximum negative SCA effects (-0.467) were recorded in cross IR-1525 x NIA Perkh (Table 3).

Number of bolls plant-1: Among the six parents, two parents showed positive GCA effects while the four parents revealed negative GCA effects as presented in Table 2. The highest positive GCA effects (8.651) were observed for the parent NIA Sadori and highest (-6.970) negative GCA effects were recorded in NIA ufaq. Out of 9, four crosses showed positive SCA effects. The maximum positive SCA effects (5.10) were indicated by the cross Bt-008 x NIA Perkh and the maximum negative SCA effects (-2.65) were expressed by the cross IR-1525 x NIA Perkh (Table 3).

Boll weight: Two parents Neelam-131 and NIA Ufaq exhibited positive GCA effects (0.064 and 0.264) and may be regarded as good general combiner for boll weight, whereas rest of parents showed negative GCA effects and maximum negative GCA (-0.1981) effects was recorded in parent NIA Perkh (Table 2). Among 9 crosses, four crosses showed positive SCA effects and five crosses indicated negative SCA effects. Cross IR-1525 x NIA Perkh exhibited maximum positive SCA effects (0.257). Maximum negative SCA effects (-1.155) were obtained in the cross Bt-008 x NIA Perkh (Table 3).

Seed index: The parents Bt-008, Neelam-131, NIA Sadori and NIA Ufaq produced positive GCA effects and were good general combiners for seed index (Table 2). Negative GCA effects however, imply poor combining ability. The parent NIA Ufaq indicated highest positive GCA effects (0.491) and NIA Perkh had highest negative GCA effects (-0.613). Among 9 crosses, four crosses exhibited positive SCA effects where the highest positive SCA effects (0.316) were shown by the cross IR-1525 x NIA Perkh and the highest negative effects (-0.266) by the cross Neelam-131 x NIA Perk (Table 3).

Lint index: Among the six parents, three parents displayed positive and three showed negative GCA effects (Table 2). The highest positive GCA effects (0.171) were shown by the parent NIA Perkh whereas the highest negative GCA effects (-0.184) were exhibited by NIA Sadori. Out of 9 progenies, five showed negative SCA effects and remaining four crosses had positive SCA effects. The highest positive SCA effects (0.307) were recorded in the cross Neelam-131 x NIA Perkh and the highest negative (-0.308) value was attained by the progeny IR-1525 x NIA Perkh (Table 3).

Ginning outturn (G.O.T.%): Among the six parents, four revealed positive GCA effects and two parents indicated negative GCA effects as presented in Table 2. The higher positive CGA effects (1.958 and 1.080) were displayed by parents Neelam-131 and NIA Ufaq while the higher negative GCA effects (-2.331) were recorded for parent IR-1525 followed by -1.397 in NIA Perkh. Out of 9 crosses, four crosses revealed positive and five displayed negative SCA effects (Table 3). The highest positive SCA effects (2.259) were produced by the progeny Neelam-131 x NIA Perk followed by 2.257 SCA effects in cross of IR-1525 x NIA Ufaq.

While, the highest negative SCA effects (-4.385) were recorded in the cross Neelam-131 x NIA Ufaq. Staple length: Estimation of general combining ability (GCA) for staple length showed that among six parents, three parents revealed positive GCA effects and three parents indicated negative GCA effects as depicted in Table 2. Higher positive GCA effects (2.356) were found in parent NIA Perkh and the maximum negative GCA effects (-2.011) were revealed by the parent NIA Sadori (Table 14). Out of 9 crosses, four crosses showed positive SCA effects and five crosses indicated negative SCA effects (Table 15). The highest positive SCA effects (0.889) were produced by the progeny Neelam-131 x NIA Ufaq followed by the cross Neelam-131 x NIA Perkh (0.644) and maximum negative SCA effects (0.880) were shown by the cross Bt-008 x NIA NIA Perkh (Table 3).

Seedcotton yield plant-1: Estimation of general combining ability (GCA) for seedcotton yield palnt-1 showed that among six parents, two parents revealed positive GCA effects and four parents indicated negative

GCA effects as depicted in Table 2. The highest positive GCA effects (5.952) were noted for parent NIA Ufaq followed by GCA effects of 5.429 in parent Neelam-131. Whereas, the higher negative GCA effects (-4.159) were shown by parent Bt-008. Among the nine crosses, four progenies exhibited positive SCA effects while five progenies showed negative SCA effects (Table 3). Maximum positive SCA value (3.169) was produced by the cross IR-1525 x NIA Perkh and the highest negative (-5.064) SCA effects were exhibited by Neelam-131 x NIA Perkh.

The manipulation of qualitative traits through breeding is successful because its genetic background can be analyzed easily. Instead, the quantitative traits require a better understanding of inheritance, and its extent of success is associated with a level of improvement that is observed during the selection process. The genetic variability for yield and yield contributing factors were investigated through analysis of combining ability in this study. In plant breeding programs the idea of combining ability place a special position due to two reasons. Firstly, it helps in identification of best parents' performance, secondly it predicts what kind of gene action involve in controlling the quantitative traits. Further, we can evaluate lines' performance in hybrid combinations. On these backgrounds, two terms were introduced in plant breeding such as GCA (general combining ability) and SCA (specific combining ability) (Sprague and Tatum, 1942). In general combinations, the average performance of parents is analyzed in GCA while the hybrid performance is studied in SCA. In hybrid combination, the genetic potential of inbred parents shows great attraction for cotton breeders (Baloch and Bhutto, 2003).

In the present study, The GCA values of lines were found statistically highly significant ($p \leq 0.01$) for the quantitative trait included plant height, sympodial branches plant-1, monopodial branches plant-1, bolls plant-1, boll weight, seed index, GOT%, and staple length. Whereas, other traits like sympodial branches plant-1, seed index, and seedcotton yield plant-1 anifested significant differences for GCA values. But in case of testers, the GCA effects were significant for sympodial branches plant-1, bolls plant-1 and seedcotton yield plant-1 as well as highly significant

for staple length only. The remaining parameters of GCA for testers revealed non-significant differences. While, mean squares values for the interaction of line x tester revealed highly significant SCA effects for plant height, monopodial branches plant-1, bolls weight and GOT%. While mean square values due to SCA for rest of the parameters showed non-significant variations. The higher value of GCA variances was might be due to influence of additive gene action and its combination that control the expression of quantitative trait in the investigated genetic materials. Our results are in line with Basal et al. (2011) who recorded greater GCA's mean square values significant for all the studied variables and SCA for lint percentage and seed index.

Similar findings were reported by Bharad et al. (2000) and Mert and Boyaci (2003) who observed higher GCA variances over SCA variances that was might be due to the involvement of additive gene actions. Nevertheless, the higher GCA of parents does not inevitably consult higher SCA, therefore both combining abilities are sovereign (Khan et al., 2007; Basal et al., 2009).

The quantitative characteristics of plant such as yield and its components are importantly controlled by both additive and non-additive gene. According to BingTangs (1992) that dominance gene action is responsible for seedcotton yield and additive gene actions is involved in controlling the yield contributing characters. While, working on cotton breeding, he found significant variances of GCA and SCA for seedcotton yield and its components in F1 and F2 population. Nonetheless, Baloch (2004) reported that both additive and non-additive gene actions are involved in controlling seedcotton yield and yield contributing traits are controlled by additive gene actions. Such information support the evidences behind the inheritance that both additive and non-additive gene actions are responsible in controlling the traits pertaining of yield and its factors during cotton breeding (Mühleisen et al., 2013; Klykov et al., 2018).

As regard to GCA, Bt-008 was found as good general combiner for plant height, monopodial branches plant-1 and seed index while, parent IR-1525 was noted a good combiner for monopodial branches plant-1. Similarly, the



parent Neelam-131 was good general combiner for sympodial branches plant-1, boll weight, GOT%, staple length and seedcotton yield plant-1. Whereas, NIA Sadori was good general combiner for plant height, sympodial branches plant-1, monopodial branches plant-1, bolls plant-1, seed index and GOT%. Likewise, the parent NIA Ufaq was good general combiner for sympodial branches plant-1, boll weight, seed index, GOT% and seedcotton yield. Together with that, the parent NIA Perkh also expressed combining ability and was good general combiner for monopodial branches plant-1, lint index and staple length respectively (Table 2). A group of researchers reported positive GCA effects for plant height, bolls plant-1 and staple length (Irfanullah et al., 1993; Syed et al., 1993). For bolls plant-1 and seedcotton yield, positive GCA effect was reported by Keerio et al. (1995a, b) and Soomro et al. (1995).

According to Kalwar and Babar (1999) that nonadditive gene action is responsible for controlling the traits like bolls plant-1, boll weight and seedcotton yield plant-1 demonstrating higher SCA effects than GCA. It means that for carrying out breeding program for improvement in a specific trait, both additive and nonadditive gene action must be investigated for better understanding of genetic architecture. In most cases, the magnitude of GCA was higher than SCA in all cases, which indicated the importance of additive gene action and in that case transgressive segregates could be selected in early generations (Fujimoto et al., 2018). Among the nine

crosses, two crosses such as IR- 1525 x NIA Ufaq and IR- 1525 x NIA Perkh displayed significantly higher specific combining ability effects and were the best specific combiners for most of the studied traits particularly for boll weight, seed index and seedcotton yield plant-1 followed by the cross of Neelam-131 x NIA Sadori which showed positive SCA effects and was best specific combiner for plant height, bolls weight, GOT%, staple length and seedcotton yield plant -1 and Neelam-131 x NIA Ufaq manifested positive SCA effects and was the best specific combiner for plant height, monopodial branches plant-1, bolls plant-1, staple length and seedcotton yield plant-1. Therefore, crosses showing high SCA along with good general combining parents should be selected for improvement of a particular character. Significant GCA and SCA effects for various traits among parents and their crosses showed that these traits are governed by additive and nonadditive gene action (Basal et al.2011). Earlier studies reported positive SCA effects for plant height (Nirania et al., 1992), sympodial branches plant-1 (Bhatade and Bhale, 1983), number of bolls plant-1 (Waldi et al., 1980), and lint yield plant-1 (Chaudari et al., 1990) and lint index (Bhatade and Bhale, 1983; Avtar et al., 1992). For yield contributing characters, Bt-008 x NIA Perkh, IR-1525 x NIA Ufaq, IR-1525 x NIA Perkh, Neelam-131 x NIA Sadori and Neelam-131 x NIA Ufaq showed significant SCA effects among the rest of crosses under this study. Among them, the crosses IR-1525 x NIA Perkh, IR-1525 x Perkh perform well for seedcotton yield plant-1.s



Table 1: Analysis of variance (mean squares) for combining ability in F1 generation for quantitative and qualitative traits in *Gossypium hirsutum* L.

Source of variation	D.F.	Plant height (cm)	Monopodial branches Plant ⁻¹	Sympodial branches Plant ⁻¹	Bolls plant ⁻¹	Boll weight (g)	Seed index (g)	Lint index (g)	GOT %	Staple length (mm)	Seedcotton yield plant ⁻¹ (g)
Replications	2	15.929	0.027	1.949	57.290	0.016	0.061	0.652	1.236	0.758	110.51
Genotypes	14	320.730**	1.065**	46.079**	137.425**	0.159**	0.717**	1.486**	28.619**	26.503**	445.43**
Parents (P)	5	153.652*	2.268**	74.674**	95.784*	0.142**	0.736**	3.869**	32.319**	52.337**	1012.17**
P vs C	1	332.889*	0.428**	27.329**	234.827*	0.046	0.052	0.039	11.957*	1.008	95.88
Crosses	8	423.634**	0.392*	30.550**	151.276**	0.183**	0.788**	0.178	28.389**	13.543**	134.90*
Lines (L) GCA	2	309.200**	0.733**	112.100**	568.206**	0.510**	2.843**	0.284	14.495**	43.703**	240.29*
Testers (T) GCA	2	119.939	0.212**	4.483*	1.596	0.036	0.148*	0.035	42.328**	9.421**	217.77*
L x T (SCA)	4	632.698**	0.312**	2.809	17.650	0.094**	0.081	0.196	28.367**	0.524	40.78
Error	28	48.488	0.013	1.495	43.897	0.021	0.053	0.366	2.236	1.132	70.74

* = Significant at $P \leq 0.05$ level of probability

** = Significant at $P \leq 0.01$ level of probability

Table 2: Estimation of general combining ability (GCA) effects in F1 generation for various quantitative and qualitative traits in *Gossypium hirsutum* L.

Source of variation	Plant height (cm)	Monopodial branches Plant ⁻¹	Sympodial branches Plant ⁻¹	Bolls plant ⁻¹	Boll weight (g)	Seed index (g)	Lint index (g)	GOT %	Staple length (mm)	Seedcotton yield plant ⁻¹ (g)
Bt-008	2.837	0.089	-0.548	-0.270	-0.063	0.114	-0.028	0.373	-1.133	-4.159
IR-1525	1.281	0.088	-0.248	0.485	-0.014	-0.139	0.071	-2.331	0.278	-1.274
Neelam-131	-4.118	-0.177	0.796	-0.215	0.064	0.025	-0.043	1.958	0.856	5.429
NIA Sadori	6.737	0.039	2.207	8.651	-0.066	0.120	-0.184	0.318	-2.011	-2.615
NIA Ufaq	-2.807	-0.302	1.863	-6.970	0.264	0.491	0.013	1.080	-0.344	5.952
NIA Perkh	-3.92963	0.263	-4.070	-1.681	-0.1981	-0.613	0.171	-1.397	2.356	-3.337
S.E.	2.385	0.038	0.377	0.945	0.048	0.085	0.157	0.498	0.356	2.586

Table 3: Estimates of specific combining ability (SCA) effects in F1 generation for various quantitative and qualitative traits in *Gossypium hirsutum* L.

Source of variation	Plant height (cm)	Monopodial branches Plant ⁻¹	Sympodial branches Plant ⁻¹	Bolls plant ⁻¹	Boll weight (g)	Seed index (g)	Lint index (g)	GOT %	Staple length (mm)	Seedcotton yield plant ⁻¹ (g)
Bt-008 x NIA Sadori	4.736	0.033	0.422	-0.311	0.165	0.108	-0.069	-0.829	-0.125	-0.350
Bt-008 x NIA Ufaq	-7.575	-0.103	1.222	1.700	-0.059	0.032	-0.069	2.128	-0.502	-3.506
Bt-008 x NIA Perkh	7.892	0.099	0.011	5.100	-1.155	-0.049	0.000	-1.061	-0.880	1.894
IR-1525 x NIA Sadori	-11.305	0.163	1.414	-0.594	-0.085	-0.060	0.203	-0.248	-0.108	-1.375
IR-1525 x NIA Ufaq	-1.483	0.077	-0.053	-1.983	0.026	0.113	0.114	2.257	-0.386	2.669
IR-1525 x NIA Perkh	10.683	-0.467	0.036	-2.650	0.257	0.316	-0.308	-1.198	0.326	3.169
Neelam-131 x NIA Sadori	6.570	-0.195	-1.836	0.906	-0.079	-0.048	-0.135	1.772	0.233	1.7250
Neelam-131 x NIA Ufaq	9.058	0.026	-1.169	0.283	0.033	-0.145	-0.045	-4.385	0.889	0.836
Neelam-131 x NIA Perkh	-18.575	0.368	-1.047	-2.450	-0.103	-0.266	0.307	2.259	0.644	-5.064
S.E.	4.130	0.065	0.652	1.638	0.083	0.147	0.272	0.863	0.617	4.480

CONCLUSION

The pooled data obtained through this study have shown the importance of North Carolina Design-II analysis in identifying parents with general and specific combining ability that help to choose appropriate breeding procedure. Additive gene action predominated in all characters of the study. Among the six parents, two parents Neelam-131 and NIA Ufaq exhibited significantly higher GCA effects and were the best general combiners for yield and yield components. Crosses IR-1525 x NIA Ufaq and IR-1525 x Perkh showed significant SCA effects among the rest of crosses under this study. From this study, it is suggested that crosses showing high SCA and with good general combining parents should be selected for improvement of a particular character.

AUTHOR'S CONTRIBUTION:

HOCLAB, Z.: Designed the study, wrote the protocol, managed the literature searches, wrote the draft of the manuscript and interpreted the statistical analysis

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