R E S E A R C H   A R T I C L E

Trends in Biotechnology and Plant Sciences

Genetic Analysis for Seed Cotton Yield and CLCuD Resistance in Upland Cotton

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Abstract

Cotton is the primary source of valuable textile fiber, belongs to the Malvaceae family and the genus Gossypium. Cotton is widely referred to be a problem plant because it is a high maintenance crop that is influenced by a variety of biotic and abiotic variables that significantly reduce cotton output each year. That's why there is continuous need to develop varieties with high seed cotton yield and CLCuD resistance. The study is planned to determine the combining ability effects of parental lines and crosses in upland cotton (*Gossypium hirsutum* L.) using line x tester mating design. The four lines Kehkashan, Tarzen, BS-80, CRS-2 and four testers MNH-998, NS-131, AGC-2, KZ-191 were crossed in line tester fashion to study the genetic analysis of different yield related traits in cotton and CLCuD resistance. Four lines were crossed with four testers at the time of flowering in line × tester design in glass house. Eight parents along with 16 crosses (F_1) were grown in the field with three replications by using a randomized complete block design. Among lines CRS-2 showed significant GCA effects for plant height and number of sympodial branches, boll weight while line Tarzen showed highly significant GCA effect for plant height and number of bolls. A significant GCA result was observed for Kehkashan and BS-80, showing that both lines combine well for number of bolls. Among testers, KZ-191 showed a highly significant GCA effect for seed cotton yield, boll weight, while MNH-998 showed highly significant GCA effects for plant height and sympodial branches. The tester AGC-2 showed highly significant GCA for number of sympodial branches. Tester NS-131 showed emerged out as a good general combiner for fiber maturity and fiber elongation. Among crosses Kehkashan x AGC-2 showed significant SCA for plant height, boll weight and kehkashan × NS-131 for plant height. Other crosses CRS-2 × AGC-2 showed significant SCA for sympodial branches, ginning out turn while Kehkshan × KZ-191 proved good SCA for monopodial branches per plant. The results showed that germplasm has potential for development of cotton varieties, and may be used in cotton breeding program.

K E Y W O R D S
Disease resistance, Varieties, Combining ability, CLCuD

1 | INTRODUCTION

Cotton is the world's top producer of natural fibers, with commercial production in more than 50 countries. The cotton has 45 diploid species (2n=2x=26) and 7 tetraploid species (2n=4x=52) having widely different phenotypes.

Cotton is Pakistan's most significant cash crop, and 55% of the country's profits in foreign exchange come from cotton exports. Cotton is widely referred to be a problem plant because it is a high-maintenance crop that is influenced by a variety of biotic and abiotic variables that

significantly reduce cotton output each year. The most destructive of these is the cotton leaf curl disease complex which is the cause of considerable decreases in cotton. CLCuD resistance is quantitatively inherited with predominance additive gene effects (Khan et al. 2007; Riaz et al. 2017). Additionally, it was shown that R1 CLCuD hir and R2 CLCuD hir two of the three genes serve as CLCuD resistance while the third gene a suppressor gene helps in lowering resistance (sCLCuDhir) (Rahman et al. 2005). Seed cotton yield and growth of cotton are highly sensitive to temperature fluctuations. High temperature reduces the boll growth and boll size due to this seed cotton yield decreases. In addition, cotton will be vulnerable to ClCuD due to sudden changing climatic conditions (Khalid et al. 2022). Understanding the level of association of yield with other traits is very important for the selection of desired characteristics (Zafar et al. 2023). Seed-cotton yield had shown a positive association with other traits like plant height, number of bolls, and number of monopodial branches per plant. There is a need of time to pay attention to knowledge of the inheritance of these yield-contributing traits for the enhancement of seed cotton yield. Other plant traits like days to flowering and days to maturity are very important in short-duration breeding projects.

The utilization of line × tester analysis is most important biometrical tool in a breeding program for selection of suitable parents and F_1 hybrids (Chattha et al., 2021). Combining ability has two types general combining ability and specific combining ability. General combining ability (GCA) pertains to average genotypic prffresrxsererformance in matrix of crosses, whereas specific combining ability (SCA) pertains to individual hybrid that perform better in hybrid combinations (Sajjad et al. 2016; Farooq et al. 2020). SCA has vital role in hybrid development but GCA has advantageous role for selection of suitable parental genotypes for hybridization program and performance of GCA is caused by the additive genes of parental lines whereas performance of SCA exhibited by the novel genes that may have dominant or epistatic effects. Several lines or testers are used to estimate the GCA and SCA of genotypes and their cross combinations, respectively (Kempthorne 1957). Most important tool for selection is combining ability analysis through which we can select desirable parents and we can determine the magnitude and nature of gene action which control quantitative traits. Combining ability can be determined through two ways, through line x tester mating design and Diallel mating design (Basbag et al. 2007). The line × tester analysis is an effective biometrical tool that gives most important information regarding specific and general combining ability variances and effects, supporting the findings of best general combiners and specific promising cross combinations (Muthuswamy et al. 2003; Chattha et al. 2019). The line × tester analysis is modification of top cross breeding method which is most

common strategy for expressing the genetically hidden traits (Kempthorne, 1957).

All the cotton breeders have the primary objective to create new varieties with superior yield and fiber quality (Chattha et al., 2017). A successful breeding program starts with selection of suitable parents. A systematic method for selecting the best parents and crosses for the trait under study is Line x Tester analysis. This mating design is mostly used for determining the GCA and SCA of parents and crosses. Information of GCA and SCA effects of plants and crosses are important before starting breeding programm (Ashokkumar et al. 2010).

The objective of the present study is to determine the GCA and SCA effects of the parental lines and crosses for development of high seed cotton yield and CLCuD resistance varities.

2   METERIAL AND METHOD

The research was carried out in the department of Plant Breeding and Genetics field area at the University of Agriculture Faisalabad in 2021-22. The plant material for research was collected from the department of Plant Breeding and Genetics. The material for experimentation consisting of 4 testers (MNH-998, NS-131, AGC-2, KZ-191) and 4 lines (Kehkashan, Tarzen, BS-80,CRS-2) were sown in a glasshouse to produce the F_0 generation. All the genotypes were sown at optimum conditions like the temperature of 28°C. Proper light, and humidity was maintained in a glasshouse for a maximum germination. The seed was sown in earthen pots. Four lines were crossed with four testers at the time of flowering in line x tester design. Eight parents along with 16 crosses were grown in the field with three replications by using a randomized complete block design with 75cm spacing between lines and 30cm spacing between plants. To avoid the contamination of genetic material, all precauionery measures were followed. For data collection, 5 plants of each genotype from each replication were selected randomly. Proper agronomic practices like weeding, thinning, hoeing, timely irrigation, and plant protection measures were done from sowing to picking. The data of following parameters were recorded.

Morphological and Agronomic Traits

Plant height was recorded with measuring tape from ground level to top of plant. Measurement was taken in centimeters. The vegetative or indirect fruiting branches are mostly located at the base of stem named, as monopodial branches. The number of branches from five selected plants of each line were counted at maturity, and the average number was calculated based on the number of branches from every genotype among each replication. Sympodial branches are direct fruit

bearing branches and located on the upper side of the main stem. At maturity, sympodial branches on five plants of each line were counted, and then an average number of branches was calculated from each genotype from each replication. The days to first flowering were counted from each plant in each genotype for each replication. The days to first boll opening were calculated from sowing to first boll opening. Every parental genotype and F_1 crosses were picked two times. The total number of fully opened bolls were counted from each genotype for each line in each replication. Then whole data of full opened bolls per plant summed and average was taken. It was measured in grams. Boll weight was counted by divding the seed cotton yield of each plant by the total number of picked bolls on that plant. Mean values of each replication of each genotypes were counted.

$$\text{Boll weight} = \frac{\text{Total seed cotton weight}}{\text{Total number of bolls}}$$

Seed cotton was hand-picked after 10:00 am when the dew on the plant had evaporated, then weighed in grams on an electronic balance. The average yield per plant in each replication was .

CLCuD Symptomatic Assessment

According to the disease rating system described by Akhtar et al. (2010) suggested a disease rating scale from 0 to 6 with varying disease response i.e., highly resistant to highly susceptible for CLCuD were recorded. Severity index (SI) and responses of genotype were calculated using the formula mentioned below.

Statistical Analysis

Analysis of variance was carried out following Steel et al (1997). GCA and SCA value for both parents and hybrids were calculated using Kempthorne (1957) line x tester method.

3   RESULTS

An increase in productivity was an important goal in any breeding program. The study of genetic architecture plays a vital role as knowledge of genetic components

of yield-related traits was essential for the improvement of existing varieties as well as for the development of new varieties. The selection of genotypes with desirable traits was the basic step of breeding programs. Researchers uses combining ability analysis to identify good combiners. Combining ability analysis is very important because knowledge about the mean performance of genotype was not enough to indicate the best combiners. The Line × tester was used to estimate gene action. Mean performances and analysis of variance for various yield-related traits.

Plant Height (cm)

Plant height is a very important character in cotton, which varies from tall to dwarf. In upland cotton, genotypes with tall plant height face the problem of lodging that's why genotypes with negative and high combining ability values for plant height are considered best in upland cotton.
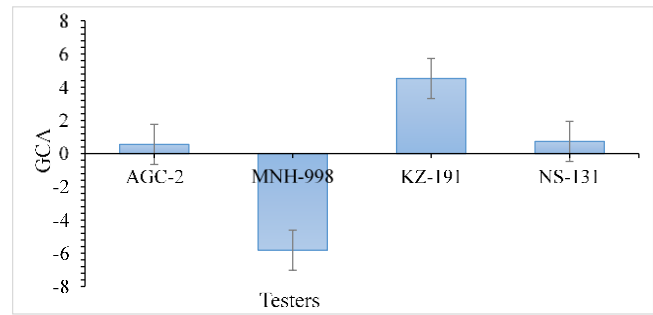
Due to significant differences among genotypes, these were further proceeded to check the variations for their combining abilities (ANOVA). Line × tester analysis of variance for plant height (Table 1) showed highly significant results for genotypes, lines (C), tester (C), crosses, LT (C), parents, and cross vs parents. It was found that the variance of GCA (0.50) was smaller than the variance of SCA (33.51) and the ratio of $(\sigma^2\text{GCA} / \sigma^{2'}\text{SCA})$ was smaller than unity (0.015) as shown in (Table 2). Non-additive gene mechanism was found responsible for controlling the plant height. Estimation of GCA and SCA effects among eight parents and their crosses for plant height were showed. Among lines CRS-2 (Fig. 1) showed significant GCA (-2.60) effects but in a negative direction indicated that it was good general combiner for plant height. Tarzen showed highly significant GCA (3.71) effects in a positive direction. Both Kehkashan and BS-80 showed non-significant GCA effects (-1.23) and (0.12) respectively for plant height. Among testers (Fig. 2) KZ-191 showed a highly significant GCA effect (4.52) in a positive direction. While MNH-998 showed highly significant GCA (-5.82) effects but in a negative direction. The other two testers, AGC-2 and NS-131 exhibited non-significant GCA effects (0.56) and (0.74) respectively (Table 2). The genotypes having negative and significant GCA values

Table 1: Analyses of variance of line × tester (including parents) for various traits in *Gossypium hirsutum* L.

SOURCE	DF	PH	NBP	SBP	MBP	DFF	DFB	SCY	CLCuD
Rep.	2	2.23	3.25	0.08	0.19	2.95	4.05	4.40	3.81
Genotypes	23	110.96**	86.3	3.8**	1.54**	43.17**	13.60**	147.20	431.04
Cross	15	132.66**	73.8	4.02**	1.32**	26.97**	11.74**	110.65	537.81
Line(C)	3	88.31**	108.03**	3.13**	0.77**	19.29**	10.95**	5.02	602.37
Test(C)	3	220.79**	75.7**	6.23**	1.76**	30.74**	1.75**	215.60	173.42
L X T (C)	9	118.07**	61.7**	3.58**	1.35**	28.27**	15.33**	110.88	637.76
Parent	7	48.41**	37.59	3.51**	2.07**	67.30**	17.97**	116.83	240.66
Cro vs par	1	223.38**	614.6**	2.16**	1.29**	117.27**	10.93	908.01	162.20

Table 2: Estimation of GCA variance (σ²GCA), SCA variance (σ²'SCA) and ratio of σ²GCA/ σ²SCA.

	GCA variance	SCA variance	GCA/SCA ratio	Additive variance	Dominance variance
PH	0.50	33.51	0.015	2.02	134.05
NBP	0.41	11.66	0.035	1.67	46.65
SBP	0.01	1.07	0.01	0.06	4.29
MBP	-0.0012	0.43	-0.002	-0.004	1.73
DFF	-0.045	8.75	35.01	-0.1809	35.0171
DFB	-0.1247	3.3534	0.03718	-0.4987	13.4136
SCY	-0.0079	28.9636	-0.00027	-0.0318	115.8544
CLCuD	-3.4704	211.50	-0.01	-13.881	846.022
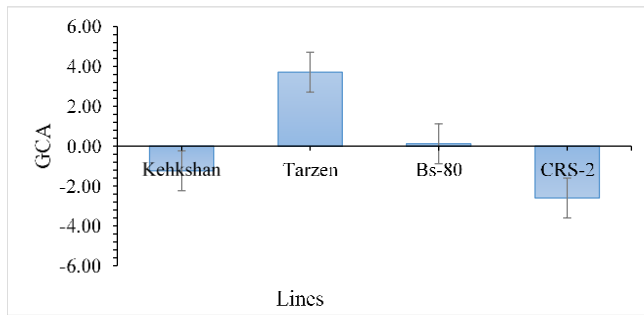
Fig. 1: Estimation of GCA effects of four lines of *Gossypium hirsutum* L. for plant height

Fig. 2: Estimation of GCA effects of four testers of *Gossypium hirsutum* L. for plant height.

can be used for variety development. Among cross combinations, BS-80 x MNH-998 showed highly significant SCA value (6.96) followed by Kehkashan x AGC-2 showed significant SCA (6.70) for plant height. Other crosses i.e., Tarzan x MNH-998 (-7.14) and kehkashan × NS-131(-6.08) and BS-80 × KZ-191 (-6.13) showed significant results in negative direction (Fig. 3). Line CRS-2, tester MNH-998 and cross Tarzan × MNH-998 can be exploited for reduction in height.

Number of Bolls per Plant

Due to significant differences among genotypes, these were further proceeded to check the variations for their combining abilities. The analysis revealed that number of bolls per plant showed highly significant results for genotypes, crosses, line (C), tester (C), LT (C), while parents showed non-significant results, as shown in (Table 4.2.1). The Cross Vs Parent showed highly significant results (Table 1).

In contrast to the GCA (11.66) variance, the SCA variance (11.66) was higher, suggesting that non-additive gene action was important for determining the number of bolls per plant inheritance. As indicated by the ratio between SCA and GCA (0.0351), dominant genes are responsible for controlling the trait, showed in (Table 2).

The performance of eight parents was studied to check out the general combining stability for number of bolls per plant. Among lines Tarzan showed highly significant GCA values (4.17) which indicated that it was a good general combiner for number of bolls per plant. The line Kehkashan (-0.69), BS-80 (-0.51) and CRS-2 (-2.98) showed non-significant GCA values in negative

direction which indicates that it was a poor general combiner for this trait as showed in (Fig. 4). Among testers, MNH-998 showed significant GCA value (-3.26) but in negative direction which indicated that it was not good general combiner for number of bolls per plant. There was a non-significant factor in the GCA value for KZ-191 (2.56), NS-131 (-0.51) and AGC-2 (1.21), which was an indication that they were poor general combiners as shown in (Fig. 5). Eight parents were analyzed in their cross combinations as shown in (Fig. 4.2.3). On the basis of cross combinations, CRS-2 × NS-131 showed maximum highly significant SCA value (-9.25) but in negative direction. Crosses like Kehkshan × AGC-2, Kehkshan × MNH-998, Kehkshan × KZ-191, Kehkshan × NS-131, Tarzen × AGC-2, Tarzen × MNH-998, Tarzen × KZ-191, Tarzen× NS-131, BS-80 × AGC-2, BS-80 × MNH-998, BS-80 × KZ-191, BS-80 × NS-131, CRS-2 × AGC-2, CRS-2 × MNH-998, CRS-2 × KZ-191 showed non-significant results which indicated that these crosses were very poor specific combiner for number of bolls per plant (Fig. 6).

Symodial Branches per Plant

Due to significant differences among genotypes, these were further proceeded to check the variations for their combining abilities. The results indicated that mean square of general combing ability (GCA) and specific combining ability (SCA) were highly significant (P<0.01). There were highly significant results in the analysis of variance of line testers for number of sympodials per plant for genotypes, crosses, lines, testers, parents, and cross-parental crosses as shown in (Table 1).

Based on the fact that SCA (1.0747) showed a greater variance than GCA (0.0153), it was concluded this trait is controlled by non-additive gene mechanism. According to the ratio GCA-SCA (4.2888), the dominant gene controlled sympodial numbers per plant showed in (Table 2).
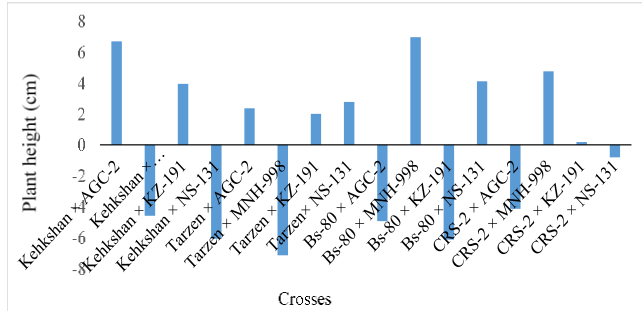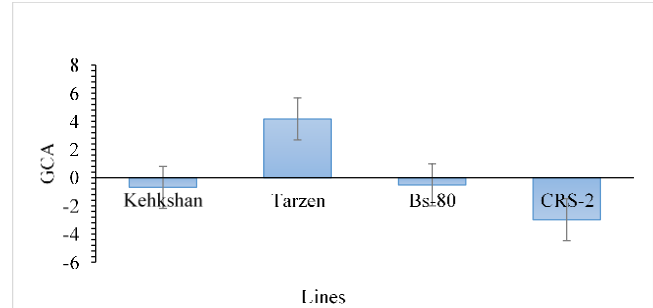
The performance of eight parents was studied to check out the general combining stability for a number of sympodial branches per plant. Among lines Tarzen displayed highly significant GCA values (0.58) in a positive direction, indicated it was very effective general

Fig. 3: SCA effects of sixteen crosses of *Gossypium hersutum* L. for plant height.

Fig. 4: Estimation of GCA effects of four lines of *Gossypium hirsutum* L. for number of bolls per plant.
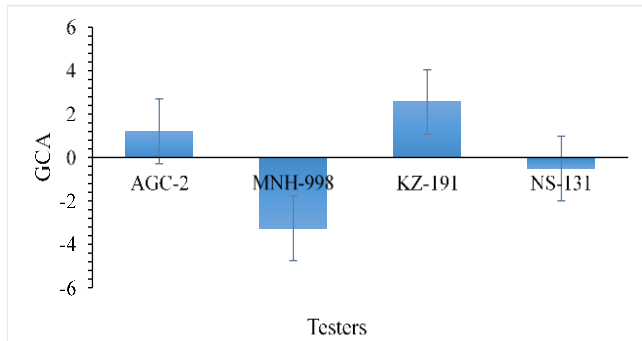
Fig. 5: Estimation of GCA effects of four testers of *Gossypium hirsutum* L. for number of bolls.
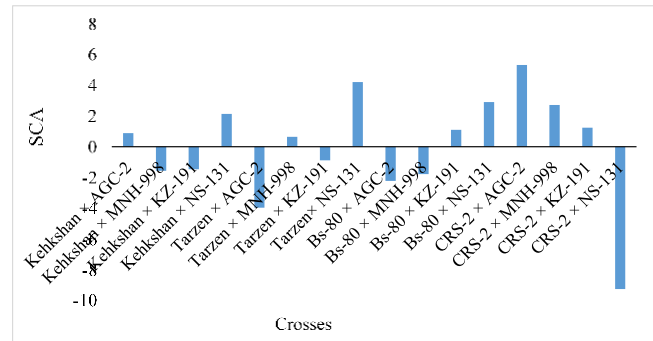
Fig. 6: SCA effects of sixteen crosses of *Gossypium hersutum* L. for number of bolls.
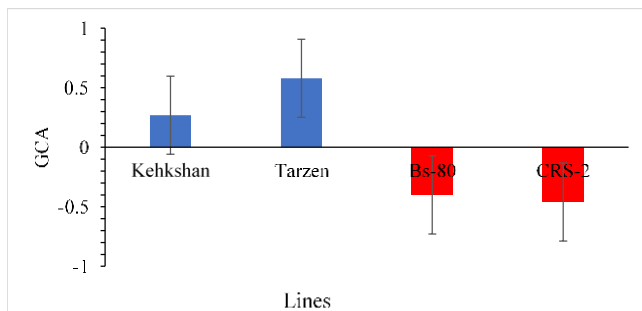
Fig. 7: Estimation of GCA effects of four lines of *Gossypium hirsutum* L. for sympodial branches.
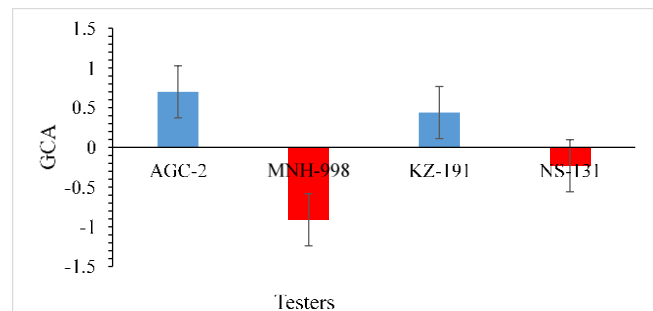
Fig. 8: Estimation of GCA effects of four testers of *Gossypium hirsutum* L. for sympodial branches.

combiner for the number of sympodials per plant. In contrast, line CRS-2 (-0.46) and BS-80 (-0.40) showed negative GCA values, which indicated that they performed poorly as general combiners for the number of sympodial branches per plant. Line Kehkshan showed non-significant result indicated that it was poor general combiner as (Fig. 7).

In comparison to other general combiners, AGC-2 showed a highly significant GCA value (0.71), which indicated that the it was a good general combiner in terms of the number of sympodia's per plant. Among testers, KZ-191 showed significant GCA value (0.44) while MNH-998 showed highly-significant GCA value (-0.91) but in a negative direction which indicated that it

was a poor general combiner. Among testers NS-131 showed non-significant GCA value (-0.23) as shown in (Fig. 8). The performance of eight parents were studied in their cross combinations as shown in Fig. 9. On the basis of cross combinations, CRS-2 × AGC-2 showed maximum highly significant SCA value (1.42) while CRS-2 × NS-131, Tarzen × AGC-2 and Kehkshan ×
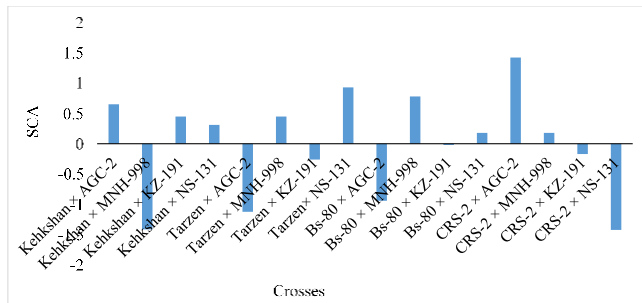

Fig. 9: SCA effects of sixteen crosses of *Gossypium hersutum* L. for sympodial branches.

negative direction indicated that it was poor specific combiner. Among crosses Kehkshan × AGC-2 (0.65), Kehkshan × KZ-191 (0.45), Kehkshan × NS-131 (0.31), Tarzen × MNH-998 (0.45), Tarzan × KZ-191 (-0.26), BS-80 × KZ-191 (0.02), BS-80 × NS-131(0.18), CRS-2 × MNH-998 (0.18), CRS-2 × KZ-191(-0.17) showed non-significant results.

Monopodial Branches per Plant

As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities.

Analysis of variance of line testers for number of monopodial branches per plant showed highly significant results for genotypes, crosses, line (C), tester (C), L x T (C), parents and crosses Vs parents as shown in (Table 1).

Variances of SCA (0.4348) and GCA (-0.0012) indicated a non-additive type of gene action that had an important role in inheritance of monopodial branches. It was found that the dominant gene (1.7391) was responsible for the number of monopodial branches per plant showed in (Table 2).

The performance of eight parents was studied to check out the general combining stability for a number of monopodial branches per plant. The CRS-2 showed highly significant GCA values (0.30) in positive direction. According to the GCA values for BS-80 (-030), showed the poor general combining ability for the number of sympodial branches per plant, as it showed high significant GCA values in a negative direction. The results for Kehkshan (-0.08) and Tarzen (0.08) revealed non-significant results indicating a poor general combiner (Fig. 10).

Among testers MNH-998 showed highly significant GCA value (0.42) which indicated that it was good

MNH-998 showed highly significant negative SCA values (-1.42), (-1.12) and (-0.41) respectively which indicated that these crosses were very poor specific combiners for number of sympodial branches per plant. Tarzen × NS-131(0.93) and BS-80 × MNH-998 (0.78) showed significant SCA value. Cross BS-80 × AGC-2(-0.94) showed significant result for SCA value but in general combiner for number of monopodial per plant. NS-131 showed highly significant GCA value (-0.47) but in a negative direction. While KZ-191 showed significant GCA value (0.17). Which indicated that it was a good general combiner. Among testers AGC-2 showed non-significant GCA value (-0.11) as showed in (Fig. 4.4.2). The performance of eight parents was studied in their cross combinations showed in (Fig. 11). On the basis of cross combinations, Kehkshan × KZ-191 showed maximum highly significant value SCA value (0.98) followed by Tarzen × AGC-2 (0.71), Kehkshan x NS-131 (0.42), CRS-2 × MNH-998 (0.41) and BS-80 × KZ-191(0.26). Crosses Kehkshan × MNH-998 ,Tarzen × KZ-191 , BS-80 × NS-131, CRS-2 × KZ-191, Kehkshan × AGC-2 showed highly significant negative SCA values (-0.74), (-0.78) ,(-0.49), (-0.47) and (-0.67) respectively. These crosses don't provide good specific combiners for monopodial branches per plant. Among crosses Tarzen × MNH-998 (0.17), CRS-2 × NS-131 (0.17), Tarzen× NS-131(-0.1), BS-80 × AGC-2 (0.08), BS-80 × MNH-998 (0.15) and CRS-2 × AGC-2(-0.12) showed non-significant SCA value (Fig. 12).

Days to First Flowering

As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities (Table 1).

SCA variance (8.7543) was greater than GCA variance (-0.0452), suggested non-additive gene action played a role in the inheritance of days to first flowering. The ratio between GCA and SCA showed the dominant gene (35.0171) that controlled the days to first flowering showed in (Table 2).

The performance of eight parents was studied to check out the general combining stability for days to first flowering. Among lines, Tarzen showed highly significant GCA values (1.73) in positive direction which indicated that it was a good general combiner for days to first flowering. The line Kehkshan (-1.32) showed highly significant GCA values in a negative direction which indicates that it was a poor general combiner for days to first flowering. Among lines BS-80 and CRS-2 showed non-significant GCA value (-0.19), (-0.22) respectively as shown in (Fig. 13).

Among testers AGC-2 showed highly significant GCA value (2.37). Among tester KZ-191 (-1.03) and NS-131 (-0.87) showed significant GCA value but in a negative direction showed these were the poor general combiner for days to first flowering as shown in (Fig.

4.5.2). The performance of eight parents was studied in their cross combinations as shown in (Fig. 14).

On the basis of cross combinations, cross CRS-2 × KZ-191 showed highly significant SCA value (3.91) followed by Tarzen× NS-131 (3.46), BS-80 × NS-131 (2.85). Among crosses CRS-2 × NS-131 (-4.01) showed highly significant SCA value (-4.01) but in negative direction followed by BS-80 × KZ-191 (-2.86), Kehkshan

× NS-131 (-2.29), CRS-2 × MNH-998 (-1.99) showed highly significant but negative SCA value. CRS-2 × MNH-998 (-1.99) showed significant but negative SCA value. Among crosses Tarzen × AGC-2 (-0.76), Tarzen × MNH-998 (-1.32), (Tarzen × KZ-191) (-1.38), BS-80 × AGC-2 (-1.2), BS-80 × MNH-998 (1.21), Kehkshan × KZ-191 (0.33) and Kehkshan × AGC-2 (-0.14) showed non-significant SCA value for days to first flowering (Fig. 15).
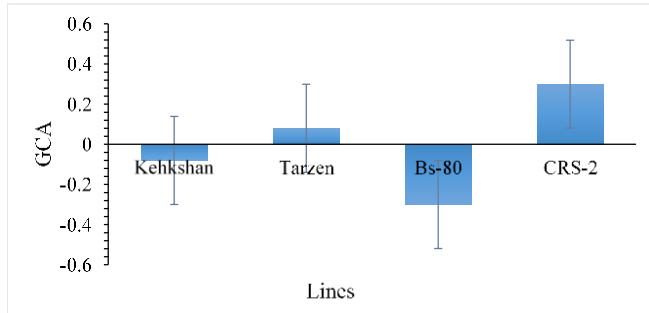
Fig. 10: Estimation of GCA effects of four lines of *Gossypium hirsutum* L. for monopodial branches.
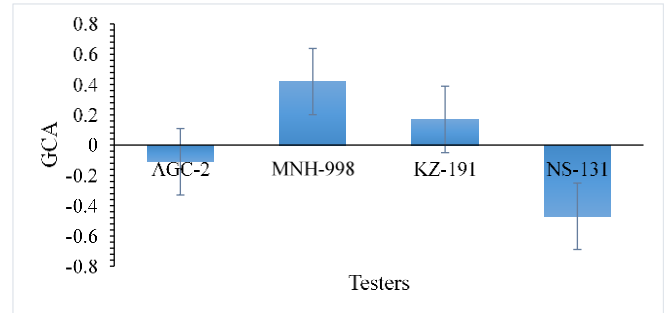
Fig. 11: Estimation of GCA effects of four testers of *Gossypium hirsutum* L. for monopodial branches.
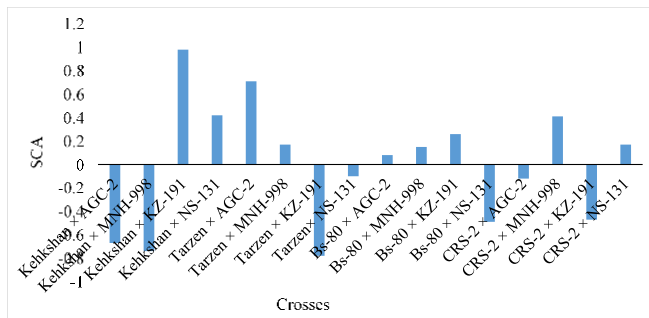

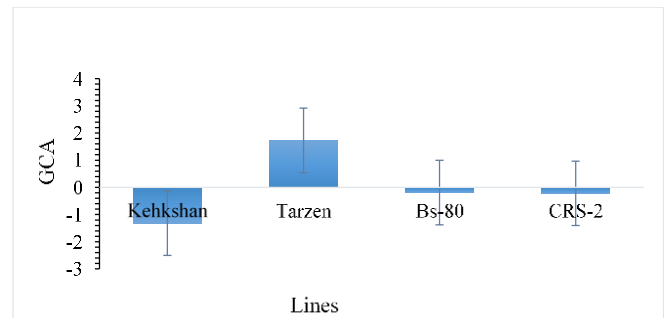**Fig. 12:** SCA effects of sixteen crosses of *Gossypium hersutum* L. for monopodial branches.

Fig. 13: Estimation of GCA effects of four lines of *Gossypium hirsutum* L. for days to first flowering.
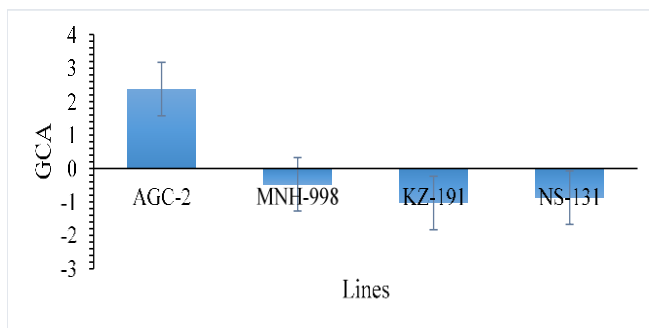

Fig. 14: Estimation of GCA effects of four testers of *Gossypium hirsutum* L. for days to first flowering.
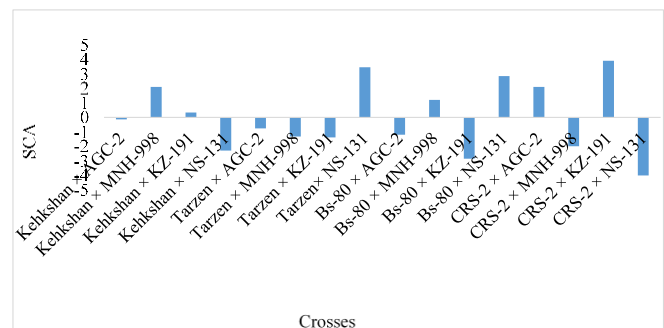

Fig. 15: SCA effects of sixteen crosses of *Gossypium hersutum* L. for days to first flowering.

Days to First Boll Opening

As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities.

Analysis of variance of line testers for days to first boll opening plant showed highly significant results for genotypes, crosses, L x T (C), parents and tester (C). Line (C), showed significant results. Crosses Vs parents showed non-significant results as showed in (Table 1).

A higher variance of SCA (3.3534) was observed than a variance of GCA (-0.1247), indicating that the non-additive nature of gene action played a significant role in inheritance. In the ratio of GCA to SCA, it was determined that days to first boll opening were affected by a dominant gene (-0.03718) as shown in (Table 2).

The performance of eight parents was studied to check out the general combining stability for days to first boll opening. Among lines BS-80 showed maximum GCA value (0.81) but non- significant results followed by Kehkshan (0.55), CRS-2 (-0.03) and Tarzen (-1.33) as shown in (Fig. 16).

Among testers MNH-998 showed maximum GCA value (0.42) but non-significant results followed by KZ-191(0.23), AGC-2 (-0.27) and NS-131(-0.37) as shown in (Fig. 17). The performance of eight parents was studied in their cross combinations as shown in (Fig. 4.6.3). On the basis of cross combinations Kehkshan × MNH-998 showed maximum significant SCA value (2.98) indicated that it was good specific combiner. Cross Kehkshan × AGC-2 showed significant SCA value (-2.8) but in a negative direction showed it was poor specific combiner for days to boll opening. Among crosses CRS-2 × AGC-2 (2.29), BS-80 × KZ-191(2.22), Tarzen × AGC-2 (1.96), Kehkshan × NS-131 (1.51), Tarzen × KZ-191 (0.72), BS-80 × MNH-998 (-0.01), CRS-2 × NS-131 (-0.08), Tarzen× NS-131 (-0.68), BS-80 × NS-131 (-0.75), CRS-2 × MNH-998 (-0.97), CRS-2 × KZ-191 (-1.24), BS-80 × AGC-2 (-1.45), Kehkshan × KZ-191 (-1.7) and Tarzen × MNH-998 showed minimum SCA value (-2). The proportional contribution of lines, testers and their interactions in total variability for days to first boll opening were 18.66, 2.99 and 78.35 respectively for days to first boll opening as shown in (Fig. 18).
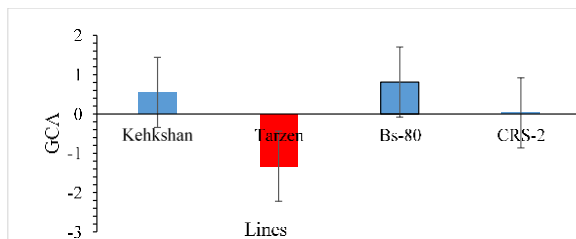

Fig. 16: Estimation of GCA effects of four lines of *Gossypium hirsutum* L. for days to first boll opening.
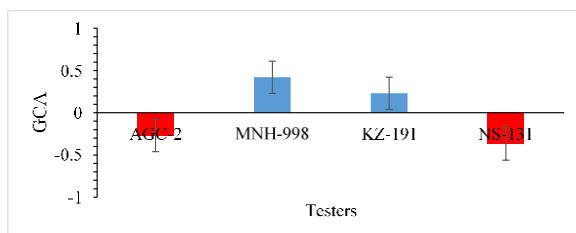

Fig. 17: Estimation of GCA effects of four testers of *Gossypium hirsutum* L. for days to first boll opening.
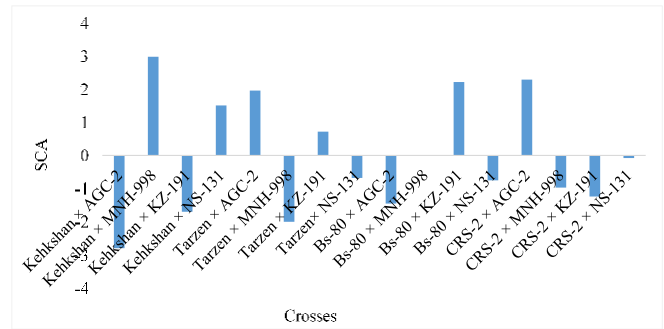

Fig. 18: SCA effects of four lines, four testers and of *Gossipium hersutum* L. for days to first boll opening.

Seed Cotton Yield (kg/ha)

As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities. Analysis of variance of line tester for ginning out percentage (Table 1) showed highly significant results for genotypes, crosses,), testers (C), parents and LT (C) and Crosses vs. Parents while Lines (C) showed non-significant results.

In this study, the variance of SCA (28.9636) was greater than the variance of GCA (-0.0079), and the ratio of GCA to SCA was lower than unity (-0.00027), indicated that this trait was influenced by a non-additive type of gene action (Table 2). All the lines showed non-significant GCA value for seed cotton yield as shown in (Fig. 19). Among testers KZ-191 showed maximum highly significant GCA values (4.75) while MNH-998 showed highly significant GCA value (-5.57) but in a negative direction indicated that it was poor general combiner for seed cotton yield (Fig. 20). The performance of eight parents was studied in their cross combinations shown in Fig. 21. Among crosses CRS-2 × MNH-998 showed maximum highly significant SCA value (9.98) while Kehkshan × AGC-2 showed significant SCA value (6.29). Among crosses CRS-2 × NS-131, Kehkshan × MNH-998 and Tarzen × MNH-998 showed significant SCA value but in a negative direction (5.92), (-5.79) and (-5.87) respectively (Fig. 21).

CLCuD Symptomatic Assessment

Based on the CLCuD symptomatic assessment and disease severity scale data were analyzed. Due to significant differences among genotypes, these were further proceeded to check the variations for their combining abilities (ANOVA).

Analysis of variance of line tester for CLCuD (Table 1) showed highly significant results for genotypes, parents, Line (C), testers (C), and LT (C) and Crosses Vs Parents. It was found that the variance of SCA (211.50) was greater than the variance of GCA (-

3.4704) and the ratio of a GCA/ SCA was smaller than unity (-0.01) as shown in (Table 2).

It's indicated that non-additive gene action was responsible for this trait. Among lines BS-80 and CRS-2 showed highly significant results (1.52) and (8.99) respectively indicated that these are good general combiners while Tarzen showed negative but significant results as shown in indicated that it can be utilized for

screening against CLCuD resistance as shown in Fig. 22. Among testers NS-131 and KZ-191 showed highly significant results (2.17) and (4.22) respectively while MNH-998 showed significant but negative values (-3.66) indicated that it can be used in the future breeding for CLCuD. The performance of eight parents were studied in their cross combinations as shown in (Fig. 23).
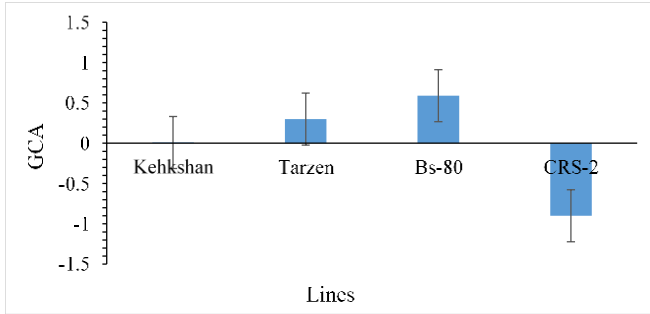

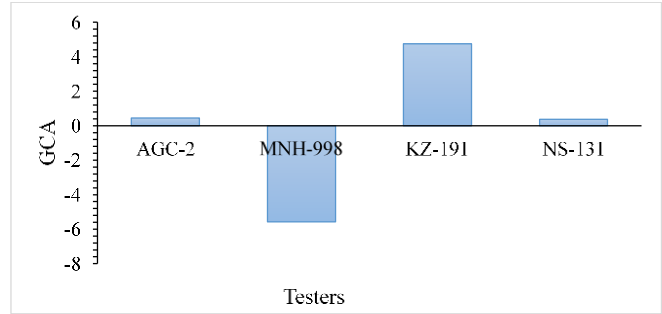**Fig. 19:** GCA effects of four lines of *Gossypium hersutum* L. for Seed cotton yield.

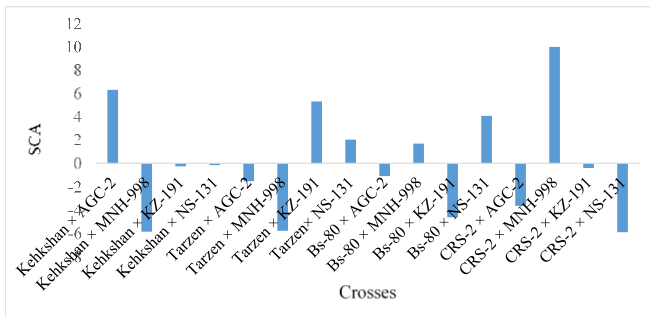**Fig. 20:** GCA effects of four testers of *Gossypium hersutum* L. for Seed cotton yield.

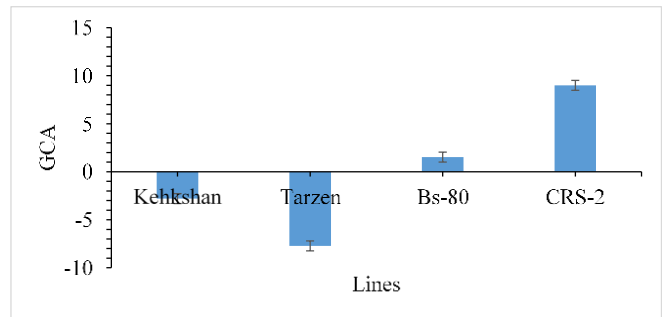**Fig. 21:** SCA effects of sixteen crosses of *Gossypium hersutum* L. for Seed cotton yield.

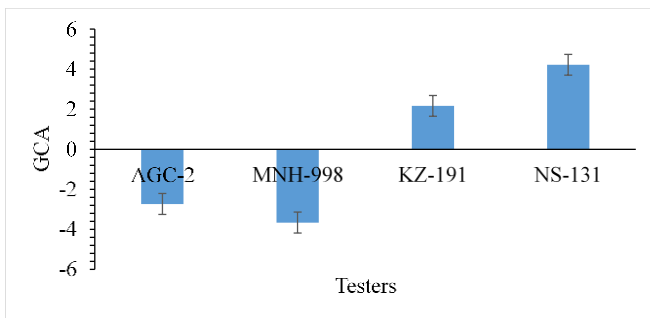**Fig. 22:** GCA effects of four lines of *Gossypium hersutum* L. for CLCuD.

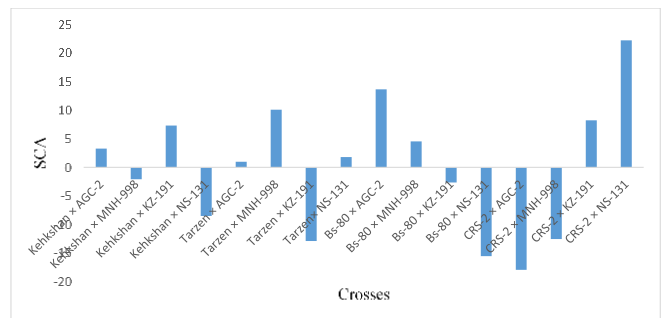**Fig. 23:** GCA effects of four testers of *Gossypium hersutum* L. for CLCuD.

Fig. 24: SCA effects of sixteen crosses of *Gossypium hersutum* L. for CLCuD.

Among crosses Kehkshan × AGC-2, Kehkshan × KZ-191, Tarzen × MNH-998, Bs-80 × AGC-2, Bs-80 × MNH-998, CRS-2 × KZ-191, CRS-2 × NS-131 showed highly significant positive values (3.29),(7.33),(10.11),(13.66),(4.53) (8.23) and (22.26) while Kehkshan × NS-131, Tarzen × KZ-191, Bs-80 ×

KZ-191, Bs-80 × NS-131, CRS-2 × AGC-2, and CRS-2 × MNH-998 showed highly significant but negative value indicated that these crosses may be utilized for screening against CLCuD (Fig. 24).

4 | DISCUSSION

Different characters contain genetic variation in various forms having useful information that aids in breeding population selection. Natural selection, which modifies plant features genetically, is a key factor in the development of genetic variation in phenotypes. Significant differences can be seen between parental traits and their progenies in traits like boll weight, number of nodes first for effective boll formation, number of monopodial branches, number of sympodial branches, no of bolls per plant. Kempthorne, 1957 divided the genetic variability into two categories: general combining ability (GCA) and specific combining ability (SCA), which make it easier to understand how genes influence character. Combining ability studies is a helpful tool for choosing parental lines in hybrid development. (Neelima et al. 2004; Chattha et al., 2019; Manan et al. 2022) identified six parents for various cotton characteristics 'based on general combining ability.

According to the findings of present research, among lines CRS-2 showed significant GCA effects for plant height, number of sympodial branches per plant and boll weight while line Tarzen showed highly significant GCA effect for plant height and number of bolls. Both lines Kehkashan and BS-80 showed significant GCA for number of bolls per plant.

Among testers KZ-191 showed a highly significant GCA effect for seed cotton yield, boll weight while tester MNH-998 showed highly significant GCA effects for number of bolls per plant, ginning out turn and sympodial branches. The tester AGC-2 proved good general combiner for number of sympodial per plant. Munir et al. (2016) reported the same results that parents proved to be good general combiners. Both type of combining abilities affect found the responsible for inheritance pattern of some economically important parameters of upland cotton (Wankhade et al. 2008; Chattha et al., 2018). Among crosses Kehkashan x AGC-2 showed significant SCA for plant height, boll weight and kehkashan x NS-131 for plant height. Other crosses CRS-2 × AGC-2 showed significant SCA for sympodial branches while Kehkshan × KZ-191 showed significant SCA for monopodial branches per plant. Cross Kehkshan × MNH-998 for days to first boll opening. Cross CRS-2 × MNH-998 showed significant SCA for seed cotton yield.

So it is cleared from above findings that parents with low combining ability can produce desirable hybrids for specific yield related traits same as findings of Solongi et al. (2019), and Khan and Qasim (2012).

It was found that gene action controlled plant height in a non-additive manner similar findings were shown by (Shaukat et al. 2013). Number of bolls per plant are controlled by the predominately non-additive gene action same as showed by Khokhar et al. (2017). Number of sympodial branches per plant was controlled non-additively confirmed by the Lakho et al. (2016). Gene action was found to be dominant for seed cotton in a non-additive manner this confirms the results found by Shaukat et al. (2013) and Raza et al. (2013). Genetic analysis based on the disease severity scale of cotton genotypes is done for resistance to cotton leaf curl disease complex same as the research done by Farooq et al. (2014) and Akhtar et al. (2010).

Conclusion

So, the experiment was conducted to perform genetic analysis for seed cotton yield and CLCuD resistance in upland cotton. Among crosses Kehkshan × NS-131, Tarzen × KZ-191, Bs-80 × KZ-191, Bs-80 × NS-131, CRS-2 × AGC-2, and CRS-2 × MNH-998 showed highly significant but negative values for CLCuD resistance indicated that these crosses may be utilized for screening against CLCuD. All the characters showed that SCA variances were greater then GCA variances, which indicated the additive gene action.All these crosses can be used in future hybrid development program.

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