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RESEARCH ARTICLE

Genetic Analysis in Upland Cotton for Fiber Quality Parameters

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ABSTRACT

Cotton is a major industrial fiber crop that is extensively grown worldwide and has a big impact on the political and socioeconomic problems that many nations face. That's why there is a dire need to develop cotton varieties with high fiber quality. The study will determine the combining ability effects of parental lines and crosses in upland cotton (*Gossypium hirsutum* L.) using line × tester mating design. The four lines Kehkashan, Tarzen, BS-80, CRS-2, and four testers MNH-998, NS-131, AGC-2, and KZ-191 were crossed in line tester fashion to study the genetic analysis of different fiber quality traits in cotton. Four lines were crossed with four testers at the time of flowering in line × tester design in the glass house. Eight parents and 16 crosses (F1) were grown in the field with three replications using a randomized complete block design. A significant GCA result was observed for Kehkashan and BS-80, showing that both lines combine well for fiber strength. Among testers, KZ-191 showed a highly significant GCA effect for fiber fineness, while MNH-998 showed highly significant GCA effects for fiber strength and fiber elongation. Tester NS-131 emerged as a good general combiner for fiber maturity and fiber elongation. The results showed that germplasm has the potential for the development of cotton varieties, and may be used in cotton breeding programs.

Key words: Fiber quality traits, cotton, genetic diversity, combining ability

INTRODUCTION

Cotton is mostly grown for its fiber, which yields a profit for the farmer, but it is also planted for its seeds (Kamal et al., 2024). Therefore, without sacrificing yield or quality, it is necessary to raise lint yield, enhance fiber quality, or lower input costs to make cotton production more economically sustainable (Zafar et al., 2022a). In upland cotton, breeding initiatives are crucial to the genetic enhancement of lint yield and fiber quality. Elite breeding lines generated by crossing create progeny lines with a variety of yield and fiber quality attributes that can be used to drive genetic yield improvement (Zafar et al., 2024a). Breeders have addressed a variety of yield components to boost upland cotton production. Breeders must have a thorough understanding of the link between lint yield and other yield components to pick favorable qualities for future improvement (Zafar et al., 2024b; Farooq et al., 2023). Seed-cotton yield correlated positively with plant height, number of bolls, and number of monopodial branches per plant (Chattha et al., 2021). There is a need to devote more time to understanding the inheritance of these yield-contributing features to increase seed cotton yield (Zafar et al., 2023a). Other plant characteristics such as days to flowering and days to maturity are critical in short-duration breeding efforts. Combining ability is classified into two types: general combining ability and specific combining ability. General combining ability (GCA) refers to the average genotypic performance in a cross matrix, whereas specialized combining ability (SCA) refers to individual hybrids that outperform hybrid combinations (Sajjad et al., 2016).

SCA has a vital role in hybrid development but GCA has an advantageous role in the selection of suitable parental genotypes for hybridization programs and performance of GCA is caused by the additive genes of parental lines whereas the performance of SCA exhibited by the novel genes that may have dominant or epistatic effects (Zafar et al., 2022b).

Several lines or testers are used to estimate the GCA and SCA of genotypes and their cross combinations, respectively. The 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 (Manan et al., 2022).

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All the cotton breeders have the primary objective to create new varieties with superior yield and fiber quality. A successful breeding program starts with the selection of suitable parents. A systematic method for selecting the best parents and crosses for the trait under study is Line \times Tester analysis. This mating design is mostly used for determining the GCA and SCA of parents and crosses. Information on GCA and SCA effects on plants and crosses is important before starting the breeding program (Ashokkumar et al., 2010; Sahar et al., 2021).

The objective of the present study is to determine the GCA and SCA effects of the parental lines and crosses for fiber quality traits.

MATERIALS AND METHODS

The Department of Plant Breeding and Genetics provided the plant material used in the study. Four lines (Kehkashan, Tarzen, BS-80, CRS-2) and four testers (MNH-998, NS-131, AGC-2, KZ-191) made up the experimental material that was sown in a glasshouse to create the F₀ generation. Every genotype was raised under ideal conditions. The seeds were planted in ceramic pots. In the line × tester design, four lines were crossed with four testers at the time of flowering. There were eight parents and sixteen crosses raised 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 precautionary 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.

Fiber Characteristics

A computerized high-volume instrument developed by Uster Spinlab Company model number HVI 900, which was used to measure fiber fineness (g/in), fiber length (mm) and fiber strength (g/tex), Fiber elongation, fiber maturity and uniformity index.

Statistical Analysis

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

RESULTS

Improving fiber quality traits was an important goal of a cotton 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 use combining ability analysis to identify good combiners. Combining ability analysis is very important because knowledge about the mean performance of the 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 yieldrelated traits.

Fiber Length (mm)

The results of the ANOVA showed that the genotypic differences between eight parents and sixteen crosses were significant (P-value 0.01) when the fiber length was calculated. 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 fiber length showed highly significant results for genotypes, LT (C), and parents while cross showed significant results. Line (C), Testers (C), and) and Crosses Vs Parents showed non-significant results (Table 1).

Table 1: MS values line x tester for fiber quality traits in cotton

SOURCE	DF	FL	FS	FF	FU	FM	FE
Rep.	2	2.93	6.25	0.07	0.18	0.001	0.09
Genotypes	23	7.52	18.78**	0.45**	6.49**	0.002**	1.09**
Cross	15	5.48**	23.1**	0.5**	4.47	0.002	0.8**
Line(C)	3	0.71	36.13**	0.52**	2.66	0.004**	0.061
Test(C)	3	0.66	22.37**	0.74**	3.01	0.004	1.51**
LXT(C)	9	8.68**	18.99**	0.42**	5.56	0.001	0.81**
Parent	7	12.25**	11.61**	0.34**	11.34	0.002	1.83**
Cro vs par	1	5.1	4.27	0.38	2.86	0.002	0.16
Error	46	2.25	5.65	0.1	2.97	0.001	0.23
*Significant at 5% probability " **significant at 1% probability							

*Significant at 5% probability," **significant at 1% probability, ^{ns} non-significant

Non-additive gene is responsible for controlling the fiber length, and the variance of the SCA (2.0186) was greater than the variance of the GCA (-0.1110), and the proportion of GCA/SCA ratio was smaller than the unity (-0.0549) as shown in (Table 2). This means that SCA is in charge of controlling fiber length via a non-additive gene mechanism. All the lines Kehkshan, Tarzan, BS-80, and CRS-2 showed non-significant GCA values 0.1, 0.27, 0.06, and -0.32 respectively (Fig. 1). All the testers showed AGC-2 (-0.26), MNH-998 (0.02), KZ-191 (0.31) and NS-131 (-0.06) showed non-significant GCA values as shown in (Fig. 2). The performance of eight parents was studied in their cross combinations as shown in (Fig. 4.12.3). Among crosses, Tarzen × KZ-191, BS-80 × AGC-2 and CRS-2 × MNH-998 showed significant SCA values 2.51, 2.15 and 2.06 respectively. Among crosses, Tarzen × MNH-998 showed a significant SCA value (-2.08) but in a negative direction indicating that it was a poor specific combiner. All other crosses showed nonsignificant SCA values as shown in (Fig. 3).

Fiber Strength (g/tex)

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

Table 2: Estimation of GCA variance (σ^2 GCA), SCA variance (σ^2 'SCA) and ratio of σ^2 GCA/ σ^2 SCA.

	GCA variance	SCA variance	GCA/SCA ratio	Additive variance
FL	-0.111	2.0186	-0.0549	-0.4441
FS	0.1424	4.6947	0.03	0.5696
FF	0.003	0.1064	0.028	0.0118
FU	-0.0379	0.9611	-0.039	-0.1516
FM	0.0002	-0.0001	-0.5	0.0002
FE	-0.0003	0.1832	-0.0016	-0.0014



Fig. 1: GCA effects of four lines in Gossypium hersutum L. for fiber length.



Fig. 2: GCA effects of four testers of Gossypium hersutum L. for fiber length.



Fig. 3: SCA effects of sixteen crosses of Gossypium hersutum L. for fiber length.



Fig. 4: GCA effects of four lines of Gossypium hersutum L. for fiber strength.

Analysis of variance of line tester for fiber strength (Table 1) showed highly significant results for genotypes, cross, Testers (C), Line (C), LT (C), and parents while Crosses vs. parents showed non-significant results.

The variance of SCA (46.5977) was greater than the variance of GCA (0.1424) and the ratio of GCA/SCA was smaller than unity (0.030). Based on the results as shown in (Table 2), it appears that fiber strength is governed by a non-additive gene action process. Among lines, the maximum highly significant GCA value (1.77) was shown by line BS-80 while line Tarzen showed a significant GCA value but in a negative direction indicating that it was a poor general combiner (Fig. 4.). Among testers, MNH-998 showed a highly significant GCA value (1.86) while all other testers AGC-2, KZ-191 and

NS-131 showed non -significant GCA values (-0.92), (0.18) and (-1.13) respectively as shown in Fig. 5.

The performance of eight parents was studied in their cross combinations as shown in Fig. 6. Among crosses, Tarzen × KZ-191 showed a highly significant SCA value (3.93) while Kehkshan × MNH-998 showed a significant SCA value (2.75).

Fiber Fineness (µg/inch)

The results of the ANOVA showed that the genotypic differences between eight parents and sixteen crosses were significant (P-value 0.01) when the fiber fineness was calculated. 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 fiber fineness (Table 1) showed highly significant results for genotypes, cross, Testers (C), Line (C), LT (C), and parents while Crosses vs. parents showed non-significant results.

It was found that the variance of SCA (0.1064) was greater than the variance of GCA (0.0030) and the ratio of a GCA/ SCA was smaller than unity (0.028). Based on these results, it was believed that fiber fineness was controlled by a type of non-additive gene action as shown in (Table 2).

Among lines, Tarzen showed a highly significant GCA value was (0.03) while Kehkshan, BS-80, and CRS-2 showed non-significant GCA values (-0.14), (-0.03) and (-0.14) respectively as shown in (Fig. 7). Among testers, MNH-998 showed significant GCA Value (-0.32) but in the negative direction indicated that it was a poor general combiner for fiber fineness as shown in (Fig. 8). Among crosses BS-80 × MNH-998 showed a highly significant SCA value (0.59) indicating that it was a good specific combiner for fiber fineness while the cross Kehkshan × KZ-191 showed a significant SCA value (0.43). The cross BS-80 × KZ-191 showed a significant SCA value (-0.44) but in the negative direction, while all other crosses showed non-significant SCA values as shown in (Fig. 9).



Fig. 5: GCA effects of four testers of Gossypium hersutum L. for fiber strength.



Fig. 6: SCA effects of sixteen crosses of Gossypium hersutum L. for fiber strength.



Fig. 7: GCA effects of four lines of Gossypium hersutum L. for fiber fineness.



Fig. 8: GCA effects of four testers of Gossypium hersutum L. for fiber fineness.

Uniformity Index

The results of the ANOVA showed that the genotypic differences between eight parents and sixteen crosses were significant (P-value 0.01) when the uniformity index was calculated. As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities, using ANOVA.



Fig. 9: SCA effects of sixteen crosses of Gossypium hersutum L. for fiber fineness.

Analysis of variance of line tester for uniformity index (Table 1) showed highly significant results for parents while genotype showed significant results. Cross, Testers (C), Line (C), LT (C), Crosses vs Parents showed non-significant results.

It was found that the variance of SCA (0.9611) was greater than the variance of GCA (-0.0379) and the ratio of a GCA to SCA was smaller than unity (0.039) as shown in (Table 4.16.2). It was indicated that the uniformity index was controlled by a non-additive type of gene action (Table 2). All the lines Kehkshan, Tarzen, BS-80, And CRS-2 showed non-significant results for GCA value (0.29), (-0.33), (0.51), and (-0.47) respectively as shown in (Fig. 10). All the testers AGC-2, MNH-998, KZ-191, and NS-131 showed non-significant GCA values 0.41, 0.06, 0.34 and -0.69 respectively for uniformity index as shown in (Fig. 11).

Based on the cross combinations as shown in (Fig. 4.16.3) the performance of eight parents was examined. Among crosses, Tarzen × AGC-2 (1.99) showed a significant SCA value for the uniformity index. All other crosses showed non-significant SCA values.

The proportional contribution of lines, testers and their interactions in total variability were 11.91, 13.47 and 74.62 respectively for the uniformity index as shown in (Fig. 12).

Fiber Maturity

The results of the ANOVA showed that the genotypic differences between eight parents and sixteen crosses were significant (P-value 0.01) when fiber maturity was calculated. As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities, using ANOVA.

Analysis of variance of line tester for fiber maturity (Table 1) showed highly significant results for Line (C) while genotypes showed significant results. Parents, Cross, Testers (C), LT (C), Crosses vs Parents showed non-significant results.

It was found that the variance of GCA (0.0002) was greater than the variance of SCA (-0.0001) and the ratio of a GCA/SCA was smaller than unity (-0.50) as shown in (Table 2). It was indicated that the uniformity index was controlled by an additive type of gene action (Table 2). All the lines Kehkshan, Tarzen,

BS-80 and CRS-2 showed non-significant GCA values (0.02), (0.01) (-0.002), and (0.02) respectively as shown in (Fig. 13). Among testers, NS-131 showed a significant GCA value for fiber maturity (0.01) as shown in (Fig. 14). All the crosses showed non-significant SCA values for maturity (Fig. 15).



Fig. 10: GCA effects of four lines of Gossypium hersutum L. for uniformity index.



Fig. 11: GCA effects of four testers of Gossypium *hirsutism* L. for uniformity index.



Fig. 12: SCA effects of sixteen crosses of Gossypium hirsutism L. for uniformity index.



Fig. 13: GCA effects of four lines of Gossypium hersutum L. for fiber maturity.



Fig. 14: GCA effects of four testers of Gossypium hersutum L. for fiber maturity.



Fig. 15: SCA effects of sixteen crosses of Gossypium hirsutism L. for fiber maturity.

Fiber Elongation

The results of the ANOVA showed that the genotypic differences between eight parents and sixteen crosses were significant (P-value 0.01) when the fiber elongation was calculated. As a result of the observed significant differences among genotypes, further investigations were conducted to assess their combining abilities, using ANOVA.

Analysis of variance of line tester for fiber elongation (Table 1) showed highly significant results for genotype parents, Cross, Testers (C), and LT (C) while Line (C), Crosses vs Parents) showed nonsignificant results.

It was found that the variance of SCA (0.1832) was greater than the variance of GCA (-0.0003) and the ratio of a GCA/ SCA was smaller than unity (-0.0016) as shown in (Table 2). Gene action-controlled fiber elongation by a non-additive mechanism.

All lines Kehkshan, Tarzen, BS-80, and CRS-2 showed non-significant GCA values for fiber elongation (Fig. 16). Among testers, MNH-998 showed a significant GCA value indicating that it was a good general combiner while NS-131 showed a highly significant GCA value (-0.42) but in the negative direction indicating that it was a poor general combiner (Fig. 17).

A study of eight parents was conducted in their cross combinations, as shown in (Fig. 4.18.3). Among crosses, CRS-2 × NS-131 and CRS-2 × MNH-998 showed significant SCA values (0.63) and (0.61) respectively. The cross CRS-2 × AGC-2 showed a significant SCA value but in a negative direction (-0.72) indicating that it was a poor specific combiner for fiber elongation. All other crosses showed non-significant SCA values (Fig. 18).



Fig. 16: GCA effects of four lines of Gossypium hersutum L. for fiber elongation.



Fig. 17: GCA effects of four testers of Gossypium hersutum L. for fiber elongation.



Fig. 18: SCA effects of sixteen crosses of Gossypium hersutum L. for fiber elongation.

DISCUSSION

Cotton is the primary source of the most valuable textile fiber, and belongs to the Malvaceae family and the genus Gossypium. Cotton (Gossypium hirsutum L.), the king of fibers, is a significant cash crop that profoundly impacts the world's economy and social affairs (Zafar et al., 2021; Zafar et al., 2023b). Significant differences can be seen between parental traits and their progenies in traits like uniformity ratio, fiber strength, and elongation, fiber fineness, and staple length, (Kempthorne, 1957). Combining ability studies is a helpful tool for choosing parental lines in hybrid development. (Neelima et al. 2004) identified six parents for various cotton characteristics 'based on general combining ability. According to the findings of my research, lines Kehkashan and BS-80 showed significant GCA for the fiber strength. Among testers, KZ-191 showed a highly significant GCA effect for fiber fineness while tester MNH-998 showed highly significant GCA effects for fiber strength and fiber elongation. Tester NS-131 showed significant GCA for fiber maturity and fiber elongation. Munir et al. (2018) reported the same results that parents proved to be good general combiners. Both types of combining abilities are the responsible inheritance pattern of some economically important parameters of upland cotton (Wankhade et al. 2008). The parents having good general combiner for specific traits proved to be high yielders in cross combinations. Cross CRS-2 × NS-131 for fiber elongation. Tarzen × AGC-2, for uniformity index. Tarzen × KZ-191, BS-80 × AGC-2 for fiber length fiber strength, Kehkshan × MNH-998 showed significant SCA for fiber strength, fiber elongation cross BS-80 × MNH-998 for fiber fineness, and CRS-2 × MNH-998 for fiber elongation. So it is clear from the 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), Patel et al. (2011) Shakeel et al. (2011) and Khan and Qasim (2012).

Fiber length was also controlled by non-additive genes which confirm the results of Isong et al. (2019) and (Sarwar et al., 2011). For fineness, non-additive genetic effects were more important same as the findings of Khan et al. (2017) and Shaukat et al. (2013). Research findings indicated that fiber strength was predominately controlled by the non-additive gene action which was also confirmed by the previous findings by Karademir et al. (2010), Ilyas et al. (2010) and (Vekariya et al., 2017). Fiber uniformity is controlled by dominant gene action, the same as the findings of Senthilkumar et al. (2010) and Patil et al. (2011).

Eight parents were selected for genetic analysis of yield-related traits such as seed index, lint index, and fiber length. Results indicated that the variances of seed index, lint index, and fiber length were higher for specific combining ability than for general combining ability. Results revealed that significant specific combining ability effects were found between genetically diverse parents same as shown by Khan et al. (2017).

Conclusion

All the characters showed that SCA variances were greater than GCA variances except fiber maturity index which is controlled by the additive gene action. These crosses can be used in future hybrid development programs. Parents having good general combining ability for specific traits are supposed to be used in future breeding programs for the improvement of these traits.

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