ESTIMATING GENE ACTION AND COMBINING ABILITY FOR YIELD AND FIBER QUALITY IN COTTON (*Gossypium hirsutum* L.)

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Genetic evaluation of segregating populations is one of the primary activities of cotton breeders. Seven cotton genotypes were crossed in a line × tester mating design. The population of 12 F_1, 12 F_2 and their parents were tested in Randomized Complete Block Design with three replications at the Nazilli Cotton Research Institute of Türkiye during the 2014/2015 cotton-growing season. The genetic variability was significant for all characters studied. σ^2GCA / σ^2SCA indicated non-additive gene action in controlling seed cotton yield (F_2), ginning out-turn (F_1) and fiber quality traits for both generations. The highly favourable GCA effects for seed cotton yield and fiber strength were recorded in the Carmen cultivar. Carmen × Carisma hybrid exhibited high mean performance and SCA effects for seed cotton yield and fiber strength, while the performance of Gloria × ST-468 was superior in terms of ginning out-turn. We concluded that individual plants with desired traits should be selected in later generations due to the preponderance of non-additive gene actions.

Keywords: Fiber characteristics, GCA, ginning out-turn, line x tester, SCA

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INTRODUCTION

One of the main objectives of cotton breeding is to develop high-yielding cultivars by crossing genotypes with good general combining ability in terms of seed cotton yield and fiber quality and selecting promising combinations from segregating populations (AKBAR *et al.*, 2009). In other words, the success of conventional cotton breeding is based on the crossing among suitable parents, advanced genetic lines for desirable traits, and their genetic background (BOURLAND and MYERS, 2015). Many breeding studies targeting high yields have used indirect selection through yield-related attributes with high heritability. Cotton cultivars with high fiber quality need to be developed to sustain long-term cotton production for greater marketability and price.

Line × tester analysis is a modified form of a top cross by KEMPTHORNE (1957) for measuring the combining ability effects of parents and crosses and estimating gene actions of selection criteria in crop breeding (JAIN and SASTRY, 2012; RASHID *et al.*, 2013). The ratio of general and specific combining ability variance ($\sigma^2 GCA / \sigma^2 SCA$) helps estimate gene action for quantitative traits in line × tester analysis. GCA and SCA components are mainly functions of additive and dominance gene action, respectively. Previous studies using line × tester analysis in upland cotton, non-additive type of gene action for seed cotton yield and ginning out-turn was reported by SAJJAD and MALOOK (2016), SIVIA *et al.* (2017) and ROY *et al.* (2018), whereas MENDEZ-NATERA *et al.* (2012) and PRAKASH *et al.* (2018) emphasized that there is an additive gene effect. Fiber fineness, fiber length and fiber strength were controlled by non-additive gene effect according to AHUJA and DHAYAL (2007), ASHOKKUMAR *et al.* (2010), SAJJAD and MALOOK (2016), COBAN and UNAY (2017). In another study, YEHIA and EL-HASHASH (2019) explained the importance of both additive and non-additive gene actions in controlling fiber quality parameters.

Biometric analysis such as line × tester and diallel methods can be used to select the best combiners for the desired traits. For this, the parents are evaluated according to the performance of the progeny (FASAHAT *et al.*, 2016). Furthermore, estimating specific combining ability (SCA) effects allows selection superior cross combinations in developing commercial hybrids (SAMREEN *et al.*, 2008). In previous studies using the line × tester mating design, combining abilities were tested for yield, yield components and fiber quality to estimate the performance of parents and hybrid combinations in cotton (LUKONGE *et al.*, 2008; ASHOKKUMAR, 2010; MAKHDOOM *et al.*, 2019).

According to the line tester and diallel analysis methods, there are a large number of studies in which heritability, combining abilities and heterotic effects are usually performed in the F_1 generation. However, the number of studies involving parents, F_1 and F_2 populations is limited. Therefore, the present study was planned to determine the inheritance, combining abilities and heterotic effects for the traits studied in F_1 and F_2 hybrid populations of cotton (*Gossypium hirsutum* L.)

MATERIAL AND METHODS

Especially four genotypes with superior fiber colour grade, Gloria, Claudia, Carmen and Julia were used as lines, while Stoneville-468 (ST-468), Carisma and Flash were selected as testers. All parents are commercial cultivars with high-yielding and superior fiber quality, which have large cultivation areas in the Aegean Region of Turkey. The seven parents were crossed to

generate 12 F_1 hybrids by line × tester mating design. Thirty-one genotypes consisting of F_1, F_2 and parents were sown in a Randomized Complete Block Design with three replications. The study was conducted in Nazilli Cotton Research Institute in 2015 cotton growing season. Each plot comprised a single row of 12 m length with space of 0.7 m between rows and seeds were planted 0.2 m apart. Agricultural practices, fertilization, irrigation, hoeing and plant protection recommended for cotton cultivation in the Aegean region were managed. We randomly sampled 20 plants from each plot at harvest time, and data were recorded for the seed cotton yield per plant (g) and ginning out-turn (%). Fiber fineness (micronaire), fiber length (mm), and fiber strength (g tex^{-1}) were determined by HVI analysis.

The estimation of general and specific combining abilities, including the variance and its contribution effects, was performed by Line × Tester analysis (SINGH and CHAUDHARY, 1979) in TARPOPGEN Software (OZCAN and ACIKGOZ, 1999). The significance of combining ability effects was performed using a t-test. The mean of genotypes was separately compared using the LSD test at a 5% probability level (STEEL *et al.*, 1997).

RESULTS AND DISCUSSION

The significant genotypic differences indicated that there was sufficient genetic variability for all observed traits in both generations. Therefore, line × tester analysis was performed to estimate gene action, GCA and SCA variances and combining abilities for all traits (Table 1). The mean square of the line for seed cotton yield (F_1), ginning out-turn (F_1 and F_2), fiber fineness (F_1) and fiber strength (F_1) was significant. Similarly, the mean square of tester for ginning out-turn (F_1 and F_2), fiber fineness (F_2) and mean squares of line × tester ginning out-turn (F_2), fiber length (F_1), fiber fineness (F_1) and fiber strength (F_1) were significant. The results indicated that line × tester analysis showed differences between F_1 and F_2 in this study.

Table 1. Analysis of variance for combining ability of different characters in F_1 and F_2 generations

Source	df	SCY (F_1)	SCY (F_2)	GOT (F_1)	GOT (F_2)	FL (F_1)	FL (F_2)	FF (F_1)	FF (F_2)	FS (F_1)	FS (F_2)
Blocks	2	120.85	111.93	0.16	0.01	0.04	0.71	0.02	0.02	0.29	4.06
Genotypes	18	302.63*	321.29*	5.57**	4.61**	2.18**	0.98*	0.27**	0.07**	11.48**	5.18**
Parents	6	165.23	244.98	4.40**	4.40**	2.22*	1.83*	0.30*	0.04	23.84**	10.77**
Parents vs Hyrids	1	617.72*	1676.32**	3.63**	0.53	4.45*	0.16	0.01	0.19*	3.53	4.03
Hybrids	11	348.94*	239.73	6.39**	5.10**	1.95*	0.59	0.28**	0.07*	5.55*	2.24
Lines	3	576.65*	301.56	12.69**	3.81**	1.85	0.57	0.40**	0.07	7.22*	1.06
Testers	2	443.93	180.05	13.00**	3.59**	0.33	1.21	0.01	0.10*	0.81	1.19
Lines x Testers	6	203.49	228.70	1.04	6.25**	2.54**	0.39	0.31**	0.06	6.13*	3.17
Error	36	137.29	128.14	0.54	0.38	0.69	0.43	0.09	0.03	2.36	1.60
σ^2 (GCA)		41.47	8.10	0.01	1.29	-0.08	0.01	0.01	0.01	0.12	-0.23
σ^2 (SCA)		22.04	33.52	0.07	0.17	0.61	-0.01	0.07	0.01	1.26	0.52
$\sigma^2_{GCA} / \sigma^2_{SCA}$		1.89	0.24	0.14	7.72	-0.12	-0.98	0.14	0.09	0.09	-0.44
Cont. of Lines		45.07	34.30	39.58	54.14	25.91	26.42	39.58	28.20	36.06	12.96
Cont. of Testers		23.13	13.65	0.07	36.98	3.05	37.50	0.07	25.28	2.68	9.70
Cont. of L x T		31.79	52.03	60.35	8.87	71.04	36.09	60.35	46.52	61.24	77.34

*, **; significant at 5% and 1% probability level, respectively. SCY: Seed Cotton Yield per Plant, GOT: Ginning Out-turn, FL: Fiber Length, FF: Fiber Fineness, FS: Fiber Strength.

σ^2GCA / σ^2SCA, which was detected high than unity for seed cotton yield (F$_1$) and ginning out-turn (F$_2$), indicated higher additive gene action than non-additive gene action in the inheritance of traits. On the other hand, fiber fineness, fiber length and fiber strength in both generations and ginning out-turn in F$_2$ exhibited only non-additive gene action. The difference in gene action for seed cotton yield and ginning out-turn between F$_1$ and F$_2$ clearly showed that selecting a single plant in further generations is complicated. In addition, the higher proportion of maternal and paternal interaction (line × tester) than lines and testers was a sign of non-additive gene effects. Although MENDEZ-NATERA et al. (2012) and PRAKASH et al. (2018) found the preponderance of additive genes in the inheritance of seed cotton yield and ginning out-turn, the non-additive gene effect was reported by SAJJAD and MALOOK (2016), SIVIA et al. (2017), ROY et al. (2018) and MAKHDOOM et al. (2019). Our findings that non-additive genes were effective in the control of fiber quality traits are in line with the findings of AHUJA and DHAYAL (2007), ASHOKKUMAR et al. (2010), SAJJAD and MALOOK (2016), COBAN and UNAY (2017), whereas both additive and non-additive gene actions were reported by YEHIA and EL-HASHASH (2019).

Positive GCA effect was detected in Carisma and Carmen for seed cotton yield in both F$_1$ and F$_2$ generations (Figure 1). On the contrary, significantly negative GCA effects for seed cotton yield were recorded in Gloria, Julia and Flash in both generations. SCA effects of F$_1$ and F$_2$ indicated (Figure 1) that Carmen × Carisma had significant and positive SCA effects for seed cotton yield in both generations. It was clearly seen that Carmen and Carisma were found as the best general combiner by having a leading position for seed cotton yield in both populations. In addition, the Carmen × Carisma combination was the best promising cross regarding mean performance for both generations. LUKONGE et al. (2007) and KHAN et al. (2009) stated that the parent with the best GCA effect could produce a superior hybrid for high yield. At the same time, the F$_2$ hybrid of Carmen × Carisma surpassed its parents despite inbreeding depression.
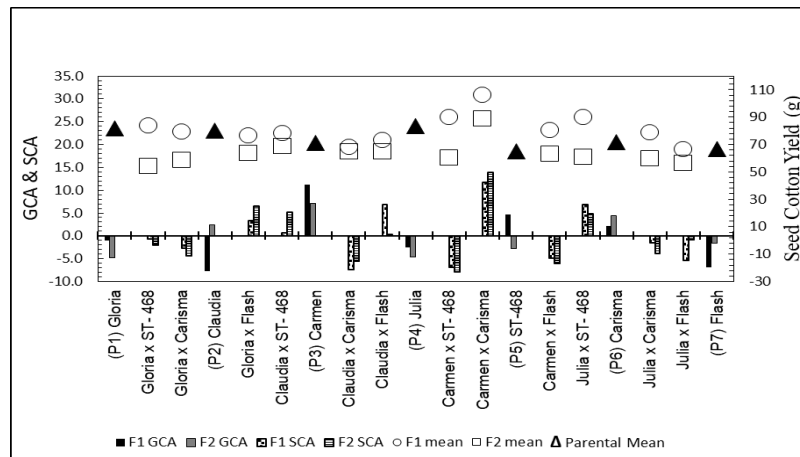

Figure 1. Graphical representation of mean performances and combining ability effects for seed cotton yield

Claudia, Carisma and ST-468 had positive and significant GCA effects, while SCA effects of Gloria × ST-468, Claudia × Carisma and Julia × Flash were positive for ginning out-turn in both generations (Figure 2). The performances of Claudia × Carisma and Gloria × ST-468 indicated that the utilization as one of a parent having the best GCA effect in a breeding program could produce promising hybrids (KHAN *et al.*, 2009).
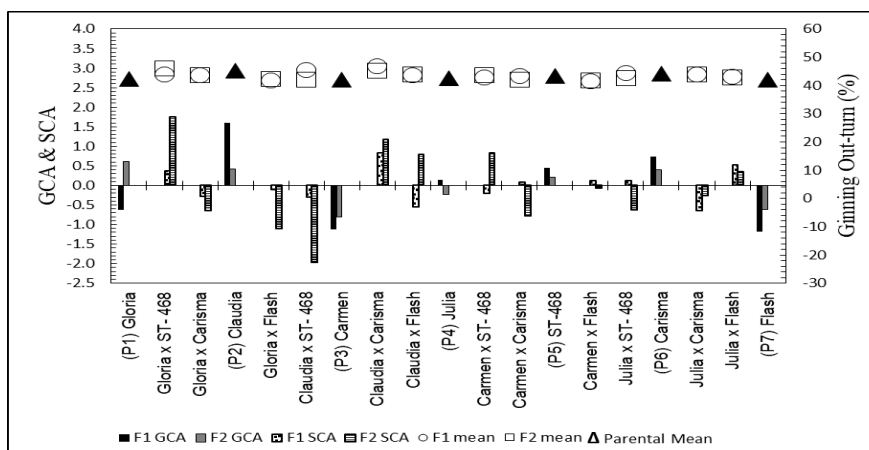

Figure 2. Graphical representation of mean performances and combining ability effects for ginning out-turn

The three major traits of cotton fiber are length, strength and fineness. It is assumed that the longer the fiber, the higher is the number of twists of the wrap fibers around the core, and hence the stronger the yarn (ANGELOVA, 2010). The Flash cultivar exhibited a positive and significant GCA effect, whereas the negative and significant GCA effect was recorded in the Julia cultivar for fiber length in both generations (Figure 3). Although most F_1 and F_2 genotypes displayed negative SCA effects, Gloria × Flash and Carmen × Carisma combinations had positive and significant SCA effects for fiber length in both generations. It was concluded that Flash as the best general combiner as well as Gloria × Flash and Carmen × Carisma as the most promising combinations for fiber length were found due to their mean performances and positive and significant combining abilities.

An ideal range of micronaire (fiber fineness) for upland cotton was from 3.9 (fine) to 4.9 (medium) (SCHENEK, 2005). The fiber fineness of parents varied between 5.35 mic. (Julia) and 4.38 mic. (Flash), while minimum fiber fineness for F_1 and F_2 generations were recorded in Gloria × ST-468 (4.26 mic.) and Julia × ST-468 (4.69 mic.), respectively (Figure 4). F_2 genotypes developed in the direction of coarse fiber, although they had lower values than their parents (Figure 4). The negative and significant GCA effects of Julia for both generations as well as ST-468 and Carmen for F_2, indicated that these cultivars could be used as general combiners in the reduction breeding of micronaire value. Gloria × ST-468 and Carmen × Flash cross combinations with negatively significant SCA effects were determined as promising populations that need to be emphasized.
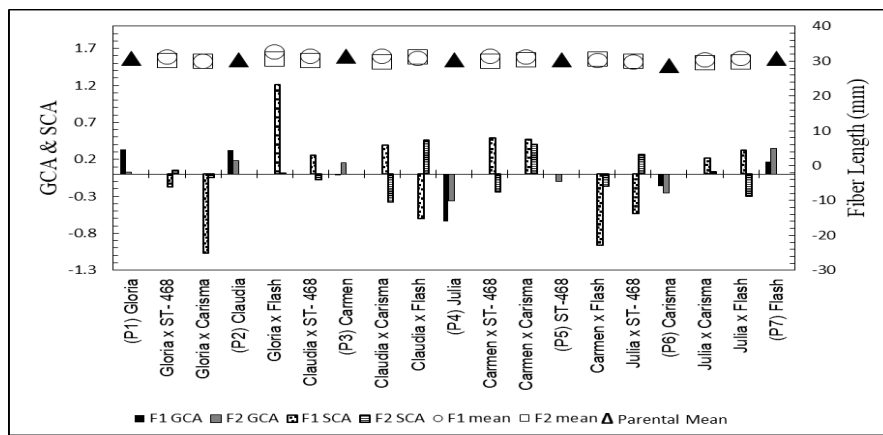
Figure 3. Graphical representation of mean performances and combining ability effects for fiber length

Fiber strength is important for the current technology, which demands stronger fiber (ACQUAAH, 2012) and tends to be highly heritable and respond well to selection (BOURLAND and MYERS, 2015). Carmen, Gloria and Claudia among parents; Carmen × Carisma combination for both generations had very strong fiber (Figure 5). Carmen having positive and significant GCA effect determined as the best general combiner, while Carmen × Carisma for F_2, Julia × Carisma, Claudia × Flash and Gloria × ST-468 for F_1 were the most promising hybrid combinations due to their positive and high SCA effects and mean performances for fiber strength. The performances of superior F_1 and F_2 involving Carmen, Gloria, and Claudia with high GCA effects indicated that cross combinations involved at least one with high GCA effects for fiber strength (AHUJA and DHAYAL, 2007; ASHOKKUMAR *et al*., 2010)
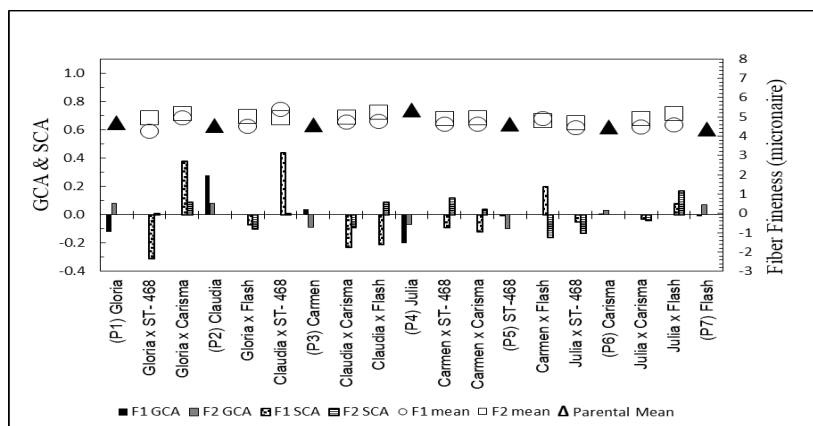

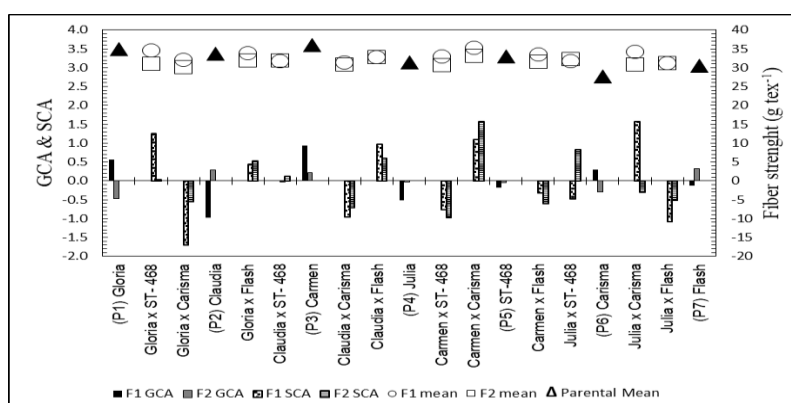Figure 4. Graphical representation of mean performances and combining ability effects for fiber fineness

Figure 5. Graphical representation of mean performances and combining ability effects for fiber strength

CONCLUSIONS

The results of the present study indicated that non-additive gene action for fiber length and fiber strength; both additive and non-additive gene actions for seed cotton yield, ginning out-turn and fiber fineness were preponderance. Therefore, superior single plants should be selected in later generations to optimize yield and fiber quality. Carmen was determined as the best general combiner for yield and fiber quality. Carmen × Carisma combination having combined performance could be used as a promising population for F_1 and F_2 hybrid production and a base population for further selection in high-yielding and quality cotton breeding. Moreover, it could be speculated that high (Carmen) × low (Carisma) GCA effect parents generated the best promising hybrid with favorable SCA for all observed characters in both generations.

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PROCENA DEJSTVA GENA I KOMBINACIONE SPOSOBNOSTI ZA PRINOS I KVALITET VLAKANA KOD PAMUKA (*Gossypium hirsutum* L.)

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Izvod

Genetička evaluacija segregirajućih populacija je jedna od primarnih aktivnosti oplemenjivača pamuka. Sedam genotipova pamuka je ukršteno u dizajnu linija × tester. Populacija od 12 F1, 12 F2 i njihovi roditelji testirani su u RCBD dizajnu sa tri ponavljanja u Nazilli Institutu za istraživanje pamuka u Turskoj tokom sezone 2014/2015. Genetska varijabilnost je bila značajna za sve proučavane osobine. s2GCA / s2SCA ukazuje na neaditivno delovanje gena u kontroli prinosa semenskog pamuka (F2), rezultata odvajanja vlakna pamuka od semena (F1) i osobina kvaliteta vlakana za obe generacije. Visoko povoljni GCA efekti na prinos semenskog pamuka i čvrstoću vlakna zabeleženi su kod sorte Carmen. Hibrid Carmen × Carisma je pokazao visoke srednje performanse i efekte SCA za prinos semenskog pamuka i jačinu vlakna, dok su performanse Gloria × ST-468 bile superiornije u pogledu rezultata odvajanja vlakana od semena. Zaključili smo da pojedinačne biljke sa željenim osobinama treba birati u kasnijim generacijama zbog preovlađivanja neaditivnog delovanja gena.