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## Combining Ability and Heterosis for Yield and Fibre Quality Traits in Line×Tester Crosses of Upland Cotton (*Gossypium hirsutum* L.)

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**Abstract:** The prime objective of cotton breeders is to develop new varieties with high yield and quality parameters. Present study aims to estimate general combining ability of the parents and specific combining ability and heterosis of hybrids for yield and fibre quality traits. Eight robust genotypes (*Gossypium hirsutum* L.) were crossed with four genotypes having compact plant type in line x tester fashion and the resulting thirty two hybrids were raised during summer 2003 in a randomized block design with two replications. Analysis of variance components indicated that 2.5% span length was predominantly controlled by additive gene action whereas the traits petiole length, length of sympodia, number of flowers per plant, days to fifty percent flowering, seeds per locule, ginning outturn, lint index, uniformity ratio and elongation percentage were governed predominantly by non-additive component. MCU 9 for seed cotton yield and 2.5% span length and KC 2 for bundle strength were the best combiners. TCH 1608×TCH 1002 exhibiting highest heterotic effect for seed cotton yield with highest *per se* performance and also highest SCA effect is the best combination in the present study, for direct exploitation. It also exhibited significant SCA effects for the important characters boll number and boll weight which is an encouraging feature in cotton breeding.

**Key words:** Cotton, line×tester analysis, general and specific combining ability, gene action

### INTRODUCTION

Cotton occupies a pre-eminent place among cash crops as it guides the destiny of a large section of the farming community as well as that of a flourishing textile industry. Cotton plays a major role in India's economy, both in terms of providing employment directly or indirectly to about 60 million people and in terms of production of wealth and earning foreign exchange for the country. Cotton breeders mainly focus on to develop cultivars earlier in maturity with high yield and good fibre quality. To combine all these traits together we need to identify suitable genotypes and use them in crossing programme. Knowledge on combining ability is useful for selection of desirable parents for exploitation of hybridity and transgressive expressions. It is also useful in assessing the ability of parents to generate potential hybrids with a reasonable level of stability. Combining ability studies also elucidate the nature and magnitude of gene action involved in the inheritance of seed cotton yield and its related characters, which will be useful to follow segregating material. The choice of parents for hybridization can be made on the basis of combining ability as well as the *per se* performance. Though the *per se* performance is important, the parents selected based on *per se* performance may not produce desirable hybrids in the event of the presence of non-additive gene action. In this context, combining ability effects provide sound basis for parental selection. Line×tester analysis would reveal General Combining Ability (GCA) effects of parents and Specific Combining Ability (SCA) effects of hybrids.

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Further evaluation of heterotic effect is essential to know whether new cross combinations are suitable for direct exploitation or whether these can be used to isolate useful and transgressive segregates from subsequent generation to develop a variety.

Earlier studies have shown that both additive and non-additive gene effects were important for controlling number of bolls and seed cotton yield (Khan and Idris, 1995; Kumaresan *et al.*, 1999). However, Shakeel *et al.* (2001) and Ahuja and Dhayal (2007) have shown that bolls and seed cotton yield are governed by genes acting non-additively. For fibre quality traits, viz., fibre length, fibre strength and micronaire non-additive gene action have been reported by Hassan *et al.* (2000) and Ahuja and Dhayal (2007). In contrast studies of Lukonge *et al.* (2007) revealed additive gene effects for fibre strength and micronaire and non-additive gene action for fibre length. The purpose of this study were to determine the GCA and SCA effects for yield parameters and fibre quality traits and to choose appropriate parents and hybrids for the investigated traits.

## MATERIALS AND METHODS

In the present study, eight *Gossypium hirsutum* L. genotypes MCU 5, TCH 1608, TCH 1452, TCH 1599, TCH 1569, MCU 12, MCU 9 and TCH 1627, robust in plant type were used as lines and four genotypes having compact plant type viz., KC 2, TCH 1002, Sahana and Sumangala were used as testers. Each of the line was crossed with all the four testers individually in a line $\times$ tester fashion (Kempthorne, 1957) to develop thirty two intra *hirsutum* hybrids. Hybridization technique described by Doak and Beasley (1934) was followed. The buds that are likely to open on the next day were emasculated by giving a cut with thumb nail and removing the staminal column. Immediately after emasculation the flowers were covered with red colour butter paper bag for easy identification. The next day, at peak anthesis the flowers from appropriate pollinator parent were collected and pollen was dusted on the stigma by gently smearing on the staminal column. After pollination the flowers were covered with white butter paper bag and proper labeling was done. A few plants of each parent were selfed by adopting clay and smear method (Ramanatha, 1936).

The thirty two intra-*hirsutum* hybrids along with their parents were raised in randomized block design with two replications during summer 2003, at Cotton Breeding Station, Tamilnadu Agricultural University, Coimbatore. They were sown in 3 m ridges spaced 75 cm apart and with an interplant distance of 30 cm so as to accommodate ten plants in each row. Recommended agronomic practices and need based plant protection measures were followed. Five randomly selected plants were tag-labelled for recording the observations. A total of 22 characters including nine metric traits, thirteen yield and quality attributes were studied. The traits are Plant Height (PH), Petiole Length (PL), Internode Length number (IL), of sympodia per plant (NOS), Length of Sympodia (LOS), No. of Flower Bearing Nodes in sympodia (NFBN), No. of Flowers (NOF), Days to First Flowering (DFF), Days to 50% Flowering (DFPF), No. of Bolls per plant (NOB), Boll Weight (BW), No. of Locules per boll (NOL), No. of Seeds per Locule (NOSL), Seed Cotton Yield (SCY), Ginning Outturn (GOT), Seed Index (SI), Lint Index (LI), 2.5 percent span length (2.5% SL), Uniformity Ratio (UR), micronaire (MIC), Bundle Strength (BS), Elongation percent (EL) were recorded on the selected plants. Average data recorded on each character from the randomly selected plants represented the mean of that replication.

The data was subjected to combining ability analysis following the method suggested by Kempthorne (1957). The ratio of GCA/SCA was worked out for each character to find out the predominance of additive or non-additive gene action, assuming simple additive dominance model. Standard heterosis was worked out as percent mean deviation of the mean  $F_1$  performance over the mean performance of the standard variety (MCU 12).

**RESULTS AND DISCUSSION**

The analysis of variance shown in Table 1 and 2 revealed significant divergence among the parents for all the characters excluding internode length, No. of flower bearing nodes in sympodia and uniformity ratio showing sufficient variability among the parents which can generate potential and promising hybrids. Significant differences among hybrids indicated the existence of variability among the cross combinations for all characters except internode length, No. of sympodia, No. of flower bearing nodes and locules per boll. The variance due to parents evrsus hybrid was significant for plant height, petiole length, number of sympodia per plant, days to first flowering, days to 50% flowering, boll weight, ginning outturn, 2.5% span length, micronaire, bundle strength and elongation percent indicating that significant heterosis could be expected in hybrids for these characters and comparison will be much relevant.

Table 1: Analysis of variance for biometrical traits from line×tester analysis

Sources of variation	df	Mean squares								
		PH (cm)	PL (cm)	IL (cm)	NOS	LOS (cm)	NFBN	NOF	DFF	DPPF
Replication	1	5.67	2.09	0.94**	20.80**	7.18	0.100	30.56	0.73	1.92
Parents	11	45.64**	2.94**	0.09	3.96**	8.60**	0.150	69.05**	23.67**	22.50**
Hybrids	31	38.90**	2.06**	0.09	1.32	12.24**	0.140	48.02**	24.48**	17.51**
Parents vs Hybrids	1	16.47**	20.79**	0.23	27.87**	3.95	0.002	155.09**	318.37**	289.55**
Error	43	6.58	0.83	0.09	0.09	2.35	0.160	10.88	1.84	1.32
Replication	1	12.36	0.67	0.40	10.14	6.05	0.180	35.94	1.00	0.25
Lines	7	50.05	2.06	0.11*	0.82	20.69*	0.080	112.85**	15.68	19.92
Testers	3	6.68	1.48	0.37**	0.83	6.11	0.200	23.68	13.08	28.52
Lines×Testers	21	39.79**	5.78*	0.04	1.55*	10.29**	0.150	29.88**	29.04**	15.14**
Error	31	6.02	0.94	0.09	0.67	2.84	0.140	9.88	2.26	1.15

\*, \*\*Means significant at 5 and 1% probability level, respectively

Table 2: Analysis of variance for yield and quality traits from line×tester analysis

Sources of variation	df	Mean squares					
		NOB	BW (g)	NOL	NOSL	SCY (g plant <sup>-1</sup> )	GOT (%)
Replication	1	15.11	0.02	0.09	0.78	49.45	0.42
Parents (P)	11	23.16*	0.53**	0.09**	0.53**	406.05**	8.62**
Hybrids (Hy)	31	15.92**	0.30**	0.04	0.56**	167.57**	9.83**
P vs Hy	1	15.99	0.87**	0.003	0.35	35.57	5.52*
Error	43	4.38	0.05	0.03	0.10	38.54	0.91
Replication	1	13.56	0.04	0.05	0.91	35.12	0.01
Lines	7	17.11	0.22	0.04	0.59	113.49	19.44*
Testers	3	8.51	0.29	0.05	0.74	56.35	12.21
Lines×Testers	21	16.58**	0.32**	0.05*	0.53**	201.49**	6.29**
Error	31	4.90	0.06	0.02	0.09	48.16	0.91

Sources of variation	df	Mean squares					
		SI	LI	2.5% SL	UR	MIC	BS (g tex <sup>-1</sup> )
Replication	0.0006	0.02	12.53	34.38	0.20	7.56	0.44
Parents (P)	0.49**	0.19**	12.92**	3.94	0.19**	8.97**	0.66**
Hybrids (Hy)	1.35**	1.32**	1.98*	5.33**	0.10**	2.71**	0.40**
P vs Hy	0.20	0.004	5.75*	6.71	0.25**	4.62**	2.76**
Error	0.15	0.05	0.93	1.96	0.01	0.58	0.02
Replication	0.07	0.02	8.85	23.77	0.16	5.06	0.28
Lines	0.92	2.16	1.68	2.00	0.11	2.66	0.37
Testers	1.33	1.04	7.79**	22.81**	0.03	1.86	0.90
Lines×Testers	1.49**	1.07**	1.26	3.95*	0.11**	2.85**	0.34**
Error	0.14	0.04	0.94	2.02	0.01	0.58	0.02

\*, \*\*Means significant at 5 and 1% probability level, respectively

The variance due to lines was significant for the characters internode length, length of sympodia, No. of flowers per plant, ginning outturn while the testers showed significant differences for internode length, 2.5% span length and uniformity ratio. The line×tester component exhibited significant variability for all the characters except internode length, No. of flower bearing nodes in sympodia and 2.5% span length indicating that the hybrids were more variable than the parents. The lines contributed a major share to the genetic variance in respect of No. of flowers per plant and ginning outturn. The contribution of tester was maximum for internode length, while the line×tester component had the maximum share of genetic variance in all other characters.

A critical comparison of the mean values of the parents and hybrids in respect of different characters revealed that hybrids were relatively shorter in duration. Plant height and length of sympodia were intermediate indicating the semicompact nature of the hybrids.

The GCA variances was predominant in 2.5% span length indicating that this character is governed by additive component of heritable variance. Under such situation improvement could be made following appropriate breeding programme of hybridization and selection which may take care of fixable gene effect. Predominance of additive component of genetic variance for 2.5% span length is in conformity with those reported by Kumar *et al.* (1992), Swati Bharad *et al.* (1999), Khorgade *et al.* (2000), El-Dahan *et al.* (2003), Iqbal *et al.* (2005) and Lukonge *et al.* (2007).

The GCA: SCA ratio was less than unity for the traits petiole length, length of sympodia, No. of flowers per plant, days to 50% flowering, seeds per locule, ginning outturn, lint index, uniformity ratio and elongation percentage suggesting that these characters were governed predominantly by non-additive component (Table 3, 4). These components can be exploited by heterotic breeding programme. The findings support earlier observation of Tang *et al.* (1993), Ahuja *et al.* (2007) (for elongation percentage), Krishna (1998) (for ginning outturn and lint index), Patel and Pethani (1998), Valarmathi and Jahangir (1998) and Ahuja and Tuteja (1999) (for ginning outturn), Khorgade *et al.* (2000) (for lint index) and Basbag *et al.* (2007) (for days to first flowering). The component of variance attributable to SCA for petiole length and uniformity ratio was relatively less in magnitude though they were larger than GCA variance. This indicated that both additive and non-additive variances were important for these two characters as reported by Nadarajan and Sree Rangaswamy (1992).

Table 3: Genetic components of variance and genetic contribution of lines, testers and line×tester to biometrical traits

Genetic parameters	PH (cm)	PL (cm)	IL (cm)	NOS	LOS (cm)	NFBN	NOF	DFF	DFFP
GCA	-	0.16	0.02	-	0.26	-	3.20	-	0.76
SCA	16.88	0.39	-	0.44	3.75	0.008	10.00	13.39	7.00
GCA/SCA	-	0.41	-	0.14	0.07	-	0.32	0.09	0.11
Lines	29.05	16.13	27.36	14.06	38.18	12.620	53.07	14.46	25.68
Testers	1.66	27.16	40.99	6.13	4.83	13.860	4.77	5.17	15.76
Line×Tester	69.28	56.70	31.65	79.81	56.99	73.510	42.16	80.36	58.56

-: Negative estimates

Table 4: Genetic components of variance and genetic contribution of lines, testers and line×tester to yield and quality traits

Genetic parameters	BW		SCY			GOT	2.5%				BS		
	NOB	(g)	NOL	NOSL	(g plant <sup>-1</sup> )	(%)	SI	LI	SL	UR	MIC	(g tex <sup>-1</sup> )	EL
GCA	-	-	-	0.01	-	0.79	-	0.04	0.29	0.70	-	-	0.02
SCA	5.84	0.13	0.01	0.22	76.67	2.69	0.67	0.51	0.16	0.96	0.05	1.14	0.16
GCA/SCA	-	-	-	0.05	-	0.29	-	0.08	1.81	0.73	-	-	0.13
Lines	24.26	17.16	19.93	23.61	15.29	44.66	15.41	37.13	19.08	8.46	24.12	22.16	20.64
Testers	5.17	9.75	10.93	12.79	3.25	12.02	9.53	7.69	38.00	41.38	2.58	6.62	21.81
Line×Tester	70.57	73.10	69.14	63.60	81.45	43.32	75.06	55.18	42.92	50.17	73.30	71.22	57.55

-: Negative estimates

In the present study, combining ability effects were studied (Table 5, 6) in which the line MCU 9 showed high GCA for seed cotton yield. In addition it also showed high GCA for plant height, number of bolls, locules per boll, seeds per locule and 2.5% span length and proved its worthiness in

**Table 5: General combining ability effects of parents for biometrical traits**

Parents	Characters						
	PH (cm)	PL (cm)	NOS	LOS	NOF	DFF	DFFP
<b>Lines</b>							
MCU 5	-0.371	0.908**	0.278	-0.706	-5.618**	0.188	0.031
TCH 1608	-1.578	-0.532	-0.597*	0.190	-3.03**	1.813**	2.031**
TCH 1599	-4.397**	-0.412	0.112	-2.886**	-4.445**	-1.313*	-0.219
TCH 1569	0.317	0.068	0.195	1.999**	0.967	0.063	0.156
TCH 1452	-0.896	-0.019	-0.367	2.133**	3.513**	-1.813**	-2.094**
MCU 12	3.579**	-0.036	0.238	0.202	2.882**	-1.063*	-1.594**
MCU 9	2.797**	0.051	-0.055	-0.133	2.513*	2.063**	2.406**
TCH 1627	0.548	-0.028	0.197	-0.798	3.217**	0.063	-0.719
SE	0.870	0.340	0.290	0.600	1.110	0.530	0.380
<b>Testers</b>							
KC2	0.103	-0.842**	-0.179	-0.048	-0.658	-0.688	-0.719**
TCH 1002	0.619	0.480*	-0.200	0.192	-0.094	-0.813*	-1.469**
Sahana	-0.908	-0.017	0.112	-0.812	-0.987	0.438	0.719**
Sumangala	0.186	0.379	0.268	0.668	1.739*	1.063**	1.469**
SE	0.610	0.240	0.200	0.420	0.790	0.380	0.270

\*, \*\*Means significant at 5 and 1% probability level, respectively

**Table 6: General combining ability effects of parents for yield and quality traits**

Parents	Characters						
	NOB	BW (g)	NOL	NOSL	SCY (g plant <sup>-1</sup> )	GOT (%)	SI
<b>Lines</b>							
MCU 5	-1.332	-0.03	-0.008	-0.299**	-3.273	-2.804**	0.277*
TCH 1608	0.665	-0.043	0.023	-0.215*	2.100	-0.554	0.56**
TCH 1599	-1.667*	-0.042	-0.039	0.276**	-4.776	1.691**	-0.147
TCH 1569	1.458	-0.247	0.017	0.303**	-1.010	0.136	0.210
TCH 1452	1.125	-0.133	-0.008	-0.095	0.579	1.201**	-0.070
MCU 12	-1.252	0.085	-0.133**	-0.316**	-2.636	1.733**	-0.363**
MCU 9	2.003*	0.096	0.116*	0.319**	7.000**	-1.215**	-0.008
TCH 1627	-1.00	0.313	0.033	0.026	2.014	-0.188	-0.460**
SE	0.78	0.090	0.050	0.110	2.450	0.340	0.130
<b>Testers</b>							
KC2	-0.126	0.009	0.041	-0.215**	0.010	-0.203	0.195*
TCH 1002	-0.812	-0.033	0.033	-0.153*	-2.008	-1.153**	0.271**
Sahana	0.959	-0.153*	0.008	0.156*	-0.508	0.677**	-0.113
Sumangala	-0.021	0.177**	-0.082*	0.213**	2.505	0.679**	-0.353**
SE	0.550	0.060	0.030	0.080	1.730	0.240	0.100

Parents	Characters						
	LI	2.5% SL	UR	MIC	BS (g tex <sup>-1</sup> )	EP	
<b>Lines</b>							
MCU 5	-0.394**	-0.159	0.047	0.022	0.431	-0.094	
TCH 1608	0.025	-0.009	-0.203	0.072	-0.244	-0.094	
TCH 1599	0.033	-0.459	0.547	0.122**	-0.019	0.206**	
TCH 1569	-0.020	0.041	0.047	0.047	0.656*	0.206**	
TCH 1452	1.203**	0.566	0.047	-0.078*	-0.144	-0.394**	
MCU 12	-0.107	-0.134	0.672	0.022	0.306	0.031	
MCU 9	-0.325**	0.741*	-0.953	-0.253**	0.231	-0.094	
TCH 1627	-0.415**	-0.584	-0.203	0.047	-1.219**	0.231**	
SE	0.070	0.340	0.500	0.040	0.270	0.050	
<b>Testers</b>							
KC2	-0.082	-0.059	0.109	-0.003	0.456*	-0.206**	
TCH 1002	-0.170**	1.003**	-1.328**	-0.028	0.031	-0.169**	
Sahana	-0.127*	-0.422	1.547**	-0.028	-0.144	0.306**	
Sumangala	0.380**	-0.522*	-0.328	0.059*	-0.344	0.069*	
SE	0.05	0.24	0.36	0.03	0.19	0.04	

\*, \*\*Means significant at 5 and 1% probability level, respectively

future hybridization programme. Further the study revealed that high and significant GCA effects for seed cotton yield resulted from combined effects of yield components viz., boll number, locules per boll and seeds per locule which indicated that this three components were jointly important in determining yield and further selection may be made on this basis of these characters. Similar results were obtained by Jagtap *et al.* (1992), Patel *et al.* (1992) and Bhatade and Sansar (1993).

Considering earliness parameters namely the days to first flowering as well as 50% flowering the lines TCH 1452 and MCU 12, testers TCH 1002 showed desirable GCA effects. Apart from this MCU 12 was also found to be a good combiner for plant height and ginning outturn while TCH 1452 showed high GCA effects for ginning outturn and lint index and moderate GCA effects for seed cotton yield, No. of bolls, 2.5% span length and uniformity ratio. Tester KC 2 was found to be a good general combiner for earliness, seed index and bundle strength. It showed moderate GCA effects for boll weight, locules per boll, seed cotton yield and uniformity ratio. In the present study, there was no relationship between *per se* performance of hybrids and *gca* effects of parents which indicated the presence of epistatic interaction also. Further studies through generation mean analysis are triple test cross analysis may bring out more useful information on the nature of gene interaction in the material.

The cross TCH 1608×TCH 1002, MCU 9×Sumangala and MCU 9×KC 2 exhibited significant standard heterosis of 61.89, 49.72 and 43.95%, respectively over MCU 12 (check) and all the three had high mean seed cotton yield (Table 7, 8). The crosses which expressed significant heterosis for seed cotton yield also expressed high heterosis for boll weight and No. of locules per boll. However no

Table 7: Expression of heterosis in hybrids(Percentage) for biometrical traits

Hybrids	Characters					
	PH (cm)	PL (cm)	NOS	NOF	DFF	DFFP
MCU5×KC2	-17.55	3.94	-7.18	-7.03**	-4.14**	-5.09
MCU5×TCH1002	8.85	-8.42	-19.66*	-7.81**	-8.97**	-6.00
MCU5×Sahana	5.59	-6.63	-10.71	1.56	-0.69	-28.12**
MCU5×Sumangala	16.96	-16.24**	-10.77	2.34	4.14**	-9.70
TCH1608×KC2	-14.61	-12.59*	-23.25*	3.13	4.14**	-17.97*
TCH1608×TCH1002	-10.40	-15.32**	-8.94	1.56	-0.69	5.06
TCH1608×Sahana	15.03	8.10	-17.89	3.13	1.38	12.44
TCH 1608×Sumangala	-30.25**	-17.71**	-35.73**	-8.59**	-3.45*	-19.82*
TCH 1599×KC2	-16.00	-9.50	-8.94	0.00	-0.69	-11.53
TCH 1599×TCH 1002	-4.75	-13.12*	-12.53	-3.13	-2.76	-17.06
TCH 1599×Sahana	-8.17	-15.33**	-8.94	-18.75**	-4.14**	-13.35
TCH 1599×Sumangala	-3.64	-23.29**	-25.01**	1.56	-3.45*	6.00
TCH 1569×KC 2	-13.25	-19.18**	-25.01**	-4.69	-2.76	-3.23
TCH 1569×TCH 1002	-20.46*	1.86	-17.84	-3.13	-1.38	7.82
TCH 1569×Sahana	0.21	-11.40*	-1.82	0.00	-2.76	6.91
TCH 1569×Sumangala	5.20	7.16	-7.18	-3.91	-2.07	12.41
TCH 1452×KC 2	-18.69	-4.10	-10.71	-7.81**	-6.90**	8.74
TCH 1452×TCH 1002	-6.41	-5.71	-23.25*	-6.25*	-6.21**	6.91
TCH 1452×Sahana	-17.19	-15.78**	-28.60**	-9.38**	-8.28**	8.76
TCH 1452×Sumangala	7.56	-6.17	-13.39	0.00	0.00	27.65**
MCU12×KC 2	-23.53*	-5.85	-21.42*	-5.47*	-6.21**	14.27
MCU12×TCH 1002	-8.68	9.25	-10.71	-5.47*	-6.90**	-2.32
MCU12×Sahana	-9.97	-7.11	-16.07	-1.56	-2.76	13.35
MCU12×Sumangala	-14.89	9.62	-1.82	-6.25*	-2.76	19.80*
MCU9×KC 2	-34.72**	-1.85	-17.84	-5.47*	-4.83**	10.59
MCU9×TCH 1002	-21.51**	8.81	-23.25*	-9.38**	-6.90**	7.38
MCU9×Sahana	-21.24*	-11.22*	-21.48*	6.25*	6.90**	-0.47
MCU9×Sumangala	-7.82	3.58	0.00	9.38**	8.28**	23.50*
TCH 1627×KC 2	-8.62	2.42	-21.42*	-5.47*	-6.21**	16.12
TCH 1627×TCH 1002	-6.03	-15.38**	-21.42*	-0.78	-2.07	22.56*
TCH 1627×Sahana	-17.97	-4.38	-5.36	0.00	-1.38	5.06
TCH 1627×Sumangala	-13.96	-2.27	-3.59	-5.47*	-4.14**	5.06

\*, \*\*Means significant at 5 and 1% probability level, respectively

Table 8: Expression of heterosis in hybrids (%) for yield and quality traits

Hybrids	Characters					
	BW	SCY	GOT	2.5%SL	MIC	BS
MCU5×KC2	2.56	-14.26	-11.86**	-3.42	20.69**	1.69
MCU5×TCH1002	-13.29	-43.32*	-11.97**	-7.88*	0.00	-18.64**
MCU5×Sahana	19.11	22.48	-12.28**	-5.48	24.14**	-5.93
MCU5×Sumangala	42.42**	6.05	-2.12	-3.77	17.24**	0.42
TCH1608×KC2	-1.17	-30.35	1.92	-7.19*	6.9	-10.17**
TCH1608×TCH1002	34.97**	61.89**	-4.54	-1.71	17.24**	-4.24
TCH1608×Sahana	7.69	26.80	0.07	-3.77	24.14**	-10.59**
TCH1608×Sumangala	6.99	-30.16	-8.85**	-5.82	20.69**	-8.90**
TCH1599×KC2	-16.08	-22.89	2.32	-3.08	24.14**	-0.42
TCH1599×TCH1002	14.69	-3.46	-7.05*	0.00	10.34*	-7.20*
TCH1599×Sahana	10.26	-16.05	7.38*	-11.30**	20.69**	-12.29**
TCH1599×Sumangala	39.86**	-2.66	12.71**	-10.27**	20.69**	-10.17**
TCH1569×KC2	6.76	7.08	4.54	-7.19*	20.69**	-10.17**
TCH1569×TCH1002	-20.51	-39.12*	-5.95*	1.03	24.14**	2.97
TCH1569×Sahana	7.93	11.84	-0.24	-3.77	6.9	-1.69
TCH1569×Sumangala	16.32	15.26	-1.53	-7.88*	13.79**	-9.75**
TCH1452×KC2	18.88	23.02	-1.70	-1.37	0.00	-5.93
TCH1452×TCH1002	3.26	-1.88	2.19	0.00	20.69**	-8.90**
TCH1452×Sahana	9.09	-15.53	8.05**	-6.16	6.9	-5.51
TCH1452×Sumangala	0.47	6.36	0.98	-3.08	20.69**	-11.86**
MCU12×KC2	42.42**	0.25	-4.19	-7.88*	24.14**	-5.51
MCU12×TCH1002	23.54	-18.75	3.43	-0.68	6.9	-3.39
MCU12×Sahana	0.47	-4.01	2.43	-4.45	10.34*	-7.20*
MCU12×Sumangala	5.83	0.24	14.20**	-7.19*	20.69**	-8.47*
MCU9×KC2	35.43**	43.95*	-1.82	-1.03	3.45	-6.78*
MCU9×TCH1002	8.39	-5.13	-8.64**	0.34	6.90	-3.81
MCU9×Sahana	3.50	-8.16	-5.14	-4.11	6.90	-8.05*
MCU9×Sumangala	27.04*	49.72*	-3.68	-3.42	6.90	-7.20*
TCH1627×KC2	27.51*	5.02	-3.65	-7.19*	17.24**	-6.78*
TCH1627×TCH1002	49.65**	18.62	-4.54	-0.34	24.14**	-15.25**
TCH1627×Sahana	-2.33	-16.56	6.27*	-9.25**	10.34*	-13.14**
TCH1627×Sumangala	40.09**	20.20	-5.11	-9.59**	13.79**	-15.25**

\*, \*\*Means significant at 5 and 1% probability level, respectively

such relationship was observed for boll number. The results suggest that high yield does not necessarily depend on high heterotic expression of all yield components and high heterosis for some or few of the component traits, which are ultimately associated with yield, can generate significant yield heterosis. Similar results were reported by Kapoor *et al.* (2002).

The hybrids that were found to be significantly heterotic had SCA in the positive direction indicating that heterosis can be dependably exploited. The hybrid TCH 1608×TCH 1002 exhibiting highest heterotic effect (61.89%) for seed cotton yield with highest *per se* performance of 60.77 g plant<sup>-1</sup> and also highest SCA effect of 22.601 is the best combination in the present study, for direct exploitation. It also exhibited significant SCA effects for the important improvement characters boll number and boll weight which is an encouraging feature in cotton breeding.

A perusal of SCA effects (Table 9, 10) showed that superior performance of the hybrids TCH 1608×TCH 1002 and MCU9×Sumangala could be attributed to the effect of maternal parent involved in the cross. However the good expression of MCU5×Sumangala, TCH 1599×Sumangala and MCU9×KC2 for boll weight indicated that Sumangala and KC 2 (compact types) were able to result in high SCA expression.

Evaluation of fibre quality is of paramount importance in varietal improvement research in cotton, as varieties not conforming to industrial standards in fibre quality will not stand the test of time. So, in present investigation importance was given to quality characters also. The hybrids TCH 1599×Sumangala and MCU 12×Sumangala for ginning outturn and hybrid TCH 1627×Sahana for elongation



Table 9: Specific combining ability effects of hybrids for biometrical traits

Hybrids	Characters						
	PH (cm)	PL (cm)	NOS	LOS	NOF	DFF	DFFP
MCU5×KC2	5.016**	-1.044	0.637	-0.084	3.24	-2.063	-0.531
MCU5×TCH1002	-1.37	0.439	-0.507	0.195	2.346	-2.438*	-3.281**
MCU5×Sahana	1.007	-0.109	0.016	0.081	-4.76*	2.313*	0.531
MCU5×Sumangala	-4.652**	0.714	-0.145	-0.192	-0.826	2.188*	3.281**
TCH1608×KC2	-1.627	0.411	0.012	0.313	-4.008	2.813**	3.469**
TCH1608×TCH1002	-3.443*	-0.116	1.368*	-0.327	3.759	1.938	0.719
TCH1608×Sahana	9.214**	1.801**	0.221	-0.026	7.322**	1.688	0.031
TCH1608×Sumangala	-4.145*	-2.096**	-1.60**	0.041	-7.074**	-6.438**	-4.219**
TCH1599×KC2	2.657	0.121	0.638	0.516*	-0.263	3.938**	2.219*
TCH1599×TCH1002	0.421	0.199	0.324	0.05	-2.826	2.063	1.469
TCH1599×Sahana	0.898	-0.254	0.347	0.021	-0.593	-9.188**	-1.719*
TCH1599×Sumangala	-3.976*	-0.066	-1.309*	-0.587*	3.681	3.188**	-1.969**
TCH1569×KC2	-6.657**	0.256	-0.946	-0.232	-2.675	-0.438	0.344
TCH1569×TCH1002	2.828	-1.296	-0.255	0.133	0.761	0.688	2.094*
TCH1569×Sahana	-1.946	0.386	0.928	0.269	1.325	1.438	-1.094
TCH1569×Sumangala	5.775**	0.654	0.272	-0.169	0.589	-1.688	-1.344
TCH1452×KC2	1.721	-0.107	0.952	3.184**	-0.890	-0.563	-0.406
TCH1452×TCH1002	0.44	0.106	-0.197	-0.72	-2.114	0.563	0.844
TCH1452×Sahana	-2.818	-0.976	-1.009	-0.867	-0.550	-2.688*	-2.844**
TCH1452×Sumangala	0.657	0.977	0.255	-1.597	3.554	2.688*	2.406**
MCU12×KC2	-3.584**	-0.086	-0.653	-1.32	1.740	0.188	-0.406
MCU12×TCH1002	3.075	0.423	0.368	-1.689	-4.824*	0.313	-0.156
MCU12×Sahana	-3.173	0.155	-0.444	-2.40*	1.740	1.563	0.656
MCU12×Sumangala	3.682*	-0.492	0.73	5.409**	1.344	-2.063	-0.094
MCU9×KC2	-0.902	-0.587	-0.026	-2.465*	0.780	-2.938**	-3.406**
MCU9×TCH1002	3.647*	-0.169	-0.51	2.231	-0.944	-5.313**	-4.156**
MCU9×Sahana	-4.341*	-0.201	-0.657	-0.925	-2.890	3.438**	3.656**
MCU9×Sumangala	1.595	0.957	1.192*	1.159	3.054	4.813**	3.906**
TCH1627×KC2	3.377	1.037	-0.612	1.215	2.075	-0.938	-1.281
TCH1627×TCH1002	-5.599**	0.415	-0.591	0.211	3.841	2.188*	2.469*
TCH1627×Sahana	1.158	-0.803	0.597	0.09	-1.595	1.438	0.781
TCH1627×Sumangala	1.064	-0.649	0.606	-1.516	-4.321	-2.688*	-1.969**
SE	1.740	0.680	0.580	1.190	2.220	1.060	0.760

\*, \*\*Means significant at 5 and 1% probability level, respectively

percentage had superior *per se* performance, significant standard heterosis with high SCA effects. The parents involved were also good general combiners. Such a combinations of all parameters may be due to additive genetic system and additive x additive gene interaction. These hybrids can be exploited as basic material for breeding. Similar results were reported by Mandloi *et al.* (1998) and Modi *et al.* (1999) (for ginning outturn). MCU 12×KC 2 (moderate×moderate general combiner) for uniformity ratio and TCH 1452×Sumangala (poor×good general combiner) for micronaire were the other crosses with high heterotic expression, high *per se* performance and high SCA effects for respective characters. The results indicate the preponderance of non-additive genetic variation in the inheritance of these characters which was in accordance with the results obtained by Krishna (1998). The hybrid combinations which were found to be heterotic with high SCA and *per se* performance for seed cotton yield failed to exhibit good performance for quality characters. But even then hybrids recording superior performance for quality characters were found to involve at least one parent showing moderate GCA effect for seed cotton yield. This indicated the possibility for simultaneous improvement of yield and quality by exploiting these hybrids. Inter crossing the hybrids showing yield heterosis and those displaying quality characters may be taken up for parallel improvement of yield and quality.

Table 10: Specific combining ability effects of hybrids for yield and quality traits

Hybrids	Characters						
	NOB	BW (g boll <sup>-1</sup> )	NOL	NOSL	SCY (g plant <sup>-1</sup> )	GOT (%)	SI (g/100 seeds)
MCU5×KC2	0.546	-0.227	0.026	0.507*	-2.637	-0.571	0.174
MCU5×TCH1002	-2.108	-0.525**	0.033	-0.456*	-11.53*	0.344	-0.357
MCU5×Sahana	2.791	0.291	-0.107	-0.030	11.675*	-1.590*	-0.774**
MCU5×Sumangala	-1.229	0.460**	0.048	-0.021	2.492	1.817**	0.957**
TCH1608×KC2	-3.792*	-0.294	0.119	0.323	-14.051**	1.804**	-0.035
TCH1608×TCH1002	5.565**	0.523**	0.067	0.260	22.601**	0.584	0.614*
TCH1608×Sahana	3.123*	0.058	0.027	-0.013	7.926	0.305	-0.357
TCH1608×Sumangala	-4.897**	-0.287	-0.213*	-0.57**	-16.477**	-2.693**	-0.222
TCH1599×KC2	1.871	-0.615**	-0.043	-0.768**	-4.375	-0.306	-0.037
TCH1599×TCH1002	1.567	0.087	-0.101	0.804**	4.938	-2.501**	-0.639*
TCH1599×Sahana	-1.544	0.112	0.089	-0.475*	-1.287	0.510	-0.180
TCH1599×Sumangala	-1.894	0.417*	0.054	0.439*	0.725	2.297**	0.856**
TCH1569×KC2	0.746	0.080	-0.164	-0.160	3.114	1.994**	0.010
TCH1569×TCH1002	-2.728	-0.463**	0.008	-0.057	-12.219*	-0.576	-1.561**
TCH1569×Sahana	1.671	0.267	0.033	-0.031	5.416	-0.490	1.323**
TCH1569×Sumangala	0.311	0.117	0.123	0.247	3.688	-0.928	0.228
TCH1452×KC2	1.418	0.226	0.026	0.238	7.510	-1.166	-0.135
TCH1452×TCH1002	0.765	-0.067	0.033	0.005	0.178	1.089	1.859**
TCH1452×Sahana	-3.997*	0.178	-0.207*	-0.468*	-6.447	1.225	0.113
TCH1452×Sumangala	1.813	-0.337	0.148	0.225	-1.24	-1.148	-1.837**
MCU12×KC2	-1.874	0.513**	0.151	0.089	2.175	-2.533**	0.409
MCU12×TCH1002	-1.848	0.15	0.158	0.562**	-2.942	0.972	-0.617*
MCU12×Sahana	1.371	-0.224	-0.017	0.053	1.093	-1.193	0.116
MCU12×Sumangala	2.351	-0.44*	-0.292**	-0.704**	-0.325	2.755**	0.092**
MCU9×KC2	1.211	0.352*	-0.098	-0.511*	8.949	1.210	-0.316
MCU9×TCH1002	-1.443	-0.186	-0.191	-0.338	-7.464	-0.13	0.368
MCU9×Sahana	-2.874	-0.17	0.264**	0.453*	-10.104*	-0.784	-0.299
MCU9×Sumangala	3.106*	0.004	0.024	0.396	8.618	-0.297	0.247
TCH1627×KC2	-0.127	-0.035	-0.016	0.282	-0.685	-0.432	-0.07
TCH1627×TCH1002	0.23	0.482**	-0.008	-0.781**	6.438	0.218	0.334
TCH1627×Sahana	-0.542	-0.513**	-0.083	0.51*	-8.272	2.018**	0.058
TCH1627×Sumangala	0.438	0.067	0.107	-0.011	2.520	-1.804**	-0.322
SE	1.570	0.180	0.100	0.210	4.910	0.670	0.260

  

Hybrids	Characters					
	LI (g/100 seeds)	2.5% SL (mm)	UR	MIC	BS (g tex <sup>-1</sup> )	EL (%)
MCU5×KC2	0.117	0.559	0.391	0.153	1.269*	-0.294**
MCU5×TCH1002	0.010	-1.803**	-1.172	-0.422**	-3.106**	0.769**
MCU5×Sahana	-0.388**	0.322	1.953	0.278**	0.069	0.194
MCU5×Sumangala	0.260	0.922	-1.172	-0.009	1.769**	-0.669**
TCH1608×KC2	0.449**	-0.691	-0.359	-0.297**	-0.856	0.206*
TCH1608×TCH1002	0.517**	-0.153	2.078*	0.028	0.969	0.069
TCH1608×Sahana	-0.052	0.672	-0.797	0.228**	-0.356	-0.106
TCH1608×Sumangala	-0.913**	0.172	-0.922	0.041	0.244	-0.169
TCH1599×KC2	0.031	0.959	-1.109	0.153	1.219*	0.306**
TCH1599×TCH1002	-0.511**	0.797	0.328	-0.222**	0.044	-0.531**
TCH1599×Sahana	0.125	-1.078	1.453	0.078	-0.981	-0.006
TCH1599×Sumangala	0.354*	-0.678	-0.672	-0.009	-0.281	0.231*
TCH1569×KC2	0.439**	-0.741	0.391	0.128	-1.756**	0.406**
TCH1569×TCH1002	-0.688**	0.597	-0.172	0.253**	1.769**	-0.131
TCH1569×Sahana	0.738**	0.622	-0.047	-0.247**	0.844	0.094
TCH1569×Sumangala	-0.488**	-0.478	-0.172	-0.134	-0.856	-0.369**
TCH1452×KC2	-1.304**	0.434	-0.609	-0.347**	0.044	-0.394**
TCH1452×TCH1002	0.099	-0.228	-0.172	0.278**	-0.231	-0.131
TCH1452×Sahana	-0.84**	-0.603	-1.047	-0.122	0.744	-0.106
TCH1452×Sumangala	2.044**	0.397	1.828	0.191*	-0.556	0.631**
MCU12×KC2	0.011	-0.766	2.266*	0.253**	-0.306	-0.019

Table 10: Continued

	Characters					
	LI (g/100 seeds)	2.5% SL (mm)	UR	MIC	BS (g tex <sup>-1</sup> )	EL (%)
Hybrids						
MCU12×TCH 1002	-0.036	0.272	-0.797	-0.222**	0.619	0.044
MCU12×Sahana	0.070	0.597	-0.672	-0.122	-0.106	-0.231*
MCU12×Sumangala	-0.046	-0.103	-0.797	0.091	-0.206	0.206*
MCU9×KC 2	0.189	0.359	-1.609	-0.072	-0.531	0.006
MCU9×TCH 1002	0.267	-0.303	-0.172	0.053	0.594	0.369**
MCU9×Sahana	-0.082	-0.178	-1.047	0.053	-0.231	-0.406**
MCU9×Sumangala	-0.373*	0.122	2.828**	-0.034	0.169	0.031
TCH 1627×KC 2	0.069	-0.116	0.641	0.028	0.919	-0.219*
TCH 1627×TCH 1002	0.342*	0.822	0.078	0.253**	-0.656	-0.456**
TCH 1627×Sahana	0.428**	-0.353	0.203	-0.147	0.019	0.569**
TCH 1627×Sumangala	-0.838**	-0.353	-0.922	-0.134	-0.281	0.106
SE	0.150	0.680	1.010	0.080	0.540	0.100

\*, \*\*Means significant at 5 and 1% probability level, respectively

The general good combiners were MCU 9 for seed cotton yield and 2.5% span length; KC 2 for bundle strength; TCH 1452, MCU 12 and TCH 1002 for earliness. Among the hybrids, TCH 1608×TCH 1002 was the best for the yield and yield related characters No. of sympodia, No. of bolls, boll weight, lint index and seed index and for fibre quality.

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