

# Electronic Journal of Plant Breeding



## Research Article

### Combining ability estimates and heterosis analysis on major yield attributing traits and lint quality in American cotton (*Gossypium hirsutum* L.)

S. Mudhalvan<sup>1\*</sup>, S. Rajeswari<sup>2</sup>, L. Mahalingam<sup>2</sup>, P. Jeyakumar<sup>3</sup>,  
M. Muthuswami<sup>4</sup> and N. Premalatha<sup>2</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, CPBG, TNAU, Coimbatore, 641003.

<sup>2</sup>Department of Cotton, CPBG, TNAU, Coimbatore, 641003.

<sup>3</sup>Department of Plant Physiology, TNAU, Coimbatore, 641003

<sup>4</sup>Department of Agricultural Entomology, TNAU, Coimbatore, 641003

\*E-Mail: muthalvanshanmugam2012@gmail.com

#### Abstract

Six cotton lines and five testers were crossed in a line x tester mating design in 2019. Thereby hybrids along with 11 parents and a standard check were evaluated for combining ability and standard heterosis. Observations on sympodial branches per plant, the number of bolls per plant, boll weight, Ginning Out Turn, staple length and seed cotton yield per plant were recorded. Among the parents, GJHV 534, TVH 002, NDLH 32, TCH 1894 and RAHC 1040 displayed higher positive *gca* effects for the number of bolls/plant, sympodial branches/plant, span length, seed cotton yield and ginning outturn percentage. Such results suggested that all these five parents were good general combiners covering the yield contributing traits studied and may be preferred for hybridization and selection programmes. The crosses viz., TVH 002 x RAHC 1040, GJHV 534 x RAHC 1040 and TCH 1894 x NDLH 32 with higher estimates of *sca* effects for almost all the traits and also were observed with higher heterotic effects. Thus these hybrids could be potential hybrids for the exploitation of heterosis in cotton.

**Key words:** Combining ability, heterosis, cotton, lint quality

#### INTRODUCTION

Upland cotton is an important cash crop primarily grown for lint in more than 65 countries of the world. It is also called 'White Gold' or 'King of Apparel Fiber'. Most of the plant breeding programmes in cotton are focused on increasing yield and improving lint quality to meet the needs of the textile industry. Sprague and Tatum (1942) used the terms general combining ability (GCA) to designate the average performance of a line in hybrid combinations and specific combining ability (SCA) as the deviation in performance of a cross combination from that predicted on the basis of the general combining abilities of the parents involved in the cross. The line x tester analysis method can be

used to estimate general and specific combining abilities in both selves and cross-pollinated plants (Kempthorne, 1957). It plays as an early testing tool in identifying parents with the good combining ability and unravelling the gene action for each biometrical trait. The destiny of any crop is resolved by deducing the magnitude of additive and non-additive components in recombination breeding. Combining ability along with useful heterosis estimates paves way for identifying potential hybrids for heterosis breeding. Many advantages were offered by hybrid cotton over conventional seed variety such as increased productivity, resistance to biotic stresses and sensitivity to inputs (Ali, 2011).

## MATERIALS AND METHODS

The experimental research was conducted at the Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University during the 2019 and 2020 cotton growing seasons. Six cotton lines (high yield and compact plant types) and five testers (good lint quality and jassid resistance donor) (Table 1) were crossed in a line x tester mating design in 2019.

**Table 1. List of lines, testers and checks used in the present study**

S. No	LINES	S. No	TESTERS
1.	CO 17	1.	RAHC 1039
2.	TVH 002	2.	RAHC 1040
3.	TCH 1894	3.	KC 2
4.	GJHV 534	4.	KC 3
5.	SHC 374	5.	NDLH 32
6.	RH-1354		

**Check (Mallika) Non Bt**

The intraspecific crosses of the upland cotton genotypes were made using hand emasculation and pollination methods (Doak, 1934). A hybridization programme was carried out during the peak flowering stage to get an adequate quantity of crossed bolls. Crossed bolls were collected separately and ginned to obtain F<sub>1</sub> seeds. Simultaneously, parental seeds were multiplied by selfing selected plants by the clay smear method (Ramanathalyer, 1936). The F<sub>1</sub> seeds of 30 hybrids along with 11 parents and a standard check non bt hybrid (Mallika) were raised during 2020. Thirty crosses were raised in two replications in a randomized block design (RBD) with each cross in two rows of 6 m length and a spacing of 90 cm between rows and 60 cm between plants so as to maintain 10 plants in each row. The parents were

also raised in the adjacent block with four rows for each entry with a spacing of 90 x 45 cm, along with a standard check hybrid for evaluating their combining ability. Recommended agronomic practices and need based plant protection measures were carried out under irrigated conditions to obtain a good crop stand.

Five plants from each genotype were selected from each replication randomly for examining the biometrical observations viz., the number of sympodial branches per plant, number of bolls per plant, boll weight (g), ginning outrun (%) and seed cotton yield per plant (g). Samples were ginned and their lint was used for the analysis of fibre quality trait span length in each replication with a minimum 10 g of lint sample by using High Volume Instrument (HVI) 900 classic. The mean data collected from entire parents, crosses and standard checks were subjected to estimate the heterosis and combining ability using TNAU STAT statistical analysis software. The total variance was partitioned into replication and treatment for all those seven characters. The mean data were tabulated for yield contributing traits and analysis of variance (ANOVA), estimation of critical difference and standard error were reported in tables for discussion. Standard heterosis (check hybrid) values were calculated. The observed mean data were statistically calculated by TNAU STAT software.

## RESULTS AND DISCUSSION

According to the analysis of variance, hybrids and their parental lines were highly significant for all the traits. Also, mean squares due to general combining ability (GCA) and specific combining ability (SCA) were significant for all the traits and allowed arbitration of the genetic components of variance due to GCA and SCA (Tables 2, 3 and 4). The results of this study reported below were in accordance with the results of Mert *et al.* (2003), Baloch *et al.* (2012) and Monicashree *et al.* (2017).

**Table 2. Mean squares from analysis of variance for various characters of cotton**

Source of variation	Df	NSP	NB	BW	GOT	SL	SCY
Replication	1	0.53	1.05	0.02	1.59	0.64	59.85
Genotypes	40	42.76**	64.65**	0.65**	12.36**	4.11**	1244.93**
Parents	10	8.13**	8.84**	0.66**	5.41*	4.50**	407.04**
Lines	5	37.40**	214.76**	0.49**	13.44**	2.08**	2661.99**
Testers	4	38.84**	37.50**	1.20**	18.39**	16.57**	2838.26**
Lines vs Testers	1	33.32**	13.55*	0.81**	2.91**	1.05*	1414.31**
Crosses	29	32.52**	78.27**	0.67**	14.74**	3.91**	1476.91**
Crosses vs Parents	1	686.06**	227.78**	0.10 NS	12.90*	6.18**	2896.51**
Error	40	1.58	2.18	0.05	2.42	0.22	62.31

\* = Significant at 5% level, \*\* = Significant at 1% level, Df = Degrees of Freedom

NSP - Number of sympodial branches per plant

NB - Number of bolls/ plant

SL - Span length

BW - Boll weight

GOT - Ginning outturn

SCY - Seed cotton yield per plant

Table 3. Analysis of variance for combining ability for six yield and fibre quality traits

Source of variation	df	NSP	NB	BW	GOT	SL	SCY
Replication	1	1.15	3.31	0.04	1.57	0.56	1.84
Crosses	29	32.52**	78.27**	0.67**	14.74**	3.91**	1476.91**
Lines	5	37.40**	214.76**	0.49**	13.44**	2.08**	2661.99**
Testers	4	38.84**	37.50**	1.20**	18.39**	16.57**	2838.26**
Line × Tester	20	30.04**	52.30**	0.61**	14.33**	1.83**	908.36**
Error	29	1.51	2.11	0.03	2.34	0.23	65.23

\* = Significant at 5% level, \*\* = Significant at 1% level, DF = Degrees of Freedom

Table 4. Genetic components for six biometrical traits

Variance	df	NSP	NB	BW	GOT	SL	SCY
$\sigma^2A$	0.5853	0.0817	0.8539	0.0020	0.0133	0.0682	18.6936
$\sigma^2D$	14.7821	14.2626	25.0932	0.2897	5.9969	0.8006	421.5641
$\sigma^2A/\sigma^2D$	0.0395	0.0057	0.0340	0.0069	0.0022	0.0851	0.0443

Table 5. Mean performance of parents for different yield attributing major traits and span length

S.No.	Parents	NSP	NB	BW (g)	GOT (%)	SL (mm)	SCY (g)
<b>Lines</b>							
1	CO 17	21.20	24.10	4.66	36.73	28.00	112.17
2	TVH 002	20.05	25.50	4.71	32.88	30.00**	120.10*
3	TCH 1894	23.90*	21.20	4.83*	34.62	28.30	102.33
4	GJHV 534	20.10	25.20	3.88	35.59	26.10	97.71
5	SHC 374	19.90	23.80	3.64	33.46	26.60	86.34
6	RHC-H 1438	20.80	21.30	4.00	36.28	28.10	84.97
	Mean (Lines)	20.99	23.51	4.28	25.95	27.85	100.60
	SEd (Lines)	0.38	0.65	0.08	0.28	0.15	3.61
	CD of lines (0.05)	1.12	1.33	0.16	0.81	0.44	7.40
<b>Testers</b>							
1	RAHC 1039	19.10	19.60	3.91	36.35	30.35**	76.70
2	RAHC 1040	18.50	20.10	5.00**	31.71	29.75**	100.40*
3	KC 2	20.00	22.60	3.64	35.62	27.50	81.67
4	KC 3	15.50	22.20	3.57	33.31	27.85	78.74
5	NDLH 32	19.50	25.20*	3.37	33.99	26.00	84.98
	Mean (Testers)	18.52	21.94	3.89	28.53	28.29	84.50
	SEd (Testers)	0.35	1.21	0.07	0.25	0.14	3.29
	CD of testers (0.05)	1.03	1.21	0.15	0.74	0.40	6.75
	<b>Grand Mean</b>	<b>24.64</b>	<b>25.55</b>	<b>4.05</b>	<b>28.39</b>	<b>28.50</b>	<b>103.10</b>

NSP - Number of sympodial branches per plant  
 NB - Number of bolls/ plant  
 SL - Span length

BW - Boll weight  
 GOT - Ginning outturn  
 SCY - Seed cotton yield per plant

\* Significant at 5% level, \*\* Significant at 1% level

The *per se* performance of parents and hybrids for yield, yield contributing characters and fibre quality traits are presented in **Table 5** and **Table 6**, respectively. The biometrical traits *viz.*, the number of sympodial branches per plant, the number of bolls per plant, boll weight, ginning outturn, span length, and seed cotton yield per plant were

regarded as positive traits; therefore, higher mean values were preferred. The significance of lines, testers and hybrids were ascertained based on their corresponding Mean and CD values (baseline). The detailed outcome emphasizing *per se* performance of each biometrical trait is discussed as under.

**Table 6. Mean performance of hybrids for yield attributing major traits and span length**

S.No.	Hybrids	NSP	NB	BW (g)	GOT (%)	SL (mm)	SCY (g)
1	CO 17 X RAHC 1039	21.43	28.20	3.80	33.85	30.05**	107.17
2	CO 17 X RAHC 1040	25.20	27.70	4.99**	38.40**	28.05	138.38**
3	CO 17 X KC 2	26.00	29.00	3.52	36.28	27.75	102.14
4	CO 17 X KC 3	29.00*	32.50**	3.49	33.56	26.15	113.39
5	CO 17 X NDLH 32	30.00**	31.30**	4.62*	30.36	28.85	144.49**
6	TVH 002 X RAHC 1039	28.00	39.60**	2.88	34.49	30.75**	113.46
7	TVH 002 X RAHC 1040	29.80**	32.60**	4.86**	35.30	30.65**	158.40**
8	TVH 002 X KC 2	28.30	31.20**	3.86	35.70	27.55	120.29
9	TVH 002 X KC 3	27.40	28.20	3.90	29.13	29.25	109.98
10	TVH 002 X NDLH 32	28.60	34.90**	3.80	30.14	29.15	132.63**
11	TCH 1894 X RAHC 1039	30.00**	23.30	4.39	33.24	29.05	101.83
12	TCH 1894 X RAHC 1040	27.50	37.10**	4.18	36.12	29.70*	155.09**
13	TCH 1894 X KC 2	24.80	33.90**	3.43	36.19	28.75	115.75
14	TCH 1894 X KC 3	29.40*	29.20	3.80	32.02	27.35	111.02
15	TCH 1894 X NDLH 32	30.10**	18.60	3.74	27.74	26.85	69.49
16	GJHV 534X RAHC 1039	30.20**	15.70	2.75	26.27	30.05**	43.07
17	GJHV 534X RAHC 1040	19.10	27.60	3.75	39.10**	31.90**	103.55
18	GJHV 534 X KC 2	21.70	29.10	4.16	28.41	28.15	121.14
19	GJHV 534 X KC 3	19.70	17.40	3.76	34.29	25.80	65.41
20	GJHV 534 X NDLH 32	26.60	17.50	4.47	32.00	27.80	78.26
21	SHC 374 X RAHC 1039	28.70	19.40	3.97	27.81	29.30	77.01
22	SHC 374 X RAHC 1040	32.00**	23.80	4.60*	34.16	29.90*	109.4
23	SHC 374 X KC 2	28.20	19.50	4.92**	32.75	29.05	96.00
24	SHC 374 X KC 3	16.36	21.20	4.11	26.32	27.80	87.08
25	SHC 374 X NDLH 32	28.80	30.95**	4.25	37.20*	27.90	131.35**
26	RHC-H 1438 X RAHC 1039	26.20	20.20	4.18	31.71	29.90*	84.53
27	RHC-H 1438 X RAHC 1040	18.30	24.80	4.80**	25.47	29.65*	119.26
28	RHC-H 1438 X KC 2	24.90	23.50	3.60	34.46	28.00	84.36
29	RHC-H 1438 X KC 3	25.60	26.80	4.89**	34.73	27.85	131.19**
30	RHC-H 1438 X NDLH 32	30.00**	22.10	3.41	33.2	27.15	75.80
	<b>Mean</b>	<b>26.40</b>	<b>26.56</b>	<b>4.03</b>	<b>28.86</b>	<b>28.67</b>	<b>106.70</b>
	<b>SE d</b>	<b>1.23</b>	<b>1.45</b>	<b>0.18</b>	<b>0.88</b>	<b>0.48</b>	<b>8.07</b>
	<b>CD (0.05)</b>	<b>2.52</b>	<b>2.98</b>	<b>0.37</b>	<b>1.82</b>	<b>0.99</b>	<b>16.55</b>

\* = Significant at 5% level, \*\* = Significant at 1% level

NSP - Number of sympodial branches per plant  
 NB - Number of bolls/ plant  
 SL - Span length

BW - Boll weight  
 GOT - Ginning outturn  
 SCY - Seed cotton yield per plant

With respect to the number of sympodial branches per plant, the hybrids viz., SHC 374 x RAHC 1040 (32.00), GJHV 534 x RAHC 1039 (30.20) and TCH 1894 x NDLH 32 (30.10) showed more while, the parent SHC 374 (19.90) showed a less number of sympodial branches per plant. The maximum number of bolls per plant was recorded in TVH 002 (25.50), GJHV 534 (25.20) and NDLH 32 (25.20). Among the hybrids, TVH 002 x RAHC 1040 recorded a maximum of 39.60 bolls per plant. In the crosses, CO 17 x RAHC 1040 (4.99 g) and SHC 374 x KC 2 (4.92) higher weight of the boll was recorded and it was least in NDLH 32 (3.37). The hybrid GJHV 534 x RAHC 1040 (39.10) showed a higher value of ginning outturn, while the parent TVH 002 (32.88) recorded a lower value. Long span length was observed in the cross GJHV 534 x RAHC 1040 (31.90 mm) and the average span length was noted in GJHV 534 x KC 3 (27.30). For seed cotton yield, hybrids viz., TVH 002 x RAHC 1040 (158.40) and TCH 1894 x RAHC 1040 (155.09) recorded higher value, while among parents TVH 002 (120.10) exhibited the maximum performance for seed cotton yield per plant, while RHC H 1438 (84.97) recorded lower seed cotton yield per plant.

The general combining ability (*gca*) effects of parents and specific combining ability (*sca*) effects of hybrids for all the six characters were presented in **Tables 7 and 8**.

Line TVH 002 and two testers RAHC 1039 and NDLH 32 expressed a positive significant *gca* effect for the trait

number of sympodial branches per plant. Among the crosses, SHC 374 x RAHC 1039, GJHV 534 x RAHC 1039 and CO 17 x KC 3 expressed positive *sca* effects for the trait number of sympodial branches per plant. It is suggested that there is a possibility of isolating potential segregating progenies in these hybrids. These results are in agreement with the outputs of Soomro *et al.* (2012) and Jatoi *et al.* (2011). In TVH 002, CO17, RAHC 1040 and TCH 1894 significant positive *gca* effects were noticed for the trait number of bolls per plant. The *sca* effects in hybrids SCH 374 x NDLH 32, GJHV 534 x KC 2 and TVH 002 x RAHC 1039 were positive and significant, while the cross TVH 002 x KC 3 recorded a negative significant *sca* effect for the trait number of bolls per plant. Similar results were reported by Natera *et al.* (2012), Thiyagu *et al.* (2019) and Gnanasekaran *et al.* (2019). The parents SHC 374 (female parent), RAHC 1039 and KC 2 (pollen parents) expressed positive additive gene action for the boll weight. However, the hybrids RHC – H 1438 x KC 3, GJHV 534 x NDLH 32, TCH 1894 x RAHC 1039 and TVH 002 x RAHC 1040 displayed positive *sca* effects for the weight of the boll. These results are supported by Natera *et al.* (2012), Huangjun and Myers (2011) and Jatoi *et al.* (2011).

Line TCH 1894 and tester RAHC 1040 showed positive *gca* effects for the trait ginning outturn. The hybrids viz., SHC 374 x NDLH 32, RHC H 1438 x KC 3 and GJHV 534 x RAHC 1040 showed positive *sca* effects for ginning

**Table 7. General combining ability effects of parents for yield attributing major traits and span length**

S.No	Parents	NSP	NB	BW	GOT	SL	SCY
Lines							
1	CO 17	-0.07	3.18**	0.06	0.79	-0.50**	14.42**
2	TVH 002	2.02**	6.74**	-0.17**	-0.35	0.80**	20.25**
3	TCH 1894	1.96**	1.86**	-0.12*	1.68**	-0.33*	3.94
4	GJHV 534	-2.94**	-5.10**	-0.25**	0.32	0.07	-24.41**
5	SHC 374	0.42	-3.59**	0.34**	-1.07*	0.12	-6.53*
6	RHC-H 1438	-1.40	-3.08**	0.15*	-1.38**	-0.16	-7.67**
	SE ( $g_i$ ) $\pm$	0.38	0.46	0.05	0.48	0.15	2.55
Testers							
1	RAHC 1039	1.03**	-2.16**	-0.37**	-1.20*	1.18**	-18.85**
2	RAHC 1040	-1.08**	2.37**	0.50**	1.81**	1.31**	23.98**
3	KC 2	-0.75**	1.14*	-0.12*	0.18	-0.46**	-0.08
4	KC 3	-1.82**	-0.68	-0.04	-1.12*	-1.30**	-3.68
5	NDLH 32	2.62**	-0.67	0.02	-0.33	-0.72**	-1.36
	SE ( $g_i$ ) $\pm$	0.35	0.42	0.05	0.44	0.14	2.33

\* = Significant at 5% level, \*\* = Significant at 1% level

NSP - Number of sympodial branches per plant  
 NB - Number of bolls/ plant  
 SL - Span length

BW - Boll weight  
 GOT - Ginning outturn  
 SCY - Seed cotton yield per plant

Table 8. Specific combining ability effects of hybrids for yield contributing major traits and span length

S.No.	Cross combinations	NSP	NB	BW	GOT	SL	SCY
1	CO 17 X RAHC 1039	-5.92**	0.62	0.08	0.56	0.70	4.90
2	CO 17 X RAHC 1040	-0.05	-4.41**	0.41**	2.1	-1.42**	-6.72
3	CO 17 X KC 2	0.42	-1.88	-0.45**	1.60	0.04	-18.89
4	CO 17 X KC 3	4.49**	3.44**	-0.56**	0.20	-0.72*	-4.04
5	CO 17 X NDLH 32	1.05	2.23*	0.51**	-4.46**	1.40**	24.74
6	TVH 002 X RAHC 1039	-1.45	8.46**	-0.61**	2.34*	0.10	5.36
7	TVH 002 X RAHC 1040	2.46**	-3.07**	0.50**	0.13	-0.12	7.47
8	TVH 002 X KC 2	0.63	-3.24**	0.11	2.16	-1.46**	-6.58
9	TVH 002 X KC 3	0.8	-4.42**	0.08	-3.10**	1.08**	-13.29*
10	TVH 002 X NDLH 32	-2.44**	2.27*	-0.07	-1.53	0.40	7.03
11	TCH 1894 X RAHC 1039	0.61	-2.96**	0.85**	-0.94	-0.47	10.05
12	TCH 1894 X RAHC 1040	0.22	6.31**	-0.23	-1.08	0.06	20.47**
13	TCH 1894 X KC 2	-2.81**	4.34**	-0.37**	0.63	0.87*	5.20
14	TCH 1894 X KC 3	2.86**	1.46	-0.07	-0.61	0.31	4.07
15	TCH 1894 X NDLH 32	-0.88	-9.15**	-0.19	2.00	-0.77*	-39.79**
16	GJHV 534X RAHC 1039	5.71**	-3.60**	-0.67**	0.17	0.13	-20.36**
17	GJHV 534X RAHC 1040	-3.28**	3.77**	-0.53**	3.27**	1.85**	-2.72
18	GJHV 534 X KC 2	-1.01	6.50**	0.50**	-2.50*	-0.13	38.94**
19	GJHV 534 X KC 3	-1.94*	-3.38**	0.02	1.40	-1.64**	-13.19*
20	GJHV 534 X NDLH 32	0.52	-3.29**	0.67**	-2.34**	-0.22	-2.67
21	SHC 374 X RAHC 1039	0.86	-1.41	-0.03	-2.72**	-0.67	-4.30
22	SHC 374 X RAHC 1040	6.27**	-1.54	-0.27*	-0.29	-0.19	-14.75*
23	SHC 374 X KC 2	2.13*	-4.61**	0.67**	-0.07	0.72*	-4.09
24	SHC 374 X KC 3	-8.63**	-1.09	-0.23	-1.17	0.31	-9.41
25	SHC 374 X NDLH 32	-0.63	8.65**	-0.14	4.24**	-0.17	32.55**
26	RHC-H 1438 X RAHC1039	0.17	-1.12	0.37**	0.59	0.21	4.35
27	RHC-H 1438 X RAHC1040	-5.62**	-1.05	0.12	-4.14**	-0.17	-3.75
28	RHC-H 1438 X KC 2	0.65	-1.12	-0.47**	-1.83	-0.05	-14.58*
29	RHC-H 1438 X KC 3	2.42**	4.00**	0.75**	3.29**	0.64	35.85**
30	RHC-H 1438 X NDLH 32	2.38*	-0.71	-0.79**	2.09	-0.64	-21.87**
	<b>SE</b>	<b>0.87</b>	<b>1.02</b>	<b>0.13</b>	<b>1.08</b>	<b>0.34</b>	<b>5.71</b>

\* = Significant at 5% level, \*\* = Significant at 1% level

outturn. Present results are supported by the report of Kumar *et al.* (2013). Three parents *viz.*, TVH 002, RAHC 1039 and RAHC 1040 showed positive *gca* effects for staple length indicating that the trait was conditioned by additive genes in these parents, suggesting the amenability of these genotypes to be used in obtaining varieties with long staple length. There were only five crosses *viz.*, CO 17 x NDLH 32, TVH 002 x KC 3, TCH 1894 x KC 2, GJHV 534 x RAHC 1040 and SHC 374 x KC 2 which displayed positive *sca* effects for the trait staple length. It is suggested that there is a probability of isolating potential segregating progeny from these five hybrids. Similar results were reported by Baloch *et al.* (2012) and

Natera *et al.* (2012). In case of *gca*, CO 17, TVH 002 and RAHC 1040 expressed the positive additive type of gene action for seed cotton yield per plant. However, hybrids *viz.*, TCH 1894 x RAHC 1040, GJHV 534 x KC 2, SHC 374 x NDLH 32 and RHC H 1438 x KC 3 showed positive *sca* effects for seed cotton yield per plant. In later generations, the selection is suggested to isolate promising genotypes for the development of cultivars/hybrids to boost seed cotton yield/unit area. similar results were also reported by Kumar *et al.* (2013), Abro *et al.* (2009), Natera *et al.* (2012), Soomro *et al.* (2012), Huangjun and Myers (2011) and Jatoi *et al.* (2011).



The percentage of standard heterosis for six characters expressed by 30 hybrids was estimated and presented in **Table 9**. The hybrid Mallika was considered a standard check for all the characters. The range standard heterosis was presented for all the six yield components and fibre quality traits.

Standard heterosis ranged from -16.93 (SHC 374 x KC 3) to 62.44 (SHC 374 x RAHC 1040). Twenty four hybrids recorded significantly positive standard heterosis. While, the crosses of SHC 374 x RAHC 1040, GJHV 534 x RAHC 1039 and TCH 1894 x NDLH 32 had greater positive value for standard heterosis for the trait sympodial branches per plant. These results agree with

those observed by Khan and Qasim (2012). Standard heterosis varied from -46.23 (GJHV 534 x RAHC 1039) to 35.62 (TVH 002 x RAHC 1039) for the trait number of bolls per plant. Six hybrids showed significant positive standard heterosis for the number of bolls per plant. The cross TVH 002 x RAHC 1039 had high positive standard heterosis for the trait number bolls per plant. These results are in agreement with the results of Soomro *et al.* (2012). Standard heterosis ranged from -30.86 (GJHV 534 x RAHC 1039) to 25.82 (CO 17 x RAHC 1040) for the trait boll weight. Nine hybrids recorded significantly positive standard heterosis for boll weight. The cross TVH 002 x RAHC 1040 had a higher value for standard heterosis. These findings are supported by Nassar (2013)

**Table 9. Estimates of standard heterosis for yield contributing major traits and span length (Per cent)**

S.No.	Cross combinations	NSP	NB	BW	GOT	SL	SCY
1	CO 17 X RAHC 1039	8.78	-3.42	-4.28	-5.68	9.67**	-7.58
2	CO 17 X RAHC 1040	27.92**	-5.14	25.82**	7.01	2.37	19.34**
3	CO 17 X KC 2	31.98**	-0.68	-11.34*	1.09	1.28	-11.91
4	CO 17 X KC 3	47.21**	11.30*	-12.09*	-6.48	-4.56*	-2.21
5	CO 17 X NDLH 32	52.28**	7.19	16.25**	-15.39**	5.29**	24.61**
6	TVH 002 X RAHC 1039	42.13**	35.62**	-27.58**	-3.90	12.23**	-2.15
7	TVH 002 X RAHC 1040	51.27**	11.64*	22.29**	-1.64	11.86**	36.61**
8	TVH 002 X KC 2	43.65**	6.85	-2.90	-0.53	0.55	3.74
9	TVH 002 X KC 3	39.09**	-3.42	-1.76	-18.84**	6.75**	-5.15
10	TVH 002 X NDLH 32	45.18**	19.52**	-4.28	-10.41*	6.39**	14.38*
11	TCH 1894 X RAHC 1039	52.28**	-20.21**	10.58*	-7.37	6.02**	-12.18
12	TCH 1894 X RAHC 1040	39.59**	27.05**	5.29	0.64	8.39**	33.75**
13	TCH 1894 X KC 2	25.89**	16.10**	-13.73**	0.85	4.93**	-0.18
14	TCH 1894 X KC 3	49.24**	0.00	-4.28	-6.26	-0.18	-4.26
15	TCH 1894 X NDLH 32	52.79**	-36.30*8	-5.92	5.07	-2.01	-40.08**
16	GJHV 534X RAHC 1039	53.30**	-46.23**	-30.86**	-8.09	9.67**	-62.86**
17	GJHV 534X RAHC 1040	-3.05	-5.48	-5.54	8.94*	16.42**	-10.70
18	GJHV 534 X KC 2	10.15	-0.34	4.79	-11.66**	2.74	4.47
19	GJHV 534 X KC 3	0.00	-40.41**	-5.16	-4.44	-5.84**	-43.59**
20	GJHV 534 X NDLH 32	35.03**	-40.07**	12.59**	-10.82*	1.46	-32.51**
21	SHC 374 X RAHC 1039	45.69**	-33.56**	0.00	-19.99**	6.93**	-33.58**
22	SHC 374 X RAHC 1040	62.44**	-18.49**	15.87**	-4.82	9.12**	-5.65
23	SHC 374 X KC 2	43.15**	-33.22**	24.06**	-8.75*	6.02**	-17.21*
24	SHC 374 X KC 3	-16.93*	-27.40**	3.40	-15.48**	1.46	-24.90**
25	SHC 374 X NDLH 32	46.19**	5.99	6.93	3.66	1.82	13.28
26	RHC-H 1438 X RAHC 1039	32.99**	-30.82**	5.42	-11.63**	9.12**	-27.11**
27	RHC-H 1438 X RAHC 1040	-7.11	-15.07*8	21.03**	-16.43**	8.21**	2.85
28	RHC-H 1438 X KC 2	26.40**	-19.52**	-9.45	-14.54**	2.19	-27.25**
29	RHC-H 1438 X KC 3	29.95**	-8.22	23.30**	-3.9	1.64	13.14
30	RHC-H 1438 X NDLH 32	52.28**	-24.32**	-14.11	-3.22	-0.91	-34.63**
	<b>SE</b>	<b>1.25</b>	<b>1.43</b>	<b>0.18</b>	<b>1.51</b>	<b>0.48</b>	<b>8.00</b>

\* = Significant at 5% level, \*\* = Significant at 1% level

and Monicashree *et al.* (2017). The range of standard heterosis was from -19.99 (SHC 374 x RAHC 1039) to 8.94 (GJHV 534 x RAHC 1040) for the trait ginning outturn. The hybrid, GJHV 534 x RAHC 1040 showed significant positive standard heterosis for ginning outturn. The hybrid GJHV 534 x RAHC 1040 showed positive standard heterosis. Nassar (2013) and Monicashree *et al.* (2017) reported a similar result. Standard heterosis varied from -5.84 (GJHV 534 x KC 3) to 16.42 (GJHV 534 x RAHC 1040) for the trait span length. Fifteen hybrids were recorded significantly positive standard heterosis. For fibre length character, more number of crosses had positive standard heterosis. Cross GJHV 534 x RAHC 1040 had a greater positive value of standard heterosis for fibre length character and could be exploited further. These results are in agreement with the reports of Geddamm *et al.* (2013) and Yuksel Bolek *et al.* (2010). The range of standard heterosis was from -62.36 (CO 17 x KC 3) to 14.23 (GJHV 534 x RAHC 1040) for seed cotton yield per plant. Five crosses showed significantly positive standard heterosis. These results are in accordance with El-Hashash (2013) and Gnanasekaran *et al.* (2019).

Cotton textile industries demand better yield and high lint quality cotton and for this reason development of varieties with good yield potential and better fibre quality is one of the important targets of all cotton breeders. The parents GJHV 534, TVH 002, NDLH 32, TCH 1894 and RAHC 1040 were found to have higher positive *gca* effects. Such results suggested that all the five parents were good general combiners for the yield attributing major traits studied and may be used for hybridization and selection programmes. The crosses like TVH 002 x RAHC 1040, GJHV 534 x RAHC 1040, CO 17 x RAHC 1039, SHC 374 x RAHC 1040 and TCH 1894 x RAHC 1040 were identified as the best hybrids for exploitation through heterosis breeding with regard to *per se*, *sca* effect and standard heterosis.

## REFERENCES

- Abro, S., Kandhro, M.M., Laghari, S., Arain, M.A. and Deho, Z.A. 2009. Combining ability and heterosis for yield contributing traits in upland cotton (*Gossypium hirsutum* L.). *Pak. J. Bot.*, **41**(4): 1769-1774.
- Ali, G.M. 2011. Cotton hybrid seed production at PARC. Technical Report, **2**(4): 1.
- Baloch, A. W., Ejaz, M., Baloch, G.A., Yasir, T.A., Hayat, S., Shah, N.M., Baloch, M.J., Ahmad, I., Rahman, S., Wasila, H. and Khan, M.A. 2012. Development of superior F1 hybrids design-ii analysis for estimating combining ability of fibre and earliness in upland cotton. *Global J. Biodiversity Sci. and Management*, **2**(1): 38-42.
- Doak, C.C. 1934. A new technique in hybridizing suggested changes in existing methods of emasculation and bagging cotton flowers. *J. Hered.*, **25**: 201-204. [[Cross Ref](#)]
- El-Hashash, E.F. 2013. Heterosis and gene action among single and double-cross hybrids performances in cotton. *American-Eurasian J. Agric. & Environ. Sci.*, **13** (4): 505-516.
- Geddamm, Sekhar Babu and Khadi, B.M. 2013. Heterosis in GMS based diploid cotton hybrids for fibre quality traits. *Asian J. Bio. Sci.*, **8**(1): 79-81.
- Gnanasekaran, M., Thiyagu, K. and Gunasekaran, M. 2019. Combining ability and heterosis studies for seed cotton yield and fibre quality traits in hirsutum cotton. *Electronic Journal of Plant Breeding*, **10**(4): 1519-1531. [[Cross Ref](#)]
- Huangjun Lu. and Myers, G.O. 2011. Combining abilities and inheritance of yield components in influential upland cotton varieties. *Aus. J. Crop Sci.*, **5**(4): 384-390.
- Jatoi, W.A., Baloch, M.J., Veesar, N.F. and Panhwar, S.A. 2011. Combining ability estimates from line x tester analysis for yield and yield components in upland cotton genotypes. *J. Agric. Res.*, **49**(2): 165-172
- Kempthorne, O. 1957. An introduction to genetic statistics. John Wiley and Sons, Inc. New York.
- Khan, T.M. and Qasim, M. U. 2012. Genetic studies of yield traits in cotton *Gossypium hirsutum* L. *J. Agric. Res.*, **50** (1): 21-28.
- Kumar, M., Nirania, K.S., Sangwan, R.S. and Yadav, N.K. 2013. Combining ability studies for yield and quality traits in upland cotton *Gossypium hirsutum* L. *J. Cotton Res. Dev.*, **27** (2): 171-174.
- Mert, M., Gencer, O., Akiscan, Y. and Boyaci, K. 2003. Determination of superiority parents and hybrid combinations in respect to lint yield and yield components in cotton (*G. hirsutum* L.). *Turkish J. Agric. Fore.*, **27**: 337-43.
- Monicashree, C., Amala Balu, P. and Gunasekaran, M. 2017. Combining ability and heterosis studies on yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Int.J.Curr.Microbiol.App.Sci.*, **6**(8): 912-927. [[Cross Ref](#)]
- Nassar, M.A.A. 2013. Some genetic parameters and heterosis in two crosses of Egyptian cotton. *J. Appl. Sci. Res.*, **9**(1): 548-553.
- Natera, J.R., Mendez., A. Rondón., Hernández, J. and Fernando Merazo Pinto, J. 2012. Genetic studies in upland cotton *Gossypium hirsutum* L. general and specific combining ability. *J. Agr. Sci. Tech.*, **14**: 617-627.



- Ramanatha Iyer. 1936. An inexpensive method of selfing cotton flowers. *Emp. Cott. Grow. Rev.*, **13**: 28–30.
- Sprague, G. F and Tatum, L. A. 1942. General versus specific combining ability in single crosses of corn. *J. Amer. Soc. Agron.*, **34**:923-952. [\[Cross Ref\]](#)
- Soomro, M. H., Markhand, G.S. and Mirbahar, A.A. 2012. Estimation of combining ability in F2 Population of upland cotton under drought and non- drought regimes. *Pak. J. Bot.*, **44**(6): 1951-1958.
- Thiyagu, K., Gnanasekaran, M. and Gunasekaran, M. 2019. Components and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, **10**(4): 1501-1511. [\[Cross Ref\]](#)
- Yuksel Bolek, Cokkizgin, H. and Bardak, A. 2010. Combining ability and heterosis for fiber quality traits in cotton. *Plant Breeding and Seed Science*, **62**: 3–16. [\[Cross Ref\]](#)