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Research Article

Heterosis and nicking ability studies for yield and fibre quality in intra-*hirsutum* hybrids

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Abstract
The present investigation aims at estimating *per se* performance, combining ability and standard heterosis for 16 biometrical traits using 40intra-*hirsutum*hybrids synthesized from eight ovule and five pollen parents in Line × Tester fashion. The analysis of variance was significant for all biometrical traits except fibre fineness. Apart from internode length and ginning outturn, all traits were predominantly governed by dominance gene action. Among the parents CPD 1701, RHCHD 1314, RHCHD 1406, MCU 9, CO 16 and CO 14 ranked as good general combiners. Based on mean, sca effects and standard heterosis, PBH 116 × CO 16, RHCHD 1314 × CO 14, CPD 1701 × CO 16 and CPD 1702 × MCU 7 was perceived as amenable for heterosis breeding.

Keywords
Gossypium hirsutum L., Line × Tester, Combining ability, Standard Heterosis

INTRODUCTION

Cotton satisfies the attire needs of millions of people across the globe singly occupying about 25% (Ministry of textiles, GoI, 2017) of total global fibre production. Due to its intrinsic production potential, *Gossypium hirsutum* L. is always favored and cultivated predominantly in India. Since 1970's (first intra-*hirsutum* hybrid, H-4), the thirst for establishing high yielding, qualitycotton has never ceased.Even now researchers fine tune the obsoleteand novel cultivarsanticipatinga remarkable breakthrough in yield and quality aspects.Agronomically as mechanization in cotton has become the need of an hour, compact genotypes are evolved with attempts to balance yield and fibre traits.

The crux of every breeding experiment lies in fixing best parents meeting the objectives. Line × Tester analysis (Kempthorne,1957) is one of the simplest and most extensively used mating design. It serves as an early testing tool in identifying parents with good combining ability and also unveils the gene action for each biometrical trait. Either heterosis breeding or recombination breeding, the destiny of the crop is determined by deducing the magnitude of additive and non-additive components.Combining ability along with useful heterosis estimates helps in identifying potential hybrids for heterosis breeding. Thus, the motive of the present experiment is to assessgeneral combining ability,specific combining abilityand economic heterosis in intra-specific crosses synthesized using compact and non-compact lines andwell-established varieties as testers.

MATERIALS AND METHODS

The experiment was carried out during *kharif* 2019 in the experimental zone of Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Forty intra-*hirsutum* hybrids were generated using eight lines (5 compact and 3 non-compact plant types) viz., TCH 1897, RHCHD1314, SHC32, F 2382, RHCHD1406, CPD 1702, CPD 1701, PBH 116 and five testers viz., MCU5, MCU7, MCU9, CO16 and CO14in Line × Tester fashion.The hybrids were synthesized as per conventional hand emasculation and dusting method devised by Doak (1934). The resultant $F_1$and its corresponding parents were raised in 6-metre-long ridge with a crop geometry of 90 cm × 60 cm in randomized complete block design (RCBD) with two replications. Necessary agronomic, plant protection measures and sufficient irrigation were ensured. From each replication, five competing plants in each entry were chosen and 16 biometrical traits viz., days to first flowering (DFF), plant height (PH), number of monopodia per plant (NMP), number of sympodial branches per plant (NSP), internode length (IL), number of bolls per plant(NBP), boll weight (BW), seed index (SI), lint index(LI) , ginning outturn (GOT), seed cotton yield (SCY), 2.5% span length (SL), uniformity ratio (UI), fibre fineness (FF), fibre strength (FS) and elongation percentage (EL) were recorded.The analysis of variance (ANOVA) for the biometrical traits were worked out as per the method formulated by Panse and Sukhatme (1985). The magnitude of general combining ability (GCA)and specific combining ability (SCA) along with computation of additive and non-additive variance for determining gene actionin various traits were performed as per the method conceived by Kempthorne (1957). Statistical analysis was done using TNAUSTAT package using the consolidated mean arrived over sampled five plants.

RESULTS AND DISCUSSION

Analysis of variance was worked out for all sixteen biometrical traits to ensure presence of adequate variability between genotypes. Genotypeswere highly significant for almost all traits except for fibre fineness **(Table 1a)**.Insignificance of genotypes in fibre fineness was also reported by Swamy *et al.,* 2013. Parents showed significance in all traits except internode length, lint index, fibre fineness and elongation percentage. Theseresults were in accordance with Thiyagu *et al.,* 2019, Gnanasekaran *et al.,* 2019 for elongation percent,Swamy *et al.,* 2013, Sawarkar *et al.,* 2015 for fibre fineness, Preetha and Raveendran., 2007 for internode length and Udaya and Patil., 2020 for lint index. Crosses were unanimously significant for all traits.

From the results of mean sum of squares obtained from combining ability variances (**Table 1b**) lines projected significant difference for all yield related traits except boll weight.In fibre quality, the lines were not significant for any traits except for elongation percentage.Similar results were obtained by Preetha and Raveendran., 2007, Sawarkar *et al.,* 2015 and Alkuddsi *et al.,* 2013. In case of testers, all traits apart from days to first flowering, plant height, internode length and elongation percentage were found to have significance. These results were akin with Preetha and Raveendran., 2007 and Kumbhalkar *et al.,* 2018 except for internode length.

Combining ability studies are decision making tool which enables the researcher to determine the journey of any genetic material. Additive gene action and dominance gene action are the two facets of combining ability. It is essential to know the nature of gene action for every trait for executing trait-specific improvements in crop. The comparative estimates of variances owing to additive (A) and non-additive (D) components for all biometrical traits are displayed in **table 1b.**The proportion between additive and non-additive components were below one for all traits excluding internode length and ginning outturn. This indicates the presence of both additive and non-additive components with primacy of non-additive gene actionfor most of the traits.Non-additive gene action was alsomajorly recorded by Sivia *etal.,* 2017, Monicashree *et al.,*2017 and Pushpam *et al.,* 2015. In contrary, prevalence of additive gene action including ginning outturn was reported by Usharani *et al.,* 2014 and Ashokkumar *et al.,* 2014.

Table 1a. Analysis of variance for different yield and fibre quality traits

Source of variation	Mean squares																
	df	DFF	PH	NMP	NSP	IL	NB	BW	SI	LI	GOT	SCY	SL	UI	FF	FS	EL
Replication	1	0.60	2.58	0.003	0.002	0.03	1.01	0.25	0.18	0.01	1.30	1.00	2.24	0.11	0.05	2.62	0.02
Genotypes	52	3.71**	419.72**	0.16**	31.32**	0.38*	52.05**	0.24**	1.86**	0.49**	9.45**	391.22**	3.83**	2.15**	0.46	1.97**	0.01*
Parents	12	5.07**	439.08**	0.22**	30.21**	0.35	36.98**	0.16*	1.76*	0.42	21.19**	108.27**	7.81**	2.97**	0.23	1.66*	0.01
Crosses	39	3.36**	285.45**	0.14**	30.61**	0.41*	55.38**	0.16**	1.34*	0.48*	6.08**	460.42**	2.49*	1.84*	0.53*	1.84**	0.01*
Crossesvs Parents	1	0.61	5423.77**	0.30**	72.54**	0.32	103.08**	4.46**	23.58**	1.86**	0.21	1087.71**	8.49*	4.56*	0.27	10.82**	0.06**
Error	52	1.01	76.27	0.009	1.78	0.24	3.68	0.07	0.73	0.24	2.12	36.91	1.30	0.98	0.32	0.77	0.01

*Significant at 5 % level of significance **Significant at 1% level of significance

DFF - Days to first flowering
PH - Plant height (cm)
NMP- Number of monopodia per plant
NSP - Number of sympodial branches per plant
IL - Internodal length (cm)

NB - Number of bolls per plant
BW - Boll weight (g)
SI - Seed index
LI - Lint index
GOT - Ginning outturn (%)
SCY - Seed cotton yield (g)

SL. - 2.5 % span length (mm)
UI - Uniformity ratio
FF - Fibre fineness (Mic.)
FS - Fibre strength (g/tex)
EL - Elongation percentage (%)

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Table 1b. Analysis of variance for combining ability for various biometrical traits

Source of variation	Mean squares																
	df	DFF	PH	**NMP**	**NSP**	**IL**	**NB**	**BW**	**SI**	**LI**	**GOT**	**SCY**	**SL**	**UI**	**FF**	**FS**	**EL**
Replication	1	0.80	9.80	0.004	0.02	0.00	0.96	0.25	0.93	0.003	1.75	2.34	0.006	0.00	0.33	3.02	0.02
Crosses	39	3.36**	285.45**	0.14**	30.61**	0.41	55.38**	0.16**	1.34	0.48*	6.08**	460.42**	2.49*	1.84**	0.53	1.84**	0.01*
Lines	7	11.54**	1222.97**	0.15**	131.29**	1.01**	163.99**	0.15	2.77**	0.78*	16.17**	1039.82**	0.59	1.60	0.58	0.51	0.02**
Testers	4	0.89	132.62	0.13**	10.97**	0.32	93.52**	0.92**	4.00**	1.73**	16.80**	694.65**	16.32**	5.94**	0.85*	8.18**	0.01
Line × Tester	28	1.67*	72.90	0.13**	8.24**	0.27	22.78**	0.06	0.60	0.23	2.02	282.11**	0.99	1.31	0.47	1.27	0.008
Error	39	0.90	87.61	0.01	1.89	0.26	4.03	0.07	0.88	0.28	1.93	38.15	1.40	0.75	0.32	0.75	0.006
Variance																	
$\sigma^2 A$		0.0448	5.6237	0.0001	0.5918	0.0037	0.8625	0.0028	0.0196	0.0067	0.1073	4.7179	0.0397	0.0140	0.0016	0.0152	0.0001
$\sigma^2 D$		0.3849	7.3542	0.0619	3.1725	0.0012	9.3769	0.0074	0.1433	0.0266	0.0454	121.9763	0.2046	0.2824	0.0769	0.2565	0.0015
$\sigma^2 A/\sigma^2 D$		0.1164	0.7647	0.0016	0.1865	3.0833	0.0920	0.3784	0.1368	0.2519	2.3634	0.0387	0.1940	0.0496	0.0208	0.0593	0.0667
% Contribution																	
Lines		61.59	76.90	19.67	77.00	44.65	53.15	16.89	37.26	29.27	47.76	40.54	4.26	15.66	19.79	5.00	36.60
Testers		2.72	4.77	9.98	3.68	8.13	17.32	58.09	30.70	36.90	28.35	15.47	67.22	33.11	16.49	45.57	10.11
Lines × Testers		35.69	18.34	70.35	19.33	47.22	29.54	25.02	32.03	33.82	23.89	43.99	28.52	51.23	63.73	49.43	53.30

*Significant at 5 % level of significance **Significant at 1% level of significance

On observing the contribution of lines, testers and their interactions for each trait studied **(table 1b)**, the proportional contribution of lines were major for days to first flowering, plant height, number of sympodial branches, number of bolls per plant, seed index and ginning outturn. The contribution of testers was negligible except for boll weight, lint index and 2.5% span length. The remaining seven traits were predominantly contributed by line × tester interactions.

In this experiment parameters such as days to first flowering,plant height, number of monopodia per plant, internode length, and fibre fineness were considered as negative traits. Based on *per se* performance of parents **(Table 2**), among lines RHCHD1406 recorded desirable significant mean performance for six biometrical traits viz., plant height, number of monopodia per plant, internode length, seed index, 2.5% span length and fibre strength. Secondly, line TCH 1897 also recordedsignificant mean performance for fiveimportant traits such as plant height, number of monopodia per plant, seed cotton yield per plant,uniformity ratio and fibre strength. Thirdly,CPD 1701 reported desirable*per se* performance for four yield parameters namelyplant height, number of monopodia per plant, internode length and ginning outturn. Lines RHCHD1314, F2382 and PBH 116 reported increased performance for three traits each.

Among testers, MCU5 secured highest significant mean performance for seven yield and fibre quality traits viz., days to first flowering,number of monopodia per plant,ginning outturn, 2.5 % span length, uniformity ratio, fibre strength and elongation percentage. Tester CO 14 also accomplished significant mean performance for plant height,boll weight,2.5% span length and fibre strength. Comparably, CO 16 also recorded significant mean values for fourquantitative traits such as number of sympodial branches per plant, number of bolls per plant, ginning outturn and seed cotton yield per plant, uniformity ratio.

According to Dhillion (1975), the estimation of general combining ability (gca) in parents guides the researchers in choosing appropriate parents with regards to expected performance of its offspring. The chance of expecting transgressive segregants in successive generations increases when parents with high general combining ability is deployed in hybridization programmes (Singh and Hari Singh, 1985). In the present study, line CPD 1701 stands to be a good general combiner for plant height

Table 2. Mean performance of parents and hybrids for various yield and fibre quality traits

S. no	Parents	DFF	PH	NMP	NSP	IL	NB	BW	SI	LI	GOT	SCY	SL	UI	FF	FS	EL
	Lines (Female)																
1	TCH 1897	58.50	62.50*	0.68*	13.70	4.03	15.40	3.48	8.31	5.25	33.67	72.70*	25.90	83.15*	3.64	26.25*	5.70
2	RHCHD 1314	57.00	87.76	1.63	23.10*	4.26	16.47*	3.21	8.57	4.22	32.98	50.70	25.30	82.45*	3.79	25.45	5.65
3	SHC 32	60.00	69.08	0.37*	13.66	3.59	11.16	3.38	8.16	4.80	35.90	45.75	25.05	81.60	4.06	25.10	5.70
4	F 2382	58.00	77.33	0.61*	15.50	3.25	15.16	3.40	8.68	5.39*	38.25*	45.17	24.40	81.35	3.56	25.30	5.70
5	RHCHD 1406	59.00	58.40*	0.68*	11.80	3.05*	10.80	3.39	9.46*	4.95	34.39	50.50	27.70*	81.20	3.46	26.25*	5.65
6	CPD 1702	55.00*	81.00	0.90	16.80*	3.50	15.60	3.43	7.92	4.42	35.89	52.00	25.65	81.65	3.77	25.35	5.60
7	CPD 1701	58.00	51.90*	0.33*	13.00	2.85*	13.10	2.99	8.24	5.20	38.98*	48.80	24.10	81.75	4.60	24.70	5.60
8	PBH 116	55.00*	90.80	0.95	16.90*	3.80	18.90*	3.50	8.70	4.63	34.75	50.70	24.05	80.15	3.97	24.55	5.60
	Line mean	57.56	72.34	0.76	15.55	3.54	14.57	3.34	8.50	4.85	35.60	51.98	25.26	81.66	3.85	25.36	5.65
	SEd	0.42	4.18	0.04	0.61	0.22	0.89	0.11	0.42	0.23	0.62	2.76	0.52	0.38	0.25	0.38	0.03
	CD (0.05)	0.85	8.41	0.08	1.23	0.46	1.80	0.23	0.84	0.47	1.24	5.55	1.06	0.77	0.50	0.78	0.06
	Testers (Male)																
1	MCU 5	55.50*	82.25	0.57*	19.63	3.95	15.82	3.47	9.81	4.75	32.57*	49.73	29.10*	85.05*	3.39	27.30*	5.75*
2	MCU 7	55.50*	93.40	0.64	20.27	3.46*	14.90	3.20	9.37	5.28	27.13	41.47	25.50	82.55	3.82	25.55	5.65
3	MCU 9	56.50	99.50	0.56*	22.40*	3.99	22.20*	4.11*	10.78*	5.80*	35.01*	51.90	28.55	80.85	3.49	26.20	5.70
4	CO 16	57.50	92.92	0.63	22.64*	3.78	26.66*	3.64	9.63	4.96	34.17*	55.10*	28.00	82.65	4.20	25.70	5.70
5	CO 14	56.50	71.50*	0.90	18.30	3.95	15.20	3.82*	10.68	4.33	29.01	51.90	29.75*	81.70	4.00	27.60*	5.70
	Tester mean	56.30	87.91	0.66	20.64	3.82	18.95	3.64	10.05	5.02	31.57	50.01	28.18	82.56	3.77	26.47	5.70
	Mallika	55.50	83.10	0.47	16.30	3.30	15.90	3.99	11.52	6.01	31.11	46.80	26.10	82.55	4.71	25.75	5.70
	SEd	0.33	3.30	0.03	0.48	0.18	0.70	0.09	0.33	0.18	0.49	2.18	0.41	0.30	0.19	0.30	0.02
	CD (0.05)	0.67	6.65	0.07	0.97	0.36	1.42	0.18	0.66	0.37	0.98	4.38	0.84	0.61	0.39	0.61	0.05

*Significant at 5 % level of significance

Standard check-Mallika

Table 2. Continual

S.no	Cross combinations	DFF	PH	NMP	NSP	IL	NB	BW	SI	LI	GOT	SCY	SL	UI	FF	FS	EL
1	TCH 1897 X MCU 5	59.00	91.38	0.78	16.70	4.20	16.43	3.97	11.29	5.77	33.99	54.88	27.40	82.85	3.67	26.50	5.70
2	TCH 1897 X MCU 7	56.50	80.00	1.00	14.90	4.00	13.60	3.84	10.01	5.05	33.57	38.80	26.20	82.80	6.11	25.70	5.80
3	TCH 1897 X MCU 9	58.00	85.10	0.80	17.10	3.80	19.00	3.97	11.84	5.63	33.33	58.70	26.55	83.05	3.88	26.90	5.75
4	TCH 1897 X CO 16	59.00	78.60	0.90	14.00	3.60	11.70	3.67	10.26	5.02	33.81	34.60	27.00	81.90	3.52	26.65	5.70
5	TCH 1897 X CO 14	57.50	96.90	0.90	18.60	3.20	17.10	4.34	11.30	5.05	30.95	53.90	29.20	83.70	3.96	28.45*	5.85
6	RHCHD-1314 X MCU 5	59.50	119.40	1.63	26.10*	5.10	22.90*	3.98	11.20	4.77	31.84	83.00*	28.85	81.95	4.01	27.70	5.80
7	RHCHD-1314 X MCU 7	56.50	109.20	0.58*	27.40*	4.10	18.10	3.43	8.72	4.19	32.30	50.90	25.65	81.70	3.73	25.75	5.65
8	RHCHD-1314 X MCU 9	55.50	109.90	0.90	28.60*	3.70	27.00*	3.80	9.32	4.65	30.46	63.20	27.05	81.90	3.98	26.30	5.80
9	RHCHD-1314 X CO 16	57.00	125.40	1.00	30.70*	5.05	24.20*	3.87	8.99	4.76	34.77	72.80*	26.90	82.55	4.18	26.00	5.65
10	RHCHD-1314 X CO 14	57.50	104.10	1.10	22.60*	4.05	39.50*	4.34	10.20	4.89	31.57	110.00*	27.40	82.50	3.33	27.05	5.70
11	SHC 32 X MCU 5	55.00*	96.30	0.80	20.00	3.75	16.50	3.64	9.70	4.96	33.78	61.50	27.70	83.20	3.80	27.20	5.75
12	SHC 32 X MCU 7	57.00	84.58	0.33*	17.85	3.52	15.10	3.29	9.16	4.22	33.98	39.63	26.10	81.25	3.64	25.75	5.65
13	SHC 32 X MCU 9	55.50	99.00	0.90	21.70	3.85	21.00	3.98	10.17	5.14	34.65	52.00	26.25	83.20	3.30	26.50	5.70
14	SHC 32 X CO 16	56.00	98.10	0.90	20.00	3.90	19.30	3.80	9.07	5.57	37.92*	64.30	26.60	81.60	3.52	26.00	5.65
15	SHC 32 X CO 14	55.50	98.50	0.90	19.80	3.50	18.70	4.11	10.50	5.28	33.51	56.70	27.70	82.85	3.65	27.30	5.75
16	F 2382 X MCU 5	56.50	91.30	0.93	19.30	3.58	14.70	4.00	11.11	5.04	31.22	35.40	27.70	83.00	3.67	28.45*	5.85
17	F 2382 X MCU 7	56.50	88.50	0.60*	18.00	3.92	12.80	3.71	10.50	5.19	33.22	34.20	26.90	81.80	4.37	26.40	5.80
18	F 2382 X MCU 9	58.00	100.40	1.10	19.70	3.20	14.60	4.12	10.42	5.29	33.71	48.70	25.95	82.65	3.78	25.60	5.75
19	F 2382 X CO 16	56.50	103.40	0.80	19.70	3.25	15.10	3.54	10.99	5.30	32.45	56.10	26.60	81.40	4.87	26.30	5.85
20	F 2382 X CO 14	57.00	89.70	1.10	18.10	3.40	16.60	4.11	10.62	5.03	32.13	49.00	27.60	82.90	4.39	26.90	5.80
21	RHCHD-1406 X MCU 5	58.00	82.10	0.78	18.50	3.70	19.40	4.20	11.41	5.61	32.89	50.90	28.65	82.85	3.20	28.85*	5.80
22	RHCHD-1406 X MCU 7	59.50	80.90	0.80	18.90	4.10	14.80	3.69	9.14	4.64	33.76	53.23	25.10	80.50	4.61	24.95	5.60
23	RHCHD-1406 X MCU 9	57.50	92.50	0.90	21.50	3.65	21.50	4.40	10.33	5.64	35.39	62.00	27.15	82.50	3.78	26.10	5.70
24	RHCHD-1406 X CO 16	58.00	90.50	0.37*	16.36	3.24	14.03	3.91	9.97	5.37	36.09	50.60	27.40	83.75	3.79	26.20	5.60
25	RHCHD-1406 X CO 14	57.50	86.00	0.48*	18.80	3.60	19.30	4.28	10.41	5.62	32.96	60.10	28.20	84.25*	3.54	26.95	5.70
26	CPD 1702 X MCU 5	55.50	99.30	0.80	19.30	3.90	21.60	4.18	9.77	5.37	35.52	51.30	26.90	82.35	4.12	26.10	5.70
27	CPD 1702 X MCU 7	55.50	100.20	1.30	18.70	3.63	23.40*	3.64	10.17	4.79	34.06	67.08	25.60	81.85	3.59	25.50	5.60
28	CPD 1702 X MCU 9	55.50	101.70	0.90	19.90	3.85	22.40	3.94	9.90	5.37	35.26	65.27	25.95	81.10	3.51	25.45	5.65
29	CPD 1702 X CO 16	56.00	96.00	0.90	20.50	3.94	21.94	4.01	11.20	5.97	37.10*	81.24*	27.55	82.15	3.85	27.25	5.80
30	CPD 1702 X CO 14	55.50	101.70	0.60*	19.80	3.85	21.30	3.92	10.33	5.08	32.88	64.60	28.45	82.90	3.82	26.60	5.65
31	CPD 1701 X MCU 5	59.00	68.50*	1.30	12.80	4.05	11.55	3.82	9.78	5.34	35.29	56.40	28.25	82.85	3.62	25.80	5.60
32	CPD 1701 X MCU 7	58.00	81.00	0.60*	14.20	3.05	12.00	3.48	8.65	4.46	34.19	53.02	24.50	82.85	4.24	25.25	5.65
33	CPD 1701 X MCU 9	57.50	80.20	0.80	16.50	3.60	14.00	3.75	9.24	5.76	38.36*	56.60	25.70	82.30	4.05	25.55	5.70
34	CPD 1701 X CO 16	56.50	87.20	0.80	15.00	3.05	18.00	3.85	9.72	5.72	36.92	51.20	27.60	84.40*	3.89	28.30*	5.80
35	CPD 1701 X CO 14	58.50	78.90	1.10	15.20	3.20	16.70	4.32	10.93	6.38*	36.80	78.60*	27.15	83.45	3.84	26.25	5.65
36	PBH 116 X MCU 5	55.50	108.30	0.88	15.40	3.50	13.70	4.12	10.95	5.10	33.34	52.00	28.10	82.40	3.55	27.65	5.80
37	PBH 116 X MCU 7	56.00	103.40	0.93	20.80	4.18	13.50	3.73	9.08	4.70	34.10	61.40	26.40	79.55	4.11	25.60	5.70
38	PBH 116 X MCU 9	55.50	104.95	0.90	18.15	3.92	22.10	4.05	10.58	5.74	35.49	58.00	26.10	83.50	4.35	25.95	5.70
39	PBH 116 X CO 16	55.00*	109.35	0.68	25.32*	4.47	24.15*	4.13	10.34	5.59	35.11	93.80*	26.25	82.10	4.64	25.90	5.80
40	PBH 116 X CO 14	56.50	95.95	0.27*	21.00	3.95	22.80*	4.62*	11.56	6.11	34.53	61.40	29.55*	83.25	4.23	27.80	5.85
	Mean of crosses	56.90	94.96	0.85	19.44	3.78	18.55	3.94	10.20	5.23	34.16	58.68	27.05	82.49	3.94	26.54	5.72
	SE	0.95	9.36	0.09	1.37	0.51	2.00	0.26	0.93	0.52	1.38	6.17	1.18	0.86	0.56	0.86	0.07
	CD (0.05)	1.90	18.81	0.20	2.76	1.03	4.03	0.53	1.88	1.06	2.79	12.41	2.37	1.73	1.12	1.74	0.15
	CV%	1.76	9.61	11.82	7.03	13.14	10.67	6.85	8.63	9.53	4.27	10.69	4.24	1.20	14.54	3.33	1.36

*Significant at 5 % level of significance

(-15.80), internode length (-0.39), ginning outturn (2.16) and uniformity ratio (0.68). Similarly, PBH 116 recorded significant gca effects for days to first flowering (-1.20), number of monopodia per plant (-0.12), boll weight (0.19) and seed cotton yield (6.64). The ovule parentsRHCHD 1314, SHC 32 and CPD 1702 reported significant gca effects for three traits each. Being a tester, CO 14 tops as best general combiner for seven characters viz., number of bolls per plant (2.95), boll weight (0.32), seed index (0.53), seed cotton yield per plant (8.11), 2.5% span length (1.11), uniformity ratio (0.74) and fibre strength (0.63). The testers, CO 16and MCU 9 share significant gca effects for three quantitative traitseach. The general combining ability effects of parents for both yield and fibre quality parameters are represented in **Table 3.**

Table 3. General combining ability effects (GCA) of parents for yield and fibre quality traits

S.No	Parents	DFF	PH	NMP	NSP	IL	NB	BW	SI	LI	GOT	SCY	SL	UI	FF	FS	EL
	Lines (Female)																
1	TCH 1897	1.10**	-8.57**	0.03	-3.18**	-0.02	-2.99**	0.02	0.74*	0.07	-1.02*	-10.50**	0.22	0.37	0.29	0.30	0.04
2	RHCHD 1314	0.30	18.64**	0.19**	7.64**	0.62**	7.79**	-0.06	-0.71*	-0.58**	-1.37**	17.30**	0.12	-0.37	-0.10	0.03	-0.00
3	SHC 32	-1.10**	0.33	-0.08*	0.43	-0.07	-0.43	-0.17*	-0.47	-0.19	0.62	-3.85	-0.18	-0.07	-0.36*	0.01	-0.03
4	F 2382	0.00	-0.30	0.06	-0.48	-0.31	-3.79**	-0.04	0.53	-0.06	-1.61**	-14.00**	-0.10	-0.14	0.27	0.20	0.09**
5	RHCHD 1406	1.20**	-8.56**	-0.19**	-0.62	-0.12	-0.75	0.16	0.06	0.15	0.06	-3.31	0.25	0.28	-0.16	0.08	-0.05
6	CPD 1702	-1.30**	4.82	0.05	0.20	0.05	3.57**	0.00	0.08	0.09	0.81	7.22**	-0.16	-0.42	-0.17	-0.36	-0.05
7	CPD 1701	1.00**	-15.80**	0.07*	-4.70**	-0.39*	-4.10**	-0.10	-0.53	0.30	2.16**	0.49	-0.41	0.68*	-0.01	-0.30	-0.05
8	PBH 116	-1.20**	9.43**	-0.12**	0.70	0.23	0.70	0.19*	0.31	0.22	0.36	6.64**	0.23	-0.33	0.24	0.05	0.05
	SE (g_i) ±	0.30	2.96	0.03	0.44	0.16	0.63	0.08	0.29	0.17	0.44	1.95	0.37	0.27	0.18	0.27	0.02
	Testers (Male)																
1	MCU 5	0.35	-0.39	0.14**	-0.92**	0.19	-1.46**	0.05	0.33	0.02	-0.67	-3.00	0.90**	0.19	-0.24	0.75**	0.03
2	MCU 7	0.04	-3.99	-0.08**	-0.59	0.04	-3.14**	-0.34**	-0.77**	-0.57**	-0.51	-8.89**	-1.24**	-0.95**	0.35*	-0.92**	-0.04*
3	MCU 9	-0.28	1.76	0.05	0.96**	-0.08	1.65**	0.06	0.03	0.17	0.80*	-0.62	-0.71*	0.03	-0.11	-0.49*	-0.01
4	CO 16	-0.15	3.61	-0.06*	0.76*	0.03	0.00	-0.09	-0.13	0.18	1.37**	4.40**	-0.06	-0.01	0.09	0.04	0.01
5	CO 14	0.04	-0.99	-0.04	-0.20	-0.18	2.95**	0.32**	0.53*	0.20	-0.99**	8.11**	1.11**	0.74**	-0.10	0.63**	0.02
	SE (g_j) ±	0.24	2.34	0.02	0.34	0.13	0.50	0.07	0.23	0.13	0.35	1.54	0.29	0.22	0.14	0.22	0.019

*Significant at 5 % level of significance **Significant at 1% level of significance

Table 4. Specific combining ability effects (SCA) for yield and fibre quality traits

	Cross combinations	DFF	PH	NMP	NSP	IL	NB	BW	SI	LI	GOT	SCY	SL	UI	FF	FS	EL
1	TCH 1897 X MCU 5	0.65	5.37	-0.24**	1.36	0.25	2.32	-0.04	0.02	0.46	1.54	9.70*	-0.77	-0.20	-0.32	-1.09	-0.09
2	TCH 1897 X MCU 7	-1.54*	-2.41	0.21**	-0.77	0.20	1.17	0.22	-0.16	0.32	0.95	-0.48	0.17	0.89	1.53**	-0.22	0.08
3	TCH 1897 X MCU 9	0.27	-3.05	-0.13	-0.12	0.12	1.79	-0.05	0.87	0.15	-0.61	11.14*	-0.01	0.16	-0.24	0.55	-0.00
4	TCH 1897 X CO 16	1.15	-11.40	0.08	-3.02**	-0.19	-3.87**	-0.20	-0.55	-0.47	-0.68	-17.98**	-0.21	-0.95	-0.80*	-0.23	-0.07
5	TCH 1897 X CO 14	-0.54	11.50	0.07	2.54*	-0.38	-1.41	0.07	-0.17	-0.45	-1.19	-2.39	0.82	0.11	-0.17	0.98	0.07
6	RHCHD-1314 X MCU 5	1.95**	6.19	0.46**	-0.06	0.51	-1.98	0.04	0.39	0.10	-0.28	10.02*	0.78	-0.36	0.40	0.39	0.05
7	RHCHD-1314 X MCU 7	-0.74	-0.41	-0.38**	0.91	-0.34	-5.10**	-0.12	-0.00	0.11	0.02	-16.19**	-0.28	0.53	-0.47	0.11	-0.03
8	RHCHD-1314 X MCU 9	-1.42*	-5.46	-0.19**	0.56	-0.62	-0.99	-0.14	-0.19	-0.17	-0.13	-12.16**	0.59	-0.26	0.24	0.23	0.09
9	RHCHD-1314 X CO 16	-0.05	8.19	0.02	2.86**	0.62	-2.14	0.07	-0.37	-0.08	0.62	-7.58	-0.21	0.44	0.25	-0.60	-0.08
10	RHCHD-1314 X CO 14	0.26	-8.51	0.10	-4.28**	-0.17	10.21**	0.15	0.18	0.04	-0.23	25.91**	-0.88	-0.36	-0.42	-0.14	-0.04
11	SHC 32 X MCU 5	-1.15	1.39	-0.10	1.05	-0.15	-0.16	-0.17	-0.35	-0.09	-0.32	9.68*	-0.07	0.59	0.46	-0.10	0.03
12	SHC 32 X MCU 7	1.16	-6.73	-0.35**	-1.43	-0.22	0.12	-0.14	0.21	-0.24	-0.28	-6.30	0.47	-0.22	-0.30	0.12	-0.01
13	SHC 32 X MCU 9	-0.02	1.95	0.08	0.87	0.23	1.23	0.15	0.42	-0.07	-0.92	-2.21	0.09	0.75	-0.17	0.44	0.01
14	SHC 32 X CO 16	0.35	-0.80	0.19**	-0.63	0.16	1.18	0.13	-0.52	0.35	1.79	5.07	-0.21	-0.81	-0.15	-0.59	-0.06
15	SHC 32 X CO 14	-0.34	4.20	0.18*	0.13	-0.02	-2.37	0.03	0.24	0.05	-0.27	-6.24	-0.28	-0.31	0.16	0.12	0.03
16	F 2382 X MCU 5	-0.75	-2.97	-0.12	1.26	-0.09	1.40	0.05	0.05	-0.15	-0.66	-6.28	-0.15	0.46	-0.30	0.97	0.02
17	F 2382 X MCU 7	-0.44	-2.17	-0.22**	-0.37	0.42	1.18	0.16	0.54	0.59	1.18	-1.59	1.19	0.40	-0.21	0.59	0.03
18	F 2382 X MCU 9	1.38*	3.98	0.14*	-0.22	-0.19	-1.81	0.16	-0.33	-0.05	0.36	4.64	-0.29	0.26	-0.33	-0.64	-0.05
19	F 2382 X CO 16	-0.25	5.13	-0.05	-0.02	-0.25	0.34	-0.26	0.39	-0.05	-1.46	7.02	-0.29	-0.94	0.56	-0.47	0.03
20	F 2382 X CO 14	0.06	-3.97	0.24**	-0.66	0.11	-1.11	-0.11	-0.64	-0.34	0.57	-3.79	-0.46	-0.18	0.28	-0.46	-0.03
21	RHCHD-1406 X MCU 5	-0.45	-3.91	-0.02	0.61	-0.15	3.05*	0.06	0.83	0.22	-0.66	-1.46	0.45	-0.11	-0.35	1.49*	0.10
22	RHCHD-1406 X MCU 7	1.36*	-1.51	0.22**	0.68	0.41	0.13	-0.07	-0.34	-0.16	0.05	6.76	-0.96	-1.32*	0.47	-0.74	-0.04
23	RHCHD-1406 X MCU 9	-0.33	4.34	0.19*	1.73	0.07	2.05	0.24	0.04	0.09	0.37	7.25	0.56	-0.30	0.11	-0.02	0.03
24	RHCHD-1406 X CO 16	0.05	0.49	-0.24**	-3.21**	-0.46	-3.77*	-0.10	-0.15	-0.19	0.51	-9.17*	0.16	0.99	-0.08	-0.45	-0.09
25	RHCHD-1406 X CO 14	-0.64	0.59	-0.14*	0.19	0.13	-1.45	-0.14	-0.38	0.04	-0.27	-3.38	-0.21	0.75	-0.15	-0.29	0.00
26	CPD 1702 X MCU 5	-0.45	-0.09	-0.24**	0.58	-0.13	0.93	0.19	-0.84	0.03	1.23	-11.59*	-0.89	0.09	0.58	-0.83	-0.01
27	CPD 1702 X MCU 7	-0.14	4.41	0.48**	-0.35	-0.24	4.41**	0.04	0.66	0.04	-0.39	10.07*	-0.05	0.73	-0.54	0.24	-0.04
28	CPD 1702 X MCU 9	0.17	0.16	-0.05	-0.70	0.10	-1.37	-0.06	-0.40	-0.12	-0.51	-0.01	-0.23	-1.01	-0.16	-0.24	-0.02
29	CPD 1702 X CO 16	0.55	-7.39	0.06	0.10	0.07	-0.19	0.16	1.06	0.48	0.77	10.93*	0.72	0.09	-0.02	1.03	0.11*
30	CPD 1702 X CO 14	-0.14	2.91	-0.26**	0.36	0.20	-3.77*	-0.33	-0.48	-0.44	-1.10	-9.41*	0.45	0.10	0.14	-0.21	-0.05
31	CPD 1701 X MCU 5	0.75	-10.27	0.24**	-1.02	0.47	-1.44	-0.07	-0.22	-0.21	-0.35	0.24	0.71	-0.51	-0.07	-1.18	-0.11
32	CPD 1701 X MCU 7	0.06	5.83	-0.24**	0.05	-0.38	0.69	-0.03	-0.24	-0.50	-1.61	2.75	-0.90	0.63	-0.04	-0.06	0.01
33	CPD 1701 X MCU 9	-0.12	-0.72	-0.17*	0.80	0.29	-2.10	-0.16	-0.45	0.05	1.25	-1.95	-0.23	-0.90	0.23	-0.19	0.03
34	CPD 1701 X CO 16	-1.25	4.43	-0.06	-0.50	-0.37	3.55*	0.10	0.19	0.00	-0.76	-12.37**	1.02	1.24*	-0.12	2.03**	0.11*
35	CPD 1701 X CO 14	0.56	0.73	0.22**	0.66	-0.01	-0.70	0.16	0.73	0.65	1.48	11.32*	-0.60	-0.46	0.01	-0.61	-0.05
36	PBH 116 X MCU 5	-0.55	4.30	0.01	-3.81**	-0.70	-4.90**	-0.06	0.12	-0.37	-0.51	-10.32*	-0.08	0.05	-0.40	0.32	0.01
37	PBH 116 X MCU 7	0.26	3.00	0.28**	1.26	0.14	-2.61	-0.07	-0.66	-0.17	0.09	4.97	0.36	-1.66**	-0.43	-0.06	-0.03
38	PBH 116 X MCU 9	0.08	-1.20	0.12	-2.94**	0.00	1.20	-0.14	0.05	0.12	0.18	-6.70	-0.47	1.31*	0.32	-0.14	-0.06
39	PBH 116 X CO 16	-0.55	1.35	0.00	4.43**	0.43	4.90**	0.09	-0.04	-0.04	-0.77	24.08**	-0.97	-0.05	0.37	-0.72	0.02
40	PBH 116 X CO 14	0.76	-7.45	-0.42**	1.06	0.13	0.60	0.17	0.53	0.46	1.01	-12.03**	1.16	0.35	0.14	0.59	0.06
	SE	0.67	6.62	0.07	0.97	0.36	1.42	0.19	0.66	0.37	0.98	4.37	0.84	0.61	0.39	0.61	0.05
	Range	-1.54 to 1.95	-11.40 to 11.50	-0.42 to 0.48	-4.28 to 4.43	-0.70 to 0.62	-5.10 to 10.21	-0.33 to 0.24	-0.84 to 1.06	-0.50 to 0.65	-1.61 to 1.79	-17.98 to 25.91	-0.97 to 1.19	-1.66 to 1.31	-0.80 to 1.53	-1.18 to 2.03	-0.11 to 0.11

*Significant at 5 % level of significance **Significant at 1% level of significance

Table 5. Estimates of Standard heterosis in hybrids for yield and fibre quality traits

S. No	Cross combinations	DFF	PH	NMP	NSP	IL	NB	BW	SI	LI	GOT	SCY	SL	UI	FF	FS	EL
		Standard heterosis (diii)															
1	TCH 1897 X MCU 5	6.31**	9.96	63.16**	2.45	27.27	3.30	-0.75	-2.08	-3.91	9.26*	17.25	4.98	0.36	-22.16	2.91	0.00
2	TCH 1897 X MCU 7	1.80	-3.73	110.53**	-8.59	21.21	-14.47	-3.75	-13.15	-15.97	7.89	-17.09	0.38	0.30	29.59*	-0.19	1.75
3	TCH 1897 X MCU 9	4.50*	2.41	68.42**	4.91	15.15	19.50	-0.63	2.78	-6.41	7.10	25.43	1.72	0.61	-17.60	4.47	0.88
4	TCH 1897 X CO 16	6.31**	-5.42	89.47**	-14.11	9.09	-26.42*	-8.14	-10.98	-16.56	8.68	-26.07	3.45	-0.79	-25.34*	3.50	0.00
5	TCH 1897 X CO 14	3.60*	16.61	89.47**	14.11	-3.03	7.55	8.76	-1.95	-15.97	-0.53	15.17	11.88*	1.39	-15.91	10.49**	2.63
6	RHCHD-1314 X MCU 5	7.21**	43.68**	244.21**	60.12**	54.55**	44.03**	-0.50	-11.45	-20.72*	2.33	77.35**	10.54*	-0.73	-14.95	7.57*	1.75
7	RHCHD-1314 X MCU 7	1.80	31.41**	21.05	68.10**	24.24	13.84	-14.27*	-24.34**	-30.28**	3.81	8.76	-1.72	-1.03	-20.89	0.00	-0.88
8	RHCHD-1314 X MCU 9	0.00	32.25**	89.47**	75.46**	12.12	69.81**	-4.88	-19.09*	-22.63*	7.54	35.04*	3.64	-0.79	-15.69	2.14	1.75
9	RHCHD-1314 X CO 16	2.70	50.90**	110.53**	88.34**	53.03**	52.20**	-3.25	-22.00*	-20.88*	11.76*	55.56**	3.07	0.00	-11.35	0.97	-0.88
10	RHCHD-1314 X CO 14	3.60*	25.27*	131.58**	38.65**	22.73	148.43**	8.76	-11.50	-18.64*	1.48	135.04**	4.98	-0.06	-29.48*	5.05	0.00
11	SHC 32 X MCU 5	-0.90	15.88	68.42**	22.70**	13.64	3.77	-8.76	-15.79	-17.39	8.56	31.41*	6.13	0.79	-19.41	5.63	0.88
12	SHC 32 X MCU 7	2.70	1.77	-30.53	9.51	6.82	-5.03	-17.77**	-20.48*	-29.70**	9.22*	-15.31	0.00	-1.57	-22.80	0.00	-0.88
13	SHC 32 X MCU 9	0.00	19.13	89.47**	33.13**	16.67	32.08*	-0.50	-11.76	-14.39	11.38*	11.11	0.57	0.79	-29.90*	2.91	0.00
14	SHC 32 X CO 16	0.90	18.05	89.47**	22.70**	18.18	21.38	-4.88	-21.26*	-7.40	21.89**	37.39**	1.92	-1.15	-25.34*	0.97	-0.88
15	SHC 32 X CO 14	0.00	18.53	89.47**	21.47*	6.06	17.61	3.00	-8.89	-12.06	7.70	21.15	6.13	0.36	-22.59	6.02	0.88
16	F 2382 X MCU 5	1.80	9.87	94.74**	18.40*	8.33	-7.55	0.13	-3.64	-16.14	0.32	-24.36	6.13	0.55	-22.06	10.49**	2.63
17	F 2382 X MCU 7	1.80	6.50	26.32	10.43	18.94	-19.50	-7.01	-8.94	-13.64	6.77	-26.92*	3.07	-0.91	-7.42	2.52	1.75
18	F 2382 X MCU 9	4.50*	20.82	131.58**	20.86*	-3.03	-8.18	3.00	-9.59	-11.98	8.34	4.06	-0.57	0.12	-19.83	-0.58	0.88
19	F 2382 X CO 16	1.80	24.43*	68.42**	20.86*	-1.52	-5.03	-11.26	-4.69	-11.81	4.31	19.87	1.92	-1.39	3.18	2.14	2.63
20	F 2382 X CO 14	2.70	7.94	131.58**	11.04	3.03	4.40	2.75	-7.90	-16.31	3.25	4.70	5.75	0.42	-6.79	4.47	1.75
21	RHCHD-1406 X MCU 5	4.50*	-1.20	63.16**	13.50	12.12	22.01	5.13	-0.95	-6.66	5.69	8.76	9.77*	0.36	-32.24**	12.04**	1.75
22	RHCHD-1406 X MCU 7	7.21**	-2.65	68.42**	15.95	24.24	-6.92	-7.63	-20.65*	-22.71*	8.52	13.75	-3.83	-2.48*	-2.33	-3.11	-1.75
23	RHCHD-1406 X MCU 9	3.60*	11.31	89.47**	31.90**	10.61	35.22**	10.14	-10.37	-6.16	13.74**	32.48*	4.02	-0.06	-19.83	1.36	0.00
24	RHCHD-1406 X CO 16	4.50*	8.90	-23.16	0.40	-1.97	-11.73	-2.13	-13.45	-10.73	16.01**	8.12	4.98	1.45	-19.51	1.75	-1.75
25	RHCHD-1406 X CO 14	3.60*	3.49	-0.00	15.34	9.09	21.38	7.01	-9.63	-6.49	5.93	28.42*	8.05	2.06	-24.92*	4.66	0.00
26	CPD 1702 X MCU 5	0.00	19.49	68.42**	18.40*	18.18	35.85**	4.76	-15.27	-10.73	14.16**	9.62	3.07	-0.24	-12.73	1.36	0.00
27	CPD 1702 X MCU 7	0.00	20.58	173.68**	14.72	9.85	47.17**	-8.76	-11.76	-20.38*	9.48*	43.32**	-1.92	-0.85	-23.97*	-0.97	-1.75
28	CPD 1702 X MCU 9	0.00	22.38*	89.47**	22.09*	16.67	40.88**	-1.38	-14.06	-10.65	13.32**	39.48**	-0.57	-1.76	-25.56*	-1.17	-0.88
29	CPD 1702 X CO 16	0.90	15.52	89.47**	25.77**	19.24	37.96**	0.50	-2.78	-0.58	19.24**	73.58**	5.56	-0.48	-18.35	5.83	1.75
30	CPD 1702 X CO 14	0.00	22.38*	26.32	21.47*	16.67	33.96**	-1.75	-10.37	-15.47	5.67	38.03**	9.00*	0.42	-19.09	3.30	-0.88
31	CPD 1701 X MCU 5	6.31**	-17.57	173.68**	-21.47*	22.73	-27.36*	-4.38	-15.18	-11.15	13.42**	20.51	8.24	0.36	-23.22	0.19	-1.75
32	CPD 1701 X MCU 7	4.50*	-2.53	26.32	-12.88	-7.58	-24.53	-13.02	-24.90**	-25.79**	9.88*	13.30	-6.13	0.36	-10.07	-1.94	-0.88
33	CPD 1701 X MCU 9	3.60*	-3.49	68.42**	1.23	9.09	-11.95	-6.26	-19.78*	-4.16	23.28**	20.94	-1.53	-0.30	-14.21	-0.78	0.00
34	CPD 1701 X CO 16	1.80	4.93	68.42**	-7.98	-7.58	13.21	-3.63	-15.62	-4.91	18.64**	9.40	5.75	2.24*	-17.39	9.90**	1.75
35	CPD 1701 X CO 14	5.41**	-5.05	131.58**	-6.75	-3.03	5.03	8.01	-5.21	6.24	18.27**	67.95**	4.02	1.09	-18.56	1.94	-0.88
36	PBH 116 X MCU 5	0.00	30.32**	84.21**	-5.52	6.06	-13.84	3.00	-4.95	-15.22	7.13	11.11	7.66	-0.18	-24.81*	7.38*	1.75
37	PBH 116 X MCU 7	0.90	24.43*	94.74**	27.61**	26.52	-15.09	-6.76	-21.26*	-21.80*	9.59*	31.20*	1.15	-3.63**	-12.94	-0.58	0.00
38	PBH 116 X MCU 9	0.00	26.29*	89.47**	11.35	18.94	38.99**	1.50	-8.20	-4.49	14.06**	23.93	0.00	1.15	-6.79	0.78	0.00
39	PBH 116 X CO 16	-0.90	31.59**	42.11	55.37**	35.30*	51.89**	3.50	-10.33	-6.99	12.84**	100.43**	0.57	-0.55	-1.59	0.58	1.75
40	PBH 116 X CO 14	1.80	15.46	-44.21*	28.83**	19.70	43.40**	15.64*	0.35	-1.58	10.99*	31.20*	13.22**	0.85	-10.29	7.96*	2.63
	SE	0.94	9.242	0.100	1.373	0.508	1.990	0.264	0.987	0.522	1.387	6.168	1.168	0.854	0.554	0.863	0.076
	Range	-0.90 to 7.21	-17.57 to 50.90	-44.21 to 244.21	-21.47 to 88.34	-7.58 to 54.55	-27.36 to 148.43	-17.77 to 15.64	-24.90 to 2.78	-30.28 to 6.24	-0.53 to 23.28	-26.92 to 135.04	-6.13 to 13.22	-3.63 to 2.24	-32.24 to 29.59	-3.11 to 12.04	-1.75 to 2.63

*Significant at 5 % level of significance **Significant at 1% level of significanceww

Selecting parents depending on either mean values or gca effectswas found to be deceptive in case of Arumugampillai and Amirthadevarathinam (1998). Ashokkumar *et al.,* (2014) and Monicashree *et al.,* (2017) have suggested that choice would be more reliable if both estimates are coupled in an experiment.In the present investigation lineCPD 1701has recorded significant mean and gca effects for three characters viz., plant height,internode length and ginning outturn. This was followed by line RHCHD 1314 recording significant mean and gca effect for number of sympodial branches per plant and number of bolls per plant. Line RHCHD 1406 also synced mean and gca effects with two traits. In case of testers, CO 14 showed significant mean performance and gca effects for boll weight,2.5% span length and fibre strength. CO 16 and MCU 9 also synced their mean and gca effects for three traits including number of sympodial branches and ginning outturn.These positively associated parents own additive genes;therefore,they can be sourced for recombination breeding programmes. Asynchrony between *per se* value and gca effectis a one of the signs of dominance gene action. Since none of the parents were fair combiners for the entire quantitative traits studied, an attempt of polycross in F_2 population helps in funneling down the traits to an individual genetic background.

Based on average performance of hybrids (**Table 2**), PBH 116 × CO 16 recorded significant mean values for days to first flowering, number of sympodial branches per plant, number of bolls per plant and seed cotton yield. In the order of merit and importance, PBH 116 × CO 14, RHCHD 1314 × CO 14,RHCHD 1314 × MCU 5,RHCHD 1314 × CO 16 andCPD 1701× CO 16 recorded significant mean performance for at most three characters.

Considering sca effects of hybrids (**Table 4**), CPD 1701 × CO 16 recorded high significant sca effects for four traits viz., number of bolls per plant (3.55), uniformity ratio (1.24), fibre strength (2.03) and elongation percentage (0.11). This was followed by hybrid PBH 116 × CO 16 for three important yield parameters such as number of sympodial branches per plant (4.43), number of bolls per plant (4.90) and seed cotton yield per plant (24.08). The hybrids TCH 1897 × MCU 5, RHCHD 1314 × MCU 9, RHCHD 1314 × CO 14, RHCHD 1406 × MCU 5, CPD 1702 × MCU 7 and CPD 1702 × CO 16 recorded significant gca effects for seed cotton yield and number of bolls in major.

According to Abro *et al*., 2009, Heterosis is one of the vital tools to assess the performance of hybrids as it increases the scope of improving the crops in F_1 generation itself. Standard heterosis, thus is a measure of degree of improvement of synthesized hybrid over a standard check. As cited by Rajan *et al.,* (2000), over three measures of heterosis, standard or useful heterosis is regarded as more pragmatic and reliable as it provides chance for replacement of ruling cultivars.In this study, standard hybrid Mallika was chosen as check to compute standard heterosis. The results (Table 5) revealed that the F_1 PBH 116 × CO 14 topped with significant standard heterosis for eight traits. Hybrid, RHCHD 1314 × MCU 5 and CPD 1702 × MCU 9 registered significant standard heterosis values for five different traits including number of sympodial branches per plant, number of bolls per plant and seed cotton yield per plant in common. Further, the hybrid PBH 116 × CO 16 reported significant standard heterosis estimates for four important characters viz., number of sympodial branches per plant (55.37), number of bolls per plant (51.89), ginning outturn (12.84) and seed cotton yield per plant (100.43). The hybrids RHCHD 1314 × CO 16, RHCHD 1314 × CO 14, CPD 1702 × MCU 7, CPD 1702 × CO 16, CPD 1702 × CO 14, SHC 32 × MCU 9, SHC 32 × CO 16 and RHCHD 1406 × MCU 9 also recorded significant standard heterosis for four different quantitative traits.

Considering per se performance, sca effects and standard heterosis estimates of hybrids, the F_1 PBH 116 × CO 16, was highly significant for three critical yield traits viz., number of sympodial branches per plant, number of bolls per plant and seed cotton yield per plant. Significance in the above dealt traits was also reported by Monicashree *et al.,*2017 and Pushpam *et al.,* 2015. This hybrid was followed by CPD 1702 × MCU 7 and RHCHD 1314 × CO 14 sharing significance for both number of bolls and seed cotton yield. Discussing about the gene action, the hybrids PBH 116 × CO 16, RHCHD 1314 × CO 14 and CPD 1701 × CO 16 are resultant of cross between parents of good general combining ability. This testifies the presence of additive × additive gene action. On the other hand, the F_1 CPD 1702 × MCU 7 specimens as cross between good and poor general combiners. The privilege of additive gene effect from good combiner and non-allelic effect from poor combiner together resulted the desired plant type. For improvement in quality traits, the F_1CPD 1701 × CO 16 reported to be highly significant for fibre strength and uniformity ratio. These hybrids are amenable to heterosis breeding for seeking improvement in above dealt aspects.

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