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Research Article

Combining ability studies for seed cotton yield in intraspecific hybrids of upland cotton (*Gossypium hirsutum* L.)

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Abstract

Thirty-two hybrid combinations were obtained by crossing four lines with eight testers in L x T fashion and F_1's along with their parents were used for assessing combining ability for different yield and fibre quality traits. Variance due to parents and hybrids showed significant differences for all the characters studied except for the number of monopodia, boll weight and elongation percentage. Variances due to GCA were larger than SCA for all the traits, indicating the preponderance of dominance gene action. The lines, TSH 0499 and TSH 04/115 and the testers, MCU 13 and TCH 1819 which registered high *per se* performance coupled with the significant *GCA* effect were identified as best parents in developing hybrids with improved yield and fibre quality traits. The hybrid combinations *viz.,* TSH 04/115 x MCU 7, TSH 0499 x SVPR 4, TSH 0499 x TCH 1819, TSH 0499 x MCU 13 and TSH 04/115 x TCH 1819 which showed significant *sca* could be used in heterosis breeding programme for improvement of both yield and fibre quality traits.

Keywords

Combining ability, Cotton, L x T, Gene action

INTRODUCTION

Cotton (*Gossypium* spp.) commonly called 'White Gold' that plays a vital role in the country's economic growth by providing substantial employment and making significant contributions to export earnings. Among the four cultivated *Gossypium* spp., upland cotton (*Gossypium hirsutum* L., 2n=52) is the most extensively cultivated species, accounting 95 per cent of its production and it has been the target of numerous genetic studies and breeding programmes. The first step in a successful breeding program is to select the appropriate parents. The parents should possess the good combining ability and wide genetic diversity for various economic traits (Kumaresan, 1999). Line x Tester analysis (Kempthrone, 1957) provides a systematic approach for the identification of suitable parents and cross combinations for most of the yield contributing traits. Combining ability provides information on the selection of parents as well as the nature and magnitude of gene action involved in the expression of various traits. The main objectives of this study were to evaluate the general combining ability of parents and specific combining ability of hybrids in order to select the superior cross combination for yield, yield components and fibre quality traits.

MATERIALS AND METHODS

The present investigation was carried out during 2016-17 at Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. Thirty-two hybrids were obtained by crossing 4 lines *viz.,* TSH 0499, TSH 04/115, BGDS 1063 and ARBC 19 with 8 testers *viz.,* MCU 7, MCU13, CO 14, SVPR 4, KC 3, Surabhi, TCH 1777 and TCH 1819 in L x T fashion. Randomized block design with two replications each in two rows of 10 m length with the spacing of 90 cm x 60 cm were adopted for this experimental trial. Five plants at random were taken in each entry and data on days to first flowering, plant height, the number of monopodia, the number of sympodia, the number of bolls per plant, boll weight, Internode length, the number of nodes per plant, seed index, lint index, single plant yield, ginning outturn, 2.5 per cent span length, bundle strength, uniformity ratio, elongation percentage and fibre fineness were recorded. The gene action for seed cotton yield and fibre quality traits and general and specific combining ability effects of the parents and hybrids were assessed by line × tester analysis (Kempthorne, 1957). Statistical analysis was carried out by using the mean values over five plants through TNAUSTAT package.

RESULTS AND DISCUSSION

Analysis of variance for randomized block design was carried out to test the significant differences among the genotypes studied and represented in **Table 1**. The data revealed that the sources of variation *viz*., genotypes, parents and crosses showed significance for all the characters except for the number of monopodial branches per plant, boll weight and fibre fineness. Giri *et al*. (2006), Reddy and Nadarajan (2006), Shakeel *et al*. (2012) and Ranganatha *et al*. (2013) reported significant differences among cotton genotypes for all characters except the above said three characters. Significant differences among the genotypes for ginning percentage, lint index, seed index, 2.5 per cent span length, fibre fineness, bundle strength, elongation percentage and uniformity ratio were reported by Dhivya *et al*. (2014) and Usharani *et al*. (2014).

Table 1. Analysis of variance for yield components and fibre quality traits among parents and crosses

Source	Mean squares																
	df	DFF	PH	NM	NS	NB	BW	SPY	IL	NN	SI	LI	GOT	SL	UR	STR	EP	MIC
Replication	1	5.25	1.00	0.44	1.48	74.01	0.01	279.21	0.01	0.18	0.01	0.02	0.35	4.06	3.09	0.14	0.01	0.07
Genotypes	43	9.49**	242.26**	0.58	15.69**	81.51**	0.55	2287.24**	0.96*	17.82**	3.34**	1.05*	7.98**	4.27**	7.63**	2.51**	0.70	0.33*
Parents	11	7.63**	119.69**	0.73	9.98**	46.08**	0.54	712.24**	0.68*	23.09**	2.52*	0.98*	6.86**	6.05**	7.84**	1.86*	0.65	0.22*
Lines	3	6.48**	202.86**	1.12	4.01*	39.06**	0.23	595.59*	0.95*	52.46**	2.71*	1.11*	1.15*	4.90**	0.42*	0.69*	1.64	0.14*
Testers	7	8.94**	100.67**	0.62	5.61**	16.99*	0.71	561.82**	0.37*	6.06*	1.54*	0.65*	9.88**	4.67**	11.87**	1.15*	0.29	0.24*
Lines vs Testers	1	1.87	3.36	0.33	58.52**	270.75**	0.31	2115.11**	2.00*	54.19**	8.83**	2.88*	2.91*	19.13**	1.84	10.36**	0.26	0.33*
Crosses	31	9.82**	285.11**	0.47	14.90**	82.68**	0.51	2720.50**	0.99*	14.55**	3.34**	1.07*	8.52**	3.45**	7.47**	2.55**	0.74	0.35*
Cross vs Parents	1	19.62**	262.23**	2.18	102.95**	435.00**	1.97	6181.34**	3.33*	61.36**	12.18**	1.21*	3.76	10.02**	10.22**	8.65**	0.03	0.86*
Error	43	1.05	7.67	0.13	2.24	3.90	0.07	79.52	0.07	3.53	0.07	0.04	2.03	0.65	2.02	0.86	0.05	0.03

*Significant (5% level) **Significant (1% level)

DFF	- Days to first flowering	IL	- First internode length	SL	- 2.5% span length (mm)
PH	- Plant height (cm)	SI	- Seed index	UR	- Uniformity ratio (%)
NM	- Number of monopodial branches per plant	LI	- Lint index	BS	- Bundle strength (g/tex)
NS	- Number of sympodial branches per plant	BW	- Boll weight (g)	EP	- Elongation percentage (%)
NB	- Number of bolls per plant	GOT	- Ginning out turn (%)	MIC	- Fibre fineness (Mic.)
NN	- Number of nodes per plant	SPY	- Single plant yield (g)		

The results from line x tester analysis of gene action were represented in **Table 2.** The predominance of dominance gene action for the traits, days to first flowering, plant height, the number of monopodial branches per plant, the number of sympodial branches per plant, the number of bolls per plant, boll weight, single plant yield, seed index, lint index, Internode length, the number of nodes per plant, ginning outturn, 2.5 per cent span length, fibre fineness, bundle strength, elongation percentage and uniformity ratio were recorded. The dominance variance was higher than the additive variances for all the biometrical traits. The ratio between additive and dominance variance was less than one. Similar findings were also reported by Ranganatha *et al*., 2013, Simon *et al*., 2013, Kannan and Saravanan, 2015, Sawarkar *et al*., 2015 and Srinivas *et al*., 2014. In contrast to our findings, Samreen *et al*. (2008) reported additive gene action for the number of bolls per plant, boll weight, seed cotton yield per plant, ginning outturn and seed index. Based on the mean performance between the lines, the genotype TSH 0499 observed significantly higher mean for seven yield and quality traits *viz*., the number of sympodial branches per plant, the number of bolls per plant, boll weight, single plant yield, seed index, lint index and 2.5 per cent span length. Similarly, the line ARBC 19 recorded high mean performance for five traits *viz*., days to first flowering, plant height, seed index, lint index and elongation percentage. The line, TSH 04/115 observed significantly higher mean for three characters *viz*., the number of bolls per plant, boll weight and single plant yield.

Among the testers, KC 3 recorded higher mean performance for seven seed cotton yield and quality traits *viz.,* days to first flowering, the number of monopodial branches per plant, single plant yield, seed index, lint index, uniformity ratio and elongation percentage. Similarly, the tester TCH 1819 recorded high mean performance for three characters *viz.,* elongation percentage, ginning outturn and plant height. The tester, MCU 13 recorded high mean performance for Internode length and single plant yield. The tester MCU 7 recorded high mean performance for three characters *viz*., days to first flowering, plant height and Internode length. The tester, Surabhi recorded higher mean value for fibre quality traits *viz*., 2.5 per cent span length and fibre fineness. Three lines *viz*., TSH 0499, TSH 04/115 and BGDS 1063 and two testers MCU 13 and KC 3 observed high *per se* performance in terms of single plant yield.

Table 2. Gene action for yield and fibre quality traits

Characters	$\sigma^2 A$	$\sigma^2 \Delta$	$\sigma^2 A/\sigma^2 \Delta$
Days to first flowering	0.138	3.2242	0.0428
Plant height	8.5942	67.0943	0.1281
Number of monopodia per plant	0.0108	0.0803	0.1345
Number of sympodia per plant	0.5038	2.0679	0.2436
Number of bolls per plant	3.1896	12.1999	0.2614
Boll weight	0.0125	0.1179	0.106
Single plant yield	100.5013	469.8472	0.2139
Internode length	0.0169	0.3198	0.0528
Number of nodes per plant	0.4596	1.7432	0.2637
Seed index	0.0207	1.4639	0.0141
Lint index	0.019	0.3562	0.0533
Ginning out turn	0.002	3.1444	0.0006
2.5 per cent span length	0.081	0.7634	0.1061
Uniformity ratio	0.0393	2.4762	0.0159
Bundle strength	0.076	0.3078	0.2469
Elongation percentage	0.0094	0.2687	0.035
Fibre fineness	0.011	0.0668	0.1647

In the present study, the line TSH 0499 possessed significantly high *GCA* effects for plant height, the number of sympodial branches per plant, the number of bolls per plant, boll weight, single plant yield, Internode length, the number of nodes per plant, seed index, single plant yield, lint index, 2.5 per cent span length and fibre fineness. The line, TSH 04/115 recorded high significantly positive *GCA* effects for nine characters *viz*., days to first flowering, the number of bolls per plant, boll weight, Internode length, single plant yield, lint index, 2.5 per cent span length, elongation percentage and fibre fineness. Among testers, SVPR 4 showed significantly favourable *GCA* effects for 8 out of 17 traits studied. This was followed by TCH 1819 which expressed significantly favourable *GCA* effects for seven traits**.** The next best tester was TCH 1777 which showed significantly favourable *GCA* effects for the six traits. From the above discussions, it was inferred that none of the parents was found to be a good general combiner for all the traits studied**.** The good general combiner, in the order of merit, was TSH 0499, TSH 04/115, SVPR 4, TCH 1819 and TCH 1777. The *GCA* of parents for yield and fibre quality traits were represented in **Table 3a and 3b.** On the basis of the mean value and *GCA* effects, the line TSH 0499 excelled higher mean and *GCA* effects for seven characters *viz.,* the number of sympodial branches per plant, the number of bolls per plant, boll weight, single plant yield, seed index, lint index and 2.5 per cent span length. It was followed by the line TSH 04/115 which showed the significantly high mean value and significantly superior *GCA* effects for three characters *viz.,* the number of bolls per plant, boll weight and single plant yield. The positive association between *per se* performance and *GCA* effects was evident in TSH 0499. Among the testers, MCU 13 registered high mean and *GCA* effects for Internode length and single plant yield. The tester TCH 1819 recorded higher mean performance and *GCA* effects for ginning outturn and elongation percentage.

Table 3a. Estimation of *GCA* effects for yield components

Parents	DFF	PH	NM	NS	NB	BW	SPY	IL	NN
Lines									
TSH 0499	0.02	8.98 **	-0.16	3.27 **	5.35 **	0.24 **	22.68 **	0.31 **	2.81 **
TSH 04/115	1.30 **	-0.78	0.29 **	-0.33	3.96 **	0.21 **	29.83 **	0.17 *	0.50
BGDS 1063	-0.77 **	-0.52	-0.17	-1.02 **	-3.87 **	-0.35 **	-25.78 **	-0.33 **	-1.19 *
ARBC 19	-0.55 *	-7.68 **	0.04	-1.91 **	-5.44 **	-0.10	-26.73 **	-0.15 *	-2.13 **
SE	**0.26**	**0.65**	**0.09**	**0.38**	**0.55**	**0.07**	**2.44**	**0.06**	**0.46**
Testers									
MCU 7	0.13	-7.20 **	-0.28 *	-1.48 **	-4.08 **	0.26 **	-12.94 **	0.28 **	-1.50 *
MCU 13	0.38	5.85 **	0.09	0.64	5.21 **	-0.20 *	9.56 **	0.40 **	0.75
CO 14	-0.12	-4.90 **	0.39 **	-0.30	-2.28 **	0.00	-12.60 **	-0.02	-0.38
SVPR 4	-0.02	15.19 **	-0.11	2.12 **	-1.14	0.45 **	13.46 **	-0.29 **	2.13 **
KC3	-2.34 **	-0.31	-0.06	-0.58	-1.17	-0.21 *	-18.46 **	0.17	-0.75
Surabhi	1.45 **	-0.23	0.37 **	-1.13 *	-0.55	-0.39 **	-19.95 **	-0.97 **	-0.63
TCH 1777	1.88 **	2.03 *	0.19	0.98	3.76 **	-0.30 **	13.98 **	-0.00	1.13
TCH 1819	-1.37 **	-10.43 **	-0.60 **	-0.25	0.26	0.38 **	26.95 **	0.42 **	-0.75
SE	**0.36**	**0.92**	**0.13**	**0.54**	**0.77**	**0.09**	**3.45**	**0.09**	**0.65**

*Significant (5% level) **Significant (1% level)

Table 3b. Estimation of *GCA* effects for yield and fibre quality traits

Parents	SI	LI	GOT	SL	UR	STR	EP	MIC
Lines								
TSH 0499	1.07 **	0.39 **	-0.32	0.47 *	0.22	0.39	-0.48 **	0.27 **
TSH 04/115	0.15 *	0.15 **	-0.23	0.52 **	-0.13	-0.59 **	0.28 **	0.14 **
BGDS 1063	-0.53 **	-0.69 **	-0.56	-1.03 **	0.30	-0.55 **	0.38 **	-0.15 **
ARBC 19	-0.69 **	0.15 **	1.11 **	0.04	-0.39	0.75 **	-0.18 **	-0.25 **
SE	**0.06**	**0.05**	**0.38**	**0.19**	**0.34**	**0.20**	**0.05**	**0.05**
Testers								
MCU 7	-0.28 **	-0.22 **	-0.23	-0.86 **	-0.69	-0.69 *	0.23 **	0.12
MCU 13	0.15	0.55 **	0.60	-0.12	-0.15	0.06	0.15	-0.10
CO 14	-0.65 **	-0.29 **	0.36	0.32	-2.01 **	-0.31	-0.17 *	-0.29 **
SVPR 4	0.64 **	-0.23 **	-1.00	-0.41	0.96	-0.30	-0.42 **	0.38 **
KC3	-0.21 *	-0.18 **	-0.04	-0.67 *	2.04 **	-0.67 *	0.05	0.15 *
Surabhi	-0.23 *	0.31 **	0.31	1.63 **	-0.79	1.07 **	-0.03	-0.33 **
TCH 1777	0.46 **	-0.30 **	-1.66 **	0.63 *	0.19	1.19 **	-0.09	-0.25 **
TCH 1819	0.11	0.37 **	1.66 **	-0.52	0.44	-0.35	0.27 **	0.33 **
SE	**0.09**	**0.07**	**0.53**	**0.27**	**0.48**	**0.29**	**0.08**	**0.07**

*Significant (5% level) **Significant (1% level)

The parents possessing positive relationship between *per se* performance and *GCA* effects might have more number of additive genes and could contribute to the accumulation of favourable genes in a varietal development programme. The lack of association between *per se* performance and the *GCA* effects of parents, either high mean with low *GCA* effect or vice versa signifies that the particular trait was probably under the influence of non-additive gene action. In the present study, considering *GCA* effects and *per se* performance together, the lines TSH 0499 and TSH 04/115 and the testers MCU 13 and TCH 1819 were identified as desirable parents for developing hybrids with improved yield and fibre quality traits. Hence, it could be concluded that these parents can be utilized in hybridization programmes to identify superior segregants with high yield and good fibre quality traits. An attempt could be made for selecting desirable hybrids through multiple crosses for yield and fibre quality traits in the segregating generations, as no parent was found to be a good combiner for all the traits.

In the present investigation, negative *SCA* effects were taken into consideration for days to first flowering and plant height, while positively significant *SCA* effects were considered for the rest of the traits. The *scaSCA* of hybrids for yield and fibre quality-related traits were represented in **Table 4.** The hybrid TSH 04/115 x MCU 7 excelled superior *scaSCA* effect for nine characters *viz.,* days to first flowering, plant height, the number of monopodial branches per plant, the number of bolls per plant, boll weight, single plant yield, Internode length, the number of nodes per plant and fibre fineness. The hybrid, TSH 04/115 x SVPR 4 recorded significantly superior *scaSCA* effect for seven characters. The next best hybrid combination ARBC 19 x KC 3 which expressed favourable significant *scaSCA* effect for six characters *viz.,* days to first flowering, the number of bolls per plant, single plant yield, seed index, lint index and 2.5 per cent span length. The hybrids, TSH 0499 x SVPR 4, TSH 0499 x TCH 1777, TSH 0499 x TCH 1819, TSH 0499 x TCH 1819, BGDS 1063 x TCH 1716 and ARBC 19 x SVPR 4 showed favourable *scaSCA* effects for five different yield and fibre quality traits.

Table 4. Estimates of *scaSCA* effects for yield and fibre quality traits

Cross	DFF	PH	NM	NS	NB	BW	SPY	IL	NN
TSH 0499 X MCU 7	-2.18 **	0.63	-0.19	-0.44	-7.51 **	-0.15	-17.63 *	-0.51 **	-0.69
TSH 0499 X MCU 13	-1.93 *	-1.42	0.43	-2.07	2.35	0.11	16.67 *	-0.12	-1.44
TSH 0499 X CO 14	-1.43	5.93 **	-0.07	2.72 *	-3.46 *	-0.09	-17.99 *	-0.51 **	1.69
TSH 0499 X SVPR 4	3.35 **	3.75 *	0.23	-1.39	-0.55	0.56 **	18.56 **	0.52 **	1.19
TSH 0499 X KC3	-0.71	-6.15 **	-0.02	-0.64	2.78	0.02	7.63	0.75 **	-0.44
TSH 0499 X Surabhi	0.38	-4.98 **	-0.04	0.11	0.92	-0.57 **	-25.31 **	-0.41 *	0.44
TSH 0499 X TCH 1777	1.32	-3.54	-0.27	1.25	4.80 **	-0.34	3.19	0.48 *	-0.31
TSH 0499 X TCH 1819	1.20	5.77 **	-0.08	0.47	0.65	0.44 *	14.88 *	-0.20	-0.44
TSH 04/115 X MCU 7	2.29 **	9.09 **	0.66 *	1.46	5.92 **	0.63 **	24.47 **	0.38 *	2.63 *
TSH 04/115 X MCU 13	1.16	5.64 **	-0.22	1.43	-2.31	-0.26	-0.55	-0.48 *	0.88
TSH 04/115 XCO 14	1.54 *	-14.11 **	-0.02	-2.03	3.42 *	-0.06	2.58	0.18	-2.50
TSH 04/115 X SVPR 4	0.32	-6.00 **	-0.32	0.56	-0.26	0.39 *	36.00 **	-0.30	0.00
TSH 04/115 X KC3	-3.24 **	13.50 **	-0.57 *	-2.64 *	-7.54 **	-0.23	-38.88 **	0.59 **	-3.63 **
TSH 04/115 X Surabhi	1.23	6.98 **	0.11	0.61	1.35	-0.02	13.77	0.28	-0.25
TSH 04/115 X TCH 1777	-0.96	-9.33 **	0.38	-1.10	-0.81	-0.21	-25.40 **	-0.08	0.00
TSH 04/115 X TCH 1819	-2.34 **	-5.77 **	-0.03	1.72	0.24	-0.24	-12.00	-0.56 **	2.88 *
BGDS 1063 X MCU 7	-0.01	-7.82 **	-0.18	-1.15	2.11	-0.27	-0.56	-0.22	-1.69
BGDS 1063 X MCU 13	-0.38	-1.77	-0.35	0.52	-4.08 *	-0.00	-17.99 *	0.82 **	0.06
BGDS 1063 XCO 14	-1.23	-0.91	-0.26	-1.95	-0.93	-0.25	0.13	0.90 **	-1.38
BGDS 1063 X SVPR 4	-1.48 *	-8.45 **	0.45	-2.15	-0.53	-0.45 *	-37.43 **	0.06	-1.81
BGDS 1063 X KC3	1.34	0.20	0.40	2.45 *	0.60	-0.15	-0.74	-0.70 **	3.06 *
BGDS 1063 X Surabhi	-1.95 *	5.27 **	0.07	0.40	1.39	0.11	7.95	-0.27	0.44
BGDS 1063 X TCH 1777	-0.01	1.56	-0.55 *	0.18	-0.33	0.35	27.25 **	-0.13	-0.31
BGDS 1063 X TCH 1819	1.37	1.92	-0.17	-1.49	-0.13	0.02	6.23	1.00 **	-1.94
ARBC 19 X MCU 7	-0.10	-1.91	-0.29	0.14	-0.53	-0.21	-6.28	0.35	-0.25
ARBC 19 X MCU 13	1.15	-2.46	0.14	0.11	4.04 *	0.15	1.87	-0.22	0.50
ARBC 19 X CO 14	-1.23	-0.91	-0.26	-1.95	-0.93	-0.25	0.13	0.90 **	-1.38
ARBC 19 X SVPR 4	-2.20 **	10.70 **	-0.36	2.99 **	1.34	-0.50 **	-17.13 *	-0.28	0.63
ARBC 19 X KC3	2.62 **	-7.55 **	0.19	0.84	4.16 **	0.36	31.99 **	-0.64 **	1.00
ARBC 19 X Surabhi	0.34	-7.27 **	-0.14	-1.11	-3.65 *	0.49 *	3.58	0.40 *	-0.63
ARBC 19 X TCH 1777	-0.35	11.32 **	0.44	-0.32	-3.66 *	0.20	-5.05	-0.27	0.63
ARBC 19 X TCH 1819	-0.23	-1.92	0.28	-0.70	-0.76	-0.23	-9.11	-0.24	-0.50
SE	**0.72**	**1.83**	**0.25**	**1.07**	**1.54**	**0.18**	**6.89**	**0.18**	**1.29**

*Significant (5% level) **Significant (1% level)

Cross	SI	LI	GOT	SL	UR	STR	EP	Mic
TSH 0499 X MCU 7	0.48 *	0.55 **	0.15	-0.21	0.00	-0.65	0.48 **	-0.05
TSH 0499 X MCU 13	0.53 **	0.30 *	0.22	0.53	-1.81	0.21	-0.50 **	-0.23
TSH 0499 X CO 14	-1.33 **	-0.25	-2.49 *	-0.56	-0.28	-0.76	-0.07	0.25
TSH 0499 X SVPR 4	0.17	0.22	1.60	-2.16 **	-0.23	-0.28	0.47 **	0.30 *
TSH 0499 X KC3	-0.21	-0.46 **	-0.14	1.24 *	-1.01	1.04	-0.19	-0.22
TSH 0499 X Surabhi	0.71 **	-0.70 **	1.35	0.54	1.37	0.01	-0.34 *	0.17
TSH 0499 X TCH 1777	0.22	0.48 **	0.60	0.55	2.47 *	0.72	0.20	0.19
TSH 0499 X TCH 1819	0.21	0.04	-1.40	0.08	-0.51	-0.30	-0.05	-0.42 **
TSH 04/115 X MCU 7	0.89 **	-0.03	-0.39	-0.15	-0.50	0.17	-0.28	-0.41 **
TSH 04/115 X MCU 13	-1.34 **	-0.65 **	0.23	1.63 **	0.49	1.39 *	-0.97 **	0.35 *
TSH 04/115 XCO 14	1.01 **	0.82 **	0.81	-0.05	1.07	0.66	0.67 **	-0.11
TSH 04/115 X SVPR 4	-1.42 **	-0.65 **	-0.88	0.50	-2.83 **	-0.80	-0.10	-0.21
TSH 04/115 X KC3	0.69 **	0.30 *	1.45	-0.55	0.24	0.06	0.04	0.01
TSH 04/115 X Surabhi	-0.60 **	0.14	0.76	-0.10	-0.78	-0.71	0.54 **	0.05
TSH 04/115 X TCH 1777	0.56 **	0.03	-0.59	-1.14 *	1.37	0.25	0.03	-0.23
TSH 04/115 X TCH 1819	-0.01	-0.34 *	2.09	-0.12	0.94	-1.02	0.08	0.56 **
BGDS 1063 X MCU 7	-1.83 **	-0.80 **	-2.92 **	0.19	0.18	0.39	0.12	-0.02
BGDS 1063 X MCU 13	0.39 *	-0.27	0.31	-0.37	-1.18	-1.05	0.13	-0.16
BGDS 1063 XCO 14	1.71 **	-0.64 **	-0.93	-1.11 *	1.09	0.08	0.27	-0.17
BGDS 1063 X SVPR 4	-1.17 **	-0.17	-1.77	0.94	-0.06	-0.14	-0.04	0.18
BGDS 1063 X KC3	0.26	0.12	-0.23	-0.06	-0.68	-0.23	-0.10	0.20
BGDS 1063 X Surabhi	1.37 **	1.31 **	1.56	-0.36	2.24 *	0.65	0.20	-0.01
BGDS 1063 X TCH 1777	-0.74 **	-0.09	2.96 **	0.60	-1.91	-0.19	-0.22	0.17
BGDS 1063 X TCH 1819	0.38 *	0.45 **	0.59	0.18	0.32	0.49	-0.37 *	-0.20
ARBC 19 X MCU 7	0.46 *	0.28 *	3.16 **	0.18	0.31	0.09	-0.32 *	0.48 **
ARBC 19 X MCU 13	0.39 *	-0.27	0.31	-1.79 **	2.50 *	-0.55	1.34 **	0.04
ARBC 19 X CO 14	-1.39 **	0.07	2.61 *	1.73 **	-1.88	0.02	-0.87 **	0.03
ARBC 19 X SVPR 4	2.42 **	0.60 **	1.05	0.73	3.12 **	1.21 *	-0.33 *	-0.27
ARBC 19 X KC3	-0.74 **	0.04	-1.08	-0.62	1.45	-0.87	0.25	0.00
ARBC 19 X Surabhi	-1.49 **	-0.76 **	-3.66 **	-0.07	-2.83 **	0.05	-0.40 *	-0.21
ARBC 19 X TCH 1777	-0.04	-0.42 **	-2.98 **	-0.01	-1.93	-0.79	-0.01	-0.13
ARBC 19 X TCH 1819	**0.17**	**0.13**	**1.06**	-0.14	-0.75	0.84	0.34 *	0.05
SE	0.48 *	0.55 **	0.15	**0.53**	**0.96**	**0.57**	**0.15**	**0.14**

*Significant (5% level) **Significant (1% level)

In general, among the 32 hybrids studied nine *viz.,* TSH 04/115 x MCU 7, TSH 04/115 x SVPR 4, ARBC 19 x KC 3, TSH 0499 x SVPR 4, TSH 0499 x TCH 1777, TSH 0499 x TCH 1819, TSH 0499 x TCH 1819, BGDS 1063 x TCH 1716 and ARBC 19 x SVPR 4 were the good specific combiners in order of merit since they expressed significantly favourable *SCA* effects for different yield and fibre quality traits. Significant *scaSCA* effects were reported by Deosarkar *et al*. (2009) for days to first flowering, plant height, the number of monopodial branches per plant, the number of sympodial branches per plants, seed index and lint index. Karademir and Gencer (2010), Hinze *et al.* (2011), Shaukat *et al.* (2013) and Thiyagu *et al.* (2019) reported significant *scaSCA* effects for fibre quality traits. Promising hybrids for heterosis breeding were selected based on two criteria *viz*., *per se* performance and *scaSCA* effects. In this perspective, the hybrid TSH 04/115 x MCU 7 satisfied five characters *viz*., the number of monopodial branches per plant, the number of bolls per plant, boll weight, Internode length and single plant yield. The above said hybrid was followed by TSH 0499 x SVPR 4 recorded the highest mean and *scaSCA* effects for three characters *viz*., boll weight, Internode length and single plant yield. The hybrid, TSH 04/115 x TCH 1819 recorded the highest mean and *scaSCA* effects for three characters *viz*., the number of nodes per plant, seed index and elongation percentage. Similarly, the hybrid TSH 0499 x MCU 13 exhibited higher mean and *scaSCA* effects for three characters *viz*., seed index, lint index and single plant yield. The hybrid TSH 0499 x TCH 1819 exhibited high mean and *scaSCA* effects for two characters *viz*., boll weight and lint index.

Hence, the above-mentioned hybrids *viz*., TSH 04/115 x MCU 7, TSH 0499 x SVPR 4, TSH 0499 x TCH 1819, TSH

0499 x MCU 13 and TSH 04/115 x TCH 1819 could be used for heterosis breeding programme. Positive and significant heterotic performance was reported by Kanimozhi (2012), Ashokkumar *et al*. (2010), Usharani *et al*. (2014) and Isong *et al*. (2019) for fibre quality traits. Abro *et al*. (2009) and Geddam *et al*. (2011) reported positive and significant heterosis for the number of sympodial branches per plant, single plant yield and ginning outturn.

The parents with significant *GCA* effects and the corresponding hybrids with non-significant *scaSCA* effects for 17 yield contributing and fibre quality traits were mentioned in **Table 6.** Among the cross combinations, TSH 04/115 x MCU 7 and BGDS 1063 x TCH 1819 showed non-significant *scaSCA* effects for yield attributing characters and hence could be used for recombination breeding to obtain segregants. In case of fibre quality traits, TSH 0499 x SVPR 4, TSH 0499 x KC 3, TSH 0499 x TCH 1819, TSH 04/115 x KC 3 and TSH 04/115 x TCH 1819 showed non-significant *scaSCA* effects and hence could be used to improve the fibre quality traits. Seed index, ginning outturn and uniformity ratio had no cross combination with non-significant *scaSCA* effects and those traits could not be improved by recombination breeding. Parents and crosses selected for recombination breeding were represented in **Table 5**.

Table 5. Parents and crosses selected for recombination breeding

S.No.	Characters	Parents with positive significant *GCA*	No. of crosses	Crosses with non-significant *scaSCA*
1.	**Early flowering**	BGDS 1063, ARBC 19, TCH 1819	3	BGDS 1063 x TCH 1819 ARBC 19 x TCH 1819
2.	**Plant height**	ARBC 19, TCH 1716, MCU 7, TCH 1819	3	ARBC 19 x TCH 1819 ARBC 19 x TCH 1716 ARBC 19 x MCU 7
3.	**Number of monopodia per plant**	TSH 04/115, Surabhi, TCH 1716	2	TSH 04/115 x Surabhi TSH 04/115 x TCH 1716
4.	**Number of sympodia per plant**	TSH 0499, SVPR 4	1	TSH 0499 x SVPR 4
5.	**Number of bolls per plant**	TSH 0499, TSH 04/115, MCU 13, TCH 1777	3	TSH 0499 x MCU 13 TSH 04/115 x MCU 13 TSH 04/115 x SVPR 4
6.	**Boll weight**	TSH 0499, TSH 04/115, SVPR 4, TCH 1819, MCU 7	2	TSH 0499 x MCU 7 TSH 04/115 x TCH 1819
7.	**Single plant yield**	TSH 0499, TSH 04/115, MCU 13, SVPR 4, TCH 1777, TCH 1819	3	TSH 0499 x TCH 1777 TSH 04/115 x MCU 13 TSH 04/115 x TCH 1819
8.	**Internode length**	TSH 0499, TSH 04/115, MCU 13, TCH 1819, MCU 7	2	TSH 0499 x MCU 13 TSH 0499 x TCH 1819
9.	**Number of nodes per plant**	TSH 0499, SVPR 4	1	TSH 0499 x SVPR 4
10.	**Lint index**	TSH 0499, TSH 04/115, ARBC 19, MCU 13, Surabhi, TCH 1819	2	TSH 04/115 x MCU 13 TSH 04/115 x TCH 1819
11.	**2.5 per cent span length**	TSH 0499, TSH 04/115, TCH 1777, Surabhi	2	TSH 04/115 x TCH 1777 TSH 04/115 x Surabhi
12.	**Bundle strength**	ARBC 19, TCH 1777, Surabhi	1	ARBC 19 x Surabhi
13.	**Elongation percentage**	TSH 04/115, BGDS 1063, MCU 7, TCH 1716	2	TSH 04/115 x MCU 7 BGDS 1063 x TCH 1819
14.	**Fibre fineness**	TSH 0499, TSH 04/115, SVPR 4, KC 3, TCH 1819	5	TSH 0499 x SVPR 4 TSH 0499 x KC 3 TSH 0499 x TCH 1819 TSH 04/115 x KC 3 TSH 04/115 x TCH 1819

In general, the cross combinations involving high × high general combiners produce crosses with significant *scaSCA* effect indicating the role of additive and additive × additive genetic component of variance which could be easily improved through simple selection procedures. The crosses between high x low or low x high general combiners resulted in superior cross combinations due to the complementary gene action which had arisen out of both additive and non-additive gene action. These crosses may likely provide superior transgressive segregants. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system.

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