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Combining Ability and Heterosis Studies on Yield and Fibre Quality Traits in Upland Cotton (*Gossypium hirsutum* L.)

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The present investigation was focused on studying combining ability and heterosis breeding for yield, fibre quality and economically important traits designed among 19 parents and 84 hybrids developed through line x tester method. The analysis of variance indicated substantial variability among the experimental material for yield and fibre quality traits. All the characters were predominantly controlled by non-additive gene action except lint index. Four parents *viz*., TCH 1705-152, TCH 1705-101, TCH 1705-250, Surabhi were identified as very good general combiners. The hybrids, TCH 1705-152 x BS-1, ARBC 1301 x KC3, DSC-1302 x COD 5-1-2 and C 10-3 x TCH 1705-250 observed significant *sca* effects and four hybrids *viz*., TCH 1705-152 x BS-1, TCH 1705-101 x COD 5-1-2, TC H 1705-152 x Surabhi and VS-9-S11-1 x Surabhi were identified as the best hybrids well suited for exploitation through heterosis breeding with regard to *per se*, *sca* effect and standard heterosis.

Introduction

Cotton, the leading natural fiber and major cash crop of India is an important agricultural commodity with global importance and high commercial value providing income to millions of farmers worldwide. The diversity of cotton cultivars and cotton agro climatic zones in India is considerably larger as compared to other major cotton growing countries in the world. *Gossypium* is a large diverse and economically viable genus which includes many diploid and tetraploid species indigenous to most of the tropical regions across the globe (Fryxell *et al.*, 1992). The cultivated tetraploid species *G. hirsutum*, also referred to as "upland cotton", accounts for about 95% of the global cotton production. In breeding high yielding varieties of crop plants for quantitative and qualitative traits, plant breeders often face the problem of selecting parents and crosses.

Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may yield poor combinations. Knowledge on genetic architecture of parents, in terms of yield and quality related characters would help in identifying superior cross combinations in early generation itself. Though cotton production in the country has registered marked improvement in recent years, the yield levels of hybrids appear to have reached stagnation. The important reasons attributed for this is the lack of systematic efforts made to develop hybrid oriented populations; derived lines with improved combining ability and develop new hybrids based on such genetically diverse high combiner lines.

The Line × Tester (LxT) analysis is one of the simplest and efficient methods of evaluating large number of inbreds/parents for their combining ability and moreover provides information regarding genetic mechanisms controlling polygenic traits to produce commercially viable hybrids. A good tester is a genotype that combines the following attributes: large variation between testcrosses; positive combining ability; high and significant correlation with average of the testers used and has acceptable *per se* performance (Castellanos *et al*., 1998). In order to choose the appropriate parents and crosses and to estimate the combining abilities of parents in the early generation, the line × tester analysis method has been widely used in self and cross-pollinated plants by plant breeders. The success of any hybridization program depends on the ability of the parents (lines and testers) having greater potential in the hybridization to yield desirable segregants/recombinants.

Parents showing high average combining ability in crosses are considered to have good general combining ability (GCA) and if their potential to combine well is bounded to a particular cross, they are considered to have good specific combining ability (SCA). Parents with good combining ability are found to be useful either in hybrid development programme to exploit heterotic gene combinations or pedigree breeding to develop inbred lines with favourable gene combinations. The purpose of the present investigation was to determine suitable parents with good general combining ability and hybrids with superior specific combining ability among 84 crosses obtained by crossing 12 lines with seven testers in line x tester fashion for 16 biometric traits to improve yield and fibre quality in cotton (*Gossypium hirsutum* L.).

Materials and Methods

The present research work was carried out during *kharif* 2014 in the experimental field of Department of Cotton, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu, India under irrigated conditions.

Plant materials

The experimental material used in the present study comprised of 19 parents viz., lines- TCH 1705-101, TCH 1705-152, TCH 1705-169, DSC-1302, F-2617, ARBC-1301, G.cot.100, VS-9-S11-1, African I-2, C 10-3, C 11-19, C 12-2 and testers- TCH 1705-250, TCH 1608, BS-1, KC 3, CD-98955, COD-5-1-2, Surabhi and 84 crosses along with one standard check. The genetic population was developed by crossing 12 female/lines with seven male/testers in a Line × Tester mating design. Genotypes of lines and testers were raised and each of the twelve lines was crossed with seven testers individually in a line × tester model (Kempthorne, 1957) to obtain 84 cross combinations summer 2014. The intraspecific crosses among the *G. hirsutum* genotypes were effected using conventional hand emasculation and pollination method developed by Doak (1934). Hybridization programme was continued for 45 days to get sufficient quantity of crossed bolls and they were collected separately and ginned to obtain F1 seeds. Simultaneously, parental seeds were also produced by selfing selected plants by adopting clay smear method (Ramanatha Iyer, 1936).

Field layout

The F1 seed of 84 hybrids along with 19 parents and a standard check hybrid (Mallika, Non- Bt) were raised during *Rabi* 2014-15. Eighty-four crosses were raised in three replications in a randomized block design (RBD) with each cross in two rows of 6 m length and 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 and 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 followed under irrigated condition to obtain good crop stand.

Data analysis

In the parents and F1's, five competitive plants from each genotype were selected at random per replication and were labelled with tags for recording the biometrical observations of ten yield attributes and five fibre quality traits. The average values of the observations from these five plants represented the mean of that genotype per replication. Thus, a total of 103 genotypes were evaluated for all the 16 characters *viz*., days to first flowering, plant height (cm), number of monopodial branches per plant, number of sympodial branches per plant, number of fruiting nodes per plant, number of bolls per plant, boll weight (g), seed index, lint index, single plant yield (g), ginning out turn (%), fibre fineness (mic.), 2.5 % span length (mm), uniformity ratio (%), bundle strength (g/tex) and elongation per cent (%). Observations on five fibre quality traits in each replication were recorded with ten grams of lint sample in High Volume Instrument (HVI).

Statistical analysis

At crop maturity, the mean data of 84 hybrids in each replication and their parents for each quantitative character were tabulated and analysed for analysis of variance, estimation of standard error and critical difference by adopting the method suggested by Panse and Sukhatme (1985). The Line x Tester analysis of combining ability to identify the GCA effects of the parents and SCA effects of the hybrids were estimated as described by Kempthorne (1957).

Results and Discussion

Analysis of variance

Analysis of variance showed highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials (Table 1a). Parents and hybrids showed significant differences between all the characters studied. The mean sum of squares of the combining ability variance (Table 1b) revealed highly significant differences in the lines for all the traits studied except boll weight showing significant difference. The testers showed high significant differences for all the yield and quality traits except days to first flowering, while the interaction between lines and testers had significant differences for a majority of the traits under study which was in accordance with the findings made by Despande *et al.*, (2008), Punitha *et al.*, (2008), Madhuri *et al.*, (2015).

The combining ability analysis provides information on the nature and importance of gene action, which determines the effective and appropriate method for breeding. Combining ability is determined mainly by two types of gene action *viz*., additive gene action, which provides fixable effects and non-additive gene action which are nonfixable results from dominance, epistasis and various other interactions. Further, heterosis breeding procedures are effective in harnessing dominance gene action to the full extent.

The relative estimates of variances due to additive and dominance components are presented in table 1b. The dominance variance is higher than the additive variance for all the biometric traits indicating the preponderance of dominance gene action except lint index which showed higher additive variance. The ratio between additive and dominance variance is less than one for fifteen characters studied. Similar findings have been reported by Deshpande *et al.*, (2008). In contrary, ginning outturn was found to be equally governed by both additive and dominance gene action whereas, lint index showed the predominant role of additive gene action.

Proportional contribution of lines, testers and line × tester interactions

The proportional contribution of the lines, testers and their interactions are presented in table 2. The proportional contribution of lines was higher for number fruiting nodes per plant, number of bolls per plant and ginning out turn, whereas line × tester interaction was higher for the remaining characters. The testers showed lowest proportional contribution for all the characters except boll weight and seed index which showed highest proportional contribution.

Evaluation of parents

Improvement of yield and other advantageous traits involves selection of parents which is considered as the crucial objective in any of the breeding programme. Information on the *per se* performance and nature of general combining ability of characters is necessary for selection of suitable parents for developing hybrids. Therefore, in the present study a total of 19 parents were evaluated based on *per se* performance and *gca* effects both individually and in combination. Inferiorly significant genotypes were chosen for the traits first flowering, plant height, monopodial branches and fibre fineness as earliness, short stature, less number of monopodial branches and finer fibre are the characteristics most preferred.

Mean performance

High performing parents are expected to yield desirable F1's in the segregating generation and the potentiality of such genotypes will also reflect in the performance of the hybrids. The *per se* performance of the parents (Table 3) showed significant differences among the genotypes which was evident from the analysis of variance.

Based on the mean performance among the parents, the line F-2617 observed significantly higher mean for six yield and quality traits *viz*., number of fruiting nodes per plant, number of bolls per plant, boll weight, single plant yield, uniformity ratio and elongation per cent. The corresponding best parent was TCH 1705-250 (tester) which registered high mean value for days to first flowering, number of fruiting nodes per plant, single plant yield, uniformity ratio and elongation percent.

The parent's *viz*., TCH 1705-152, DSC-1302, C 11-19, C 12-2 and BS-1 registered significant mean for four traits each. Finally, with respect to single plant yield four lines *viz*., F-2617 (129.80 g), C 11-19 (112.00 g), ARBC-1301 (109.60 g) and TCH 1705-152 (107.60 g) and three testers *viz*., TCH 1608 (133.00 g), TCH 1705-250 (124.20 g) and CD-98955 (121.80 g) observed high *per se* performance.

gca effects

The general combining ability (*gca*) of parents gives useful information on the choice of parents in terms of expected performance of their progenies as pointed out by Dhillion (1975). Singh and Hari Singh (1985) suggested that parents with high *gca* would produce transgressive segregants in F2 or later generations. Plant breeders use this method to critically analyze the parents for their ability to transmit performance to their progenies.

Based on the estimates of *gca* effects, the line TCH 1705-152 recorded high significant *gca* effects for most of the traits *viz*., number of sympodial branches per plant (1.65), number of fruiting nodes per plant (14.15), number of bolls per plant (9.59), ginning outturn (2.13), uniformity ratio (0.61) and elongation per cent (0.44) and observed significance for lint index (0.55). This was followed by the genotype TCH 1705-101 which registered highly significant and significant *gca* effect for four and one trait, respectively.

Among the testers, TCH 1705-250 obtained high *gca* effect for seven characters such as number of monpodial branches per plant (-0.05), number of sympodial branches per plant (2.03), number of fruiting nodes per plant (2.67), number of bolls per plant (1.15), single plant yield (6.34), uniformity ratio (2.70) and elongation per cent (0.82), while the genotype Surabhi observed high significance and significance for five and one trait, respectively (Table 4). Furthermore, the parents VS-9-S11-1 (14.05), F-2617 (11.44) and TCH 1705-250 (6.34) showed significant *gca* effects for the trait single plant yield.

Per se and *gca* effects

Evaluation of parents based on mean and *gca* separately might result in identification of different sets of parents as promising ones. It has not been fully established that there exists a relationship between *gca* of parents and the performance of hybrids and segregants from the cross. It is still a debatable subject among the breeders. However, Kumar *et al.,* (2014) has reported that *per se* performance and *gca* effects of parents were directly related to each other. Khan (2013) also reported parallelism between *per se* performance and *gca* effects.

In the present study, considering high significant *per se* performance and *gca* effects for yield and fibre quality traits, the parent TCH 1705-250 registered higher mean and gca effect for four characters *viz*., number of fruiting nodes per plant, uniformity ratio, single plant yield and elongation percentage. Two hybrids, DSC-1302 and C-12-2 claimed the second position registering high significance for three traits each. Arumugampillai and Amirthadevarathinam (1998) had reported that identification of parents for breeding programme based on either *per se* performance or *gca* effects alone was misleading in selection programme. The parents possessing positive relationship between *per se* performance and *gca* effects may have more number of additive genes and could contribute for the accumulation of favorable 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 is probably under the influence of non-additive gene action. 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.

Evaluation of hybrids

The chief intention of any hybridization programme is to congregate the desirable genes present in two or more parents into a single genetic background which will result in novel variability. These hybrids are utilized in two ways, i) directly using the F1's to exploit the hybrid vigour and ii) forwarding to further generations and selecting the superior individuals after attaining homozygosity. The utilization of hybrids in anyone of the two ways will depend upon the genetic constitution of the parents as well as the hybrids. To exploit the hybrid vigour, the parameters like *per se* performance, *sca* effects and standard heterosis of hybrids have to be taken into account. The hybrids, obtained by line × tester fashion in the present investigation, were studied for their *per se* performance, specific combining ability effects and heterosis over a standard hybrid Mallika, in order to recommend them for heterosis and /or recombination breeding procedures. Negatively significant values were considered for the traits days to first flowering and plant height for mean performance and *sca* effects.

Mean performance

The main criterion in selecting better hybrids is through their mean performance as it reveals their real value. Shimna and Ravikesavan (2008) advised that the *per se* performance of hybrids appeared to be a useful index in judging them. Gilbert (1958) suggested that parents with good *per se* performance would result in good hybrids.

The hybrid TCH 1705-101 x COD 5-1-2 was observed to have significant *per se* performance for six characters *viz*., number of monopodial branches per plant (1.33), number of sympodial branches per plant (24.40), number of fruiting nodes per plant (61.87), number of bolls per plant (40.33), single plant yield (198.27 g) and fibre fineness (3.90 µg/inch). This was followed by TCH 1705-101 x BS-1 which exhibited significant *per se* performance for five traits *viz*., number of monopodial branches per plant (1.47), number of fruiting nodes per plant (61.20), number of bolls per plant (39.13), 2.5% span length (31.50 mm) and bundle strength (21.60 g/tex). Furthermore, the hybrids TCH 1705-101 x Surabhi, TCH 1705-152 x TCH 1608 and TCH 1705-152 x BS-1 also exhibited significant mean performance for five traits each, respectively (Appendix 1). The top five promising hybrids with high *per se* performance for single plant yield were TCH 1705-101 x COD 5-1-2 (198.27 g), VS-9-S11-1 x KC3 (188.93 g), African I-2 x TCH 1705-250 (178.80 g), F-2617 x TCH 1608 (170.07 g) and VS-9-S11-1 x TCH 1608 (168.33 g).

Hence, the aforesaid hybrids are suitable for compromising the demand in high speed spinning mills as they registered high performance with respect to yield and fibre quality traits.

sca Effects

The next major criterion for judging the hybrids is by studying their specific combining ability (*sca*) effects. *sca* is defined as the deviation from *per se* performance, predicted based on the general combining ability (Allard, 1960). Sprague and Tatum (1942) reported that *sca* effects are due to non-additive genetic interaction. Rojas and Sprague (1952) observed that specific combining ability not only involved dominance and epistasis, but also a considerable amount of genotype and environment (G × E) interaction. Jain and Virmani (1990) reported that the *sca* value of any cross is helpful in predicting the performance of the hybrids far better than the *gca* of parents.

Based on the *sca* effects, the hybrids TCH 1705-152 x BS-1 and ARBC 1301 x KC3 obtained significant *sca* effects for six characters. The F1, TCH 1705-152 x BS-1 had significant *sca* effects for number of monopodial branches per plant (-0.10), number of sympodial branches per plant (3.93), number of fruiting branches per plant (11.25), number of bolls per plant (6.81), single plant yield (31.28) and elongation per cent (0.78), while the hybrid ARBC 1301 x KC3 recorded significant *sca* effects for the traits *viz*., number of monopodial branches per plant (-0.17), number of fruiting nodes per plant (1.98), number of bolls per plant (1.16), seed index (1.89), fibre fineness (-0.55) and 2.5% span length (3.68). The hybrids DSC-1302 x COD 5-1-2 and C 10-3 x TCH 1705-250 showed favourable significant *sca* effect for five traits each (Table 5). The hybrid VS-9-S11-1 x Surabhi, showed very good *sca* effect for fibre fineness, 2.5% span length, uniformity ratio and bundle strength out of the five fibre quality traits. The *sca* effect obtained by the above hybrids is a clear indication of the presence of dominance gene action and such hybrids are highly suitable for heterosis breeding to fully exploit the dominance gene action and to improve the yield and fibre quality traits. Significant *sca* effects were also reported by Deosarkar *et al.*, (2009), Jatoi *et al.*, (2010), Natera *et al.*, (2012), Javaid *et al.*, (2014).

Standard heterosis per cent

The scope for exploiting the hybrid vigour depends on high *per se* performance of the hybrids over the standard variety or the local check; the magnitude of heterosis and the biological feasibility for large *sca*le production of hybrid seeds. Over dominance is attributed towards heterobeltiosis, while commercial superiority of the hybrid may be assessed by evaluating with a standard commercial check (Swaminathan *et al.*, 1972). Among the three kind of heterosis, the interpretation of test hybrids based on standard, useful or economic heterosis reflecting the actual superiority over the best existing cultivar to be replaced appears to be more relevant and practical (Basu *et al.*, 1995). Therefore, heterosis over the standard hybrid Mallika was chosen as the best hybrid from the present study.

The analysis revealed that the hybrid TCH 1705-101 x COD 5-1-2 topped the list for standard heterosis with significant values for number of fruiting nodes per plant (45.45), number of bolls per plant (5.22), single plant yield (44.02), fibre fineness (-13.33) and elongation per cent (17.78). Further, the hybrids TCH 1705-101 x BS-1 and TCH 1705-152 x CD-98955 also registered significant standard heterosis for five traits each (Appendix 2). The above hybrids were followed by African I-2 x TCH 1705-250, ARBC-1301 x TCH 1705-250, C 10-3 x Surabhi, G.cot 100 x TCH 1705-250, TCH 1705-101 x TCH 1705-250, TCH 1705-152 x BS-1, TCH 1705-152 x KC3, TCH 1705-152 x Surabhi and VS-9-S11-1 x TCH 1608 which showed significant standard heterosis for four traits each. Therefore, these hybrids could be selected based on standard heterosis for improvement in yield and fibre quality traits. Positive and significant heterosis has been reported for yield and fibre quality traits by Jyotiba *et al.*, (2010), Geddam *et al.*, (2011), Ashokkumar *et al.*, (2013), Solanki *et al.*, (2014).

Hybrids chosen for heterosis breeding

Hybrids for heterosis breeding were selected based on three criteria *viz*., *per se* performance, *sca* effects and standard heterosis. In this perspective, the hybrids TCH 1705-152 x BS-1, TCH 1705-101 x COD 5-1-2, TCH 1705-152 x Surabhi and VS-9-S11-1 x Surabhi were chosen as the promising hybrids as they satisfied the above criteria for most of the traits (Table 6).

Table.1 a) Analysis of variance and b) Analysis of variance for combining ability for various yield components and fibre quality traits

a) Analysis of variance

Source	Mean squares																
	df	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
Replication	2	3.15	3613.33	0.01	41.48	1.56	13.20	6.70	1872.26	7.67	10.44	14.87	2.09	4.33	11.32	5.79	3.78
Genotypes	102	6.19**	455.43**	0.47**	12.29**	202.26**	96.04**	0.76**	1570.86**	3.79**	2.33**	11.30**	0.37**	9.56**	13.62**	3.75**	1.70**
Parents	18	10.31**	433.41**	0.31**	12.44**	175.03**	92.72**	0.77**	896.30**	5.44**	2.87**	10.44**	0.43**	18.11**	19.28**	3.41**	3.68**
Crosses	83	2.60**	326.92**	0.38**	12.19**	186.39**	92.55**	0.75**	974.24**	3.47**	2.24**	11.49**	0.34**	7.70**	12.51**	3.77**	1.29**
Parents v crosses	1	228.91	11517.78	10.63	17.74	2009.23	445.20	1.04	63232.80	0.68	0.51	11.31	1.54	9.83	3.38	7.68	0.19
Error	204	1.48	104.63	0.01	5.42	4.06	2.05	0.32	312.09	1.20	1.06	4.74	0.15	0.70	1.06	0.72	0.13

b) Analysis of variance for combining ability

Source	Mean squares																
	df	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
Replications	2	2.34	4282.94	0.002	25.31	1.55	0.42	8.15	785.48	8.94	11.41	17.66	2.28	3.15	6.46	7.34	3.17
Crosses	83	2.61	326.92	0.38	12.19	186.39	92.55	0.75	974.24	3.47	2.24	11.49	0.34	7.70	12.51	3.77	1.29
Lines	11	4.64**	840.03**	1.07**	22.74**	963.04**	378.95**	0.68*	1013.93**	5.00**	4.95**	48.46**	0.46**	21.86**	14.19**	6.14**	3.16**
Testers	6	1.56	1120.76**	0.56**	47.55**	250.42**	180.39**	5.75**	1193.52**	19.61**	8.72**	14.59**	1.09**	23.40**	57.04**	6.54**	5.18**
Line v Testers	66	2.37*	169.24*	0.25**	7.22	51.13**	36.83**	0.31	947.68**	1.74	1.20	5.05	0.26**	3.91**	8.18**	3.12**	0.62**
Error	166	1.54	119.36	0.002	5.56	1.60	0.67	0.37	313.42	1.30	1.19	4.56	0.13	0.68	1.14	0.74	0.12
GCA		0.0053	3.4446	0.0029	0.1086	2.9548	1.2172	0.0097	0.5800	0.0377	0.0227	0.1408	0.0019	0.0827	0.0946	0.0142	0.0145
SCA		0.2759	16.6272	0.0814	0.5532	16.5118	12.0534	-0.0196	211.4232	0.1481	0.0020	0.1608	0.0417	1.0785	2.3461	0.7933	0.1690
GCA/SCA		0.0192	0.2071	0.0356	0.1963	0.1789	0.1009	-0.4949	0.0027	0.2545	11.35	0.8756	0.0455	0.0766	0.0403	0.0179	0.0857

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

Table.2 Proportional contribution of lines, testers and their interactions for yield components and fibre quality traits

Source	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
Lines	23.55	34.05	37.60	24.72	68.47	54.27	11.98	13.79	19.13	29.30	55.90	17.80	37.63	15.03	21.60	32.47
Testers	4.33	24.78	10.72	28.19	9.71	14.09	55.42	8.86	40.91	28.15	9.18	22.87	21.97	32.96	12.55	29.04
L x T	72.11	41.16	51.69	47.09	21.81	31.64	32.60	77.35	39.96	42.55	34.92	59.33	40.40	52.00	65.85	38.49

Table.3 Mean performance of yield components and fibre quality traits of the parents

Parents	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
TCH 1705-101	52.00*	92.00	0.80*	21.80	36.20	31.20	4.12	91.60	11.39	8.23	32.75	4.50	29.50	50.50	21.40*	4.90
TCH 1705-152	56.00	95.00	0.80*	22.00	45.00	38.40*	4.35	107.60*	9.30	8.24	36.13	5.20	26.10	52.50*	18.60	6.10
TCH 1705-169	56.00	102.80	0.80*	21.40	31.40	27.80	4.94*	97.60	10.50	7.54	32.64	5.20	30.30	51.20*	17.90	5.80
DSC-1302	56.00	79.20*	0.60*	18.00	35.00	29.60	4.69	78.60	7.57	8.47	40.11*	5.10	26.10	51.70*	18.80	6.00
F-2617	55.00	95.20	1.00	20.00	52.80*	38.20*	5.17*	129.80*	7.38	6.44	35.88	4.80	29.00	52.00*	18.80	6.70*
ARBC-1301	56.00	104.03	1.40	20.60	43.40	37.40*	4.60	109.60*	9.60	7.65	34.37	4.80	27.60	50.40	19.30	5.90
G.cot.100	54.00	82.20*	1.60	17.80	46.40	33.00	4.69	105.40	10.91	9.30	35.48	4.60	30.60	50.50	20.50	4.40
VS-9-S11-1	55.00	87.60*	1.20	18.80	39.40	24.00	5.16*	80.80	11.39	9.66*	35.39	4.40	29.90	47.90	20.90	4.80
African I-2	55.00	94.00	0.80*	23.00	39.60	25.00	4.24	92.80	9.37	7.44	34.30	4.50	31.30*	48.30	20.00	4.40
C 10-3	54.00	76.60*	1.20	17.20	43.60	29.20	4.11	98.00	8.92	7.72	35.73	4.30	29.30	49.60	18.60	5.30
C 11-19	52.00*	76.20*	1.00	19.60	44.40	24.60	4.58	112.00*	10.50	8.68	34.99	4.40	31.50*	46.70	19.40	4.30
C 12-2	52.00*	81.60*	0.80*	20.40	39.80	20.40	4.81	81.00	10.06	7.46	33.17	4.50	31.10*	47.30	20.50	3.80
TCH 1705-250	50.33*	111.20	1.30	22.00	62.80*	31.20	3.96	124.20*	10.56	7.61	32.74	4.70	24.50	55.10*	20.60	8.90*
TCH 1608	55.00	117.60	1.70	18.40	42.40	27.60	5.39*	133.00*	11.32	8.23	32.82	4.50	31.00	48.50	20.50	5.40
BS-1	56.00	104.60	1.20	15.80	39.40	34.00*	4.33	106.42	11.79*	10.47*	36.14	4.20	32.17*	48.20	20.70	5.40
KC3	54.00	105.63	1.20	18.80	41.00	38.80*	3.41	81.80	8.95	7.90	36.10	5.70	26.60	52.50*	19.60	5.30
CD-98955	56.00	84.00*	1.00	17.00	37.20	29.20	5.35*	121.80*	11.45	9.25	34.62	4.70	30.80	46.40	19.70	5.30
COD 5-1-2	54.00	87.40*	0.60*	17.00	29.20	22.00	4.76	85.20	10.88	9.56*	36.04	4.40	28.90	45.00	17.80	4.77
Surabhi	51.00*	89.60	1.40	19.40	33.80	30.60	4.42	88.20	12.01*	8.64	32.64	4.50	34.50*	48.70	20.80	5.10
Grand mean	54.18	92.97	1.07	19.42	41.2	30.12	4.58	101.34	10.20	8.34	34.84	4.68	29.51	49.63	19.71	5.40
Mallika	51	122.73	0.87	23.73	42.53	38.33	3.65	137.67	9.78	8.63	36.05	4.50	31.70	47.70	19.50	4.50
SEd	0.9	1.72	0.13	1.78	3.23	1.87	0.15	2.62	0.69	0.55	1.93	0.41	0.75	0.67	0.62	0.35
CD (0.05)	1.82	3.49	0.25	3.61	6.55	3.8	0.3	5.31	1.39	1.11	3.92	0.82	1.52	1.35	1.27	0.72
CV %	2.03	2.26	14.3	11.23	9.59	7.62	3.92	3.17	8.25	8.03	6.79	10.61	3.11	1.64	3.88	8.03

*Significant (5 % level)   Mallika – Standard check hybrid

Table.4 Estimates of gca effects for yield components and fibre quality traits

Parents	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
TCH 1705-101	0.09	1.34	0.02*	1.81**	13.48**	7.01**	-0.03	1.24	0.11	0.28	0.39	-0.20*	0.08	-0.10	0.53**	-0.02
TCH 1705-152	0.76**	6.99**	0.02*	1.65**	14.15**	9.59**	-0.39**	1.68	-0.60*	0.55*	2.13**	0.15	-0.97**	0.61**	-0.90**	0.44**
TCH 1705-169	-0.10	5.78*	-0.10**	0.52	-1.03**	-1.44**	0.08	-4.70	0.59*	-0.54*	-2.00**	0.20*	-0.55**	0.80**	-0.10	0.31**
DSC-1302	0.28	-5.15*	0.05**	-1.17*	-6.51**	-4.77**	-0.26	-5.27	-0.62*	0.41	1.86**	0.17*	-1.73**	0.88**	-0.01	0.28**
F-2617	-0.43	1.21	-0.36**	-0.81	-3.49**	-1.56**	0.11	11.44**	-0.62*	0.29	1.61**	0.20*	-0.69**	0.20	-0.18	0.61**
ARBC-1301	0.52	1.99	0.23**	-0.68	-3.09**	-2.29**	0.01	-1.64	0.48	0.36	-0.01	-0.07	0.23	-0.13	-0.38*	0.18*
G.cot.100	-0.24	0.59	0.27**	-0.01	-3.04**	-0.87**	-0.04	-2.38	0.69**	-0.37	-1.82**	-0.06	0.58**	-0.10	1.14**	-0.53**
VS-9-S11-1	-0.91**	4.86*	0.31**	0.38	-1.81**	-0.33	0.06	14.05**	0.07	0.04	-0.11	-0.22**	-0.15	-1.13**	0.10	-0.03
African I-2	0.47	5.18*	-0.36**	0.48	-0.37	-0.34	0.07	-2.98	-0.20	0.38	1.09*	-0.06	1.91**	-1.32**	0.46*	-0.05
C 10 -3	-0.24	-13.36**	0.05**	-1.33**	-4.04**	-2.14**	-0.05	-7.64*	-0.43	-0.82**	-1.08*	-0.05	-0.69**	1.30**	-0.58**	-0.11
C 11-19	0.14	0.28	0.12**	0.15	0.99**	1.34**	0.15	3.85	0.11	0.16	0.16	0.03	1.34**	-0.05	0.14	-0.62**
C 12-2	-0.34	-9.72**	-0.24**	-0.99	-5.23**	-4.18**	0.29*	-7.64*	0.42	-0.74**	-2.22**	-0.09	0.63**	-0.93**	-0.21	-0.45**
SE of lines	**0.27**	**2.38**	**0.01**	**0.51**	**0.28**	**0.18**	**0.13**	**3.86**	**0.25**	**0.24**	**0.47**	**0.08**	**0.18**	**0.23**	**0.19**	**0.07**
TCH 1705-250	-0.21	8.37**	-0.05**	2.03**	2.67**	1.15**	-0.42**	6.34*	-0.45*	-0.55**	-0.45	0.16**	-1.31**	2.70**	0.18	0.82**
TCH 1608	0.10	3.32	0.03**	0.16	2.18**	1.42**	0.01	3.32	-0.27	-0.22	-0.06	-0.08	0.03	-0.79**	-0.32*	-0.08
BS-1	-0.01	-2.77	-0.00	-0.62	-0.50*	-0.08	0.07	-6.77*	0.67**	0.19	-0.69	-0.24**	0.65**	-0.53**	0.20	0.05
KC3	0.04	-4.68*	-0.15**	-1.04**	-0.67**	0.33*	-0.53**	4.50	-1.16**	-0.60**	0.77*	0.22**	-0.78**	0.26	-0.67**	-0.12*
CD-98955	-0.29	-7.39**	0.06**	-1.29**	-3.57**	-3.31**	0.57**	-6.83*	0.91**	0.35	-0.70*	0.11	0.15	-0.05	0.18	-0.30**
COD 5-1-2	0.02	-1.30	-0.12**	-0.04	-2.92**	-2.54**	0.41**	3.89	0.55**	0.75**	0.52	-0.00	0.21	-0.82**	-0.20	-0.28**
Surabhi	0.35	4.45*	0.23**	0.79*	2.81**	3.03**	-0.11	-4.45	-0.26	0.08	0.62	-0.17**	1.04**	-0.77**	0.63**	-0.09
SE of testers	**0.21**	**1.82**	**0.01**	**0.39**	**0.21**	**0.14**	**0.1**	**2.95**	**0.19**	**0.18**	**0.36**	**0.06**	**0.14**	**0.18**	**0.14**	**0.06**

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

Table.5 Estimates of sca effects of top performing hybrids for yield components and fibre quality traits

Cross	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
TCH 1705-152×BS-1	-0.37	15.00*	-0.10**	3.93**	11.25**	6.81**	0.05	31.28**	-0.34	0.43	1.27	0.19	0.25	0.96	-1.30**	0.78**
ARBC-1301×KC3	-1.19	10.25	-0.17**	1.08	1.98**	1.16*	0.56	-5.62	1.89**	0.8	-1.54	-0.55**	3.68**	0.31	0.66	-0.3
DSC-1302×COD5-1-2	-0.25	-1.2	0.05*	-1.09	1.99**	1.57**	-0.21	16.96	0.08	0.44	0.64	0.23	-1.65**	4.58**	1.21*	0.76**
C10-3×TCH 1705-250	0.16	3.48	0.39**	1.86	2.53**	3.98**	0.33	28.75**	0.46	-0.41	-1.79	0.09	-0.78	0.25	1.41**	0.66**
TCH 1705-101×COD5-1-2	1.27	7.17	-0.12**	2.59	3.53**	2.66**	0.45	54.92**	-0.2	0.09	0.47	-0.4	0.33	-0.44	-1.33**	0.26
TCH 1705-152×Surabhi	0.27	1.78	0.21**	0.65	5.86**	6.23**	0.19	-5.12	0.64	0.09	-0.89	-0.19	1.56**	0.5	2.17**	-0.88**
DSC-1302×Surabhi	-1.25	11.39	-0.36**	1.54	3.32**	2.40**	0.06	16.83	-0.01	0.13	0.19	-0.1	-0.49	1.83**	0.39	0.38
F-2617×TCH 1705-250	0.68	10.77	-0.01	0.94	3.31**	0.33	-0.3	-0.53	0.44	0.5	0.27	-0.26	-0.38	2.25**	1.01*	0.74**
G.cot.100×TCH 1705-250	0.49	2.19	-0.17**	-1.06	1.53*	1.44**	-0.05	-15.64	0.39	-0.9	-2.62*	-0.1	1.85**	-0.35	0.28	0.08
G.cot.100×KC3	0.24	-3.49	-0.07**	-0.85	3.74**	1.40**	0.05	8.73	-0.56	-0.21	0.24	0.13	-1.68**	-0.12	-0.27	0.62**
VS-9-S11-1×TCH 1608	-0.48	0.24	0.38**	0.75	6.86**	4.30**	0.4	12.75	0.58	0.84	0.72	0.19	1.04*	2.96**	0.92	-0.02
VS-9-S11-1×KC3	0.58	-0.02	-0.11**	1.09	3.97**	4.86**	-0.13	32.16**	-0.36	0.29	1.15	0.29	-0.85	0.11	-0.73	0.12
VS-9-S11-1×COD5-1-2	-0.4	3.72	0.13**	0.29	3.96**	5.13**	0.02	-14.89	-0.5	-0.67	-0.71	-0.48*	1.26**	-2.61**	0.2	0.08
VS-9-S11-1×Surabhi	0.6	6.18	0.45**	-0.41	-3.51**	-4.24**	0.4	17.38	0.29	-0.21	-0.72	-0.42*	1.63**	1.64**	2.97**	-0.41*

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

Table.6 Performance of four promising hybrids chosen for heterosis breeding for important yield and fibre quality traits

Traits	Hybrids	Mean	sca effects	d_{iii}
Number of sympodial branches per plant	TCH 1705-152 x BS-1	25.00*	3.93**	5.34
	VS-9-S11-1 x Surabhi	20.8	-0.41	-12.36
	TCH 1705-101 x COD 5-1-2	24.40*	2.59	2.81
	TCH 1705-152 x Surabhi	23.13	0.65	-2.53
Number of fruiting nodes per plant	TCH 1705-152 x BS-1	72.67*	11.25**	70.85**
	VS-9-S11-1 x Surabhi	45.27	-3.51**	6.43
	TCH 1705-101 x COD 5-1-2	61.87*	3.53**	45.45**
	TCH 1705-152 x Surabhi	70.60*	5.86**	65.98**
Number of bolls per plant	TCH 1705-152 x BS-1	49.53*	6.81**	29.22**
	VS-9-S11-1 x Surabhi	31.67	-4.24**	-17.38**
	TCH 1705-101 x COD 5-1-2	40.33*	2.66**	5.22*
	TCH 1705-152 x Surabhi	52.07*	6.23**	35.82**
Boll weight	TCH 1705-152 x BS-1	4.16	0.05	-6.44
	VS-9-S11-1 x Surabhi	4.79	0.40	7.57
	TCH 1705-101 x COD 5-1-2	5.26	0.45	18.20
	TCH 1705-152 x Surabhi	4.12	0.19	-7.27
Single plant yield	TCH 1705-152 x BS-1	164.4	31.28**	19.42
	VS-9-S11-1 x Surabhi	165.2	17.38	20.00
	TCH 1705-101 x COD 5-1-2	198.27*	54.92**	44.02**
	TCH 1705-152 x Surabhi	130.33	-5.12	-5.33
Fibre fineness	TCH 1705-152 x BS-1	4.6	0.19	2.22
	VS-9-S11-1 x Surabhi	3.7	-0.42*	-17.78**
	TCH 1705-101 x COD 5-1-2	3.9	-0.40	-13.33*
	TCH 1705-152 x Surabhi	4.3	-0.19	-4.44
2.5% span length	TCH 1705-152 x BS-1	29.9	0.25	-5.68**
	VS-9-S11-1 x Surabhi	32.50*	1.63**	2.52
	TCH 1705-101 x COD 5-1-2	30.6	0.33	-3.47
	TCH 1705-152 x Surabhi	31.60*	1.56**	-0.32
Bundle strength	TCH 1705-152 x BS-1	17.3	-1.30**	-11.28**
	VS-9-S11-1 x Surabhi	23.00*	2.97**	17.95**
	TCH 1705-101 x COD 5-1-2	18.3	-1.33**	-6.15
	TCH 1705-152 x Surabhi	21.20*	2.17**	8.72*

Since cotton is an often-cross pollinating crop, varietal crosses are easy by hand emasculation and hence, these hybrids could be utilized in heterosis breeding programme. Hybrids with high *per se* performance, significant *sca* and heterosis for yield and fibre quality traits have also been reported (Kumar, 2007; Kanimozhi, 2012).

In conclusion, in an outline, the present investigation paves way for exposing new hybrids that could be exploited through heterosis breeding to produce elite hybrids that could outperform the present hybrids over yield and fibre quality. Furthermore, when selection is effectively done it can yield fruitful hybrids that have the potential to meet the needs of new spinning and weaving methods and remain competitive against the synthetic fibres.

Abbreviations

DFF-Days to first flowering, PH-Plant height, NM-Number of monopodial branches per plant, NS-Number of sympodial branches per plant, NFN-Number of fruiting nodes per plant, NB-Number of bolls per plant, BW-Boll weight, SI-Seed index, LI-Lint index, GOT-Ginning outturn, FF-Fibre fineness, SL-2.5% span length, UR-Uniformity ratio, BS-Bundle strength, EP-Elongation per cent, SPY-Single plant yield.

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Appendix.1 Mean performance of top performing hybrids for yield components and fibre quality traits

Hybrids	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
TCH 1705-101×COD5-1-2	53.33	115.93	1.33*	24.40*	61.87*	40.33*	5.26	198.27*	10.79	9.36	35.73	3.90*	30.6	48	18.3	5.3
TCH 1705-101×BS-1	51.67	111.47	1.47*	20.8	61.20*	39.13*	4.48	125.6	12.09	8.22	31.72	4.3	31.50*	49.5	21.60*	5.1
TCH 1705-101×Surabhi	52	117.33	1.47*	25.07*	63.93*	44.53*	4.11	118.53	9.18	9.32	38.28*	4.4	30.8	47.8	19	5.3
TCH 1705-152×TCH1608	53.67	136.07	1.40*	24.47*	61.67*	43.60*	4.17	136.47	9.99	8.92	36.26	4.6	28.6	49	17.4	5.90*
TCH 1705-152×BS-1	52.33	127.93	1.47*	25.00*	72.67*	49.53*	4.16	164.4	10.05	9.41	37.06	4.6	29.9	50.4	17.3	6.60*
TCH 1705-101×TCH 1705-250	51.33	115.13	1.8	23.4	59.33*	40.60*	4.17	131.8	10.09	8.17	34.62	4.6	27.4	52.80*	20.6	6.20*
TCH 1705-152×CD-98955	51.67	100.6	1.87	17.8	54.93*	41.27*	3.84	143	9.15	8.4	36.74	4.7	26.8	51.20*	18.1	6.30*
TCH 1705-152×Surabhi	53.33	121.93	2	23.13	70.60*	52.07*	4.12	130.33	10.1	8.96	36.21	4.3	31.60*	49.7	21.20*	4.8
F-2617×TCH 1705-250	52	129.07	1.13*	22.2	50.27*	33.13	3.83	155.47	9.7	8.48	35.77	4.6	27.6	54.50*	20.3	7.50*
VS-9-S11-1×TCH 1705-250	50.67	124.93	1.53	22.73	51.53*	35.47*	3.7	157.07	10.49	7.35	31.95	4.1	27.9	51.30*	18.6	6.30*
African-I-2×TCH 1705-250	51.33	125.53	1.20*	22.8	53.73*	38.27*	4.09	178.80*	9.44	8.23	35.69	4.7	29.2	49.6	19	5.8
VS-9-S11-1×Surabhi	52	124.2	2.53	20.8	45.27	31.67	4.79	165.2	10.42	8.14	34.14	3.70*	32.50*	49.1	23.00*	4.8
African-I-2×TCH 1608	52.33	106.8	1.00*	18.67	47.13	31.8	4.67	118.93	10.31	8.06	33.95	4.1	31.90*	49.4	21.00*	5.4
C10-3×TCH 1705-250	51.67	107.2	1.93	22.6	48.93	36.20*	4.3	165.67	9.91	6.46	31.03	4.7	27.2	53.60*	20.3	6.70*
C12-2×CD-98955	51.67	100.53	1.00*	19.93	44.93	29.93	5.44*	126.2	11.59	7.66	31.25	4.8	31.70*	47.9	19.9	3.9

* Significant (5 % level)

Appendix.2 Standard heterosis (diii) of top performing hybrids for yield and fibre quality traits

Cross	DFF	PH	NM	NS	NFN	NB	BW	SPY	SI	LI	GOT	FF	SL	UR	BS	EP
TCH 1705-101×BS-1	1.31	-9.18	69.23**	-12.36	43.88**	2.09	0.67	-8.77	23.66*	-4.75	-12.02*	-4.44	-0.63	3.77*	10.77**	13.33*
TCH 1705-101×COD5-1-2	4.58*	-5.54	53.85**	2.81	45.45**	5.22*	18.2	44.02**	10.33	8.46	-0.89	-13.33*	-3.47	0.63	-6.15	17.78**
TCH 1705-152×CD-98955	1.31	-18.03*	115.38**	-25.00**	29.16**	7.66**	-13.71	3.87	-6.44	-2.67	1.9	4.44	-15.46**	7.34**	-7.18*	40.00**
African-I-2×TCH 1705-250	0.65	2.28	38.08**	-3.93	26.33**	-0.17	-7.94	29.88**	-3.48	-4.67	-1	4.44	-7.89**	3.98*	-2.56	28.89**
ARBC-1301×TCH 1705-250	-0.65	-4.67	115.38**	-11.8	18.81**	-11.83**	26.22*	5.81	-10.3	-10.16	0.3	0	-10.09**	6.29**	-4.62	24.44**
C10-3×Surabhi	3.92*	-19.17**	107.31**	-21.07**	9.25*	-13.38**	-2.32	-23.87*	-2.01	-5.72	-1.98	-4.44	-2.52	4.40*	-1.03	15.56*
G.cot.100×TCH 1705-250	1.96	-2.34	84.62**	-11.52	15.05**	-8.87**	11.99	-8.09	12.07	-25.61*	-18.30**	0	-1.89	8.18**	7.18*	26.67**
TCH 1705-101×TCH 1705-250	0.65	-6.19	108.08**	-1.4	39.50**	5.92**	-6.22	-4.26	3.17	-5.25	-3.97	2.22	-13.56**	10.69**	5.64	37.78**
TCH 1705-152×BS-1	2.61	4.24	69.23**	5.34	70.85**	29.22**	-6.44	19.42	2.8	9.04	2.8	2.22	-5.68**	5.66**	-11.28**	46.67**
TCH 1705-152×KC3	0.65	-9.29	84.23**	-12.36	42.79**	10.78**	-15.96	-0.24	-10.09	-0.7	4.74	13.33*	-12.62**	6.29**	-6.15	31.11**
TCH 1705-152×Surabhi	4.58*	-0.65	131.15**	-2.53	65.98**	35.82**	-7.27	-5.33	3.34	3.82	0.44	-4.44	-0.32	4.19*	8.72*	6.67
VS-9-S11-1×TCH 1608	-0.65	-4.56	161.54**	-10.11	29.31**	0.7	10.26	22.28*	9.41	3.05	-3.19	-2.22	-2.52	5.66**	2.56	15.56*
African-I-2×TCH 1608	2.61	-12.98	15.38*	-21.35**	10.82*	-17.03**	4.87	-13.61	5.46	-6.57	-5.84	-8.89	0.63	3.56	7.69*	20.00**
African-I-2×BS-1	3.92*	-9.94	53.85**	-12.92	13.94**	-10.78**	1.65	0.63	4.98	1.7	-1.85	-13.33*	3.47	-0.84	0.51	17.78**
VS-9-S11-1×Surabhi	1.96	1.2	192.31**	-12.36	6.43	-17.38**	7.57	20	6.58	-5.68	-5.31	-17.78**	2.52	2.94	17.95**	6.67

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