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Research Article

Combining ability and heterosis studies for seed cotton yield and fibre quality traits in *hirsutum* cotton

M. Gnanasekaran*, K. Thiyagu and M. Gunasekaran
Cotton Research Station, Tamil Nadu Agricultural University, Srivilliputtur
***E-Mail**: gnanasekaran79@gmail.com

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Abstract

Fifty intra *hirsutum* hybrids developed by involving five female and ten testers were evaluated to study gene action, combining ability and heterosis. The analysis of variance indicated substantial variability among the experimental material for yield, its contributing components and fibre quality traits. Preponderance of non-additive gene action was obtained for seed cotton yield per plant, majority of its component traits and fibre quality traits. Three parents namely TSH 321, BGDS 1055 and GSHV 177 were identified as very good general combiners for yield and fibre quality traits. The cross combinations TSH 321 x African I-2, and CCH 15-1 x GSHV 177 for seed cotton yield per plant and fibre properties whereas the crosses BGDS 1055 x GSHV 177, TSH 321 x TCH 484-4, SHM 55 x TCH 1819 for seed cotton yield per plant and number of bolls per plant were identified as the best hybrids and these are well suited for exploitation through heterosis breeding as it recorded significant *per se, sca* effects and standard heterosis for trait as mentioned. Further, the crosses namely SHM 55 x CNH 19, SHM 55 x GSHV 177 and SHM 55 x TCH 486-7 could be recommended for recombination breeding as they satisfied the criteria of the presence of significant *gca* effects of the parents and non significant *sca* effects for yield and fibre quality traits. The study also revealed good scope for commercial hybrid development as well as isolation of pure lines among the progenies.

Key words
Cotton, Combining ability, Heterosis breeding, Recombination breeding.

Introduction

Cotton, the leading natural fibre and major cash crop of India is an important agricultural commodity with global importance and high commercial value providing income to millions of farmers. The demand of cotton is increasing at a rapid pace, more than the world’s population growth rate, so we have to increase the yield per unit area. In India, cotton is cultivated in 122.35 lakh ha producing 377 lakh bales (170 kgs) with a productivity of 524 kg/ha during 2017-18 whereas in Tamil Nadu, cotton is cultivated in 1.48 lakh ha producing 6.00 lakh bales (170 kgs) and 689 kg/ha as productivity (AICCIP Annual Report 2017-18). Eventhough India has achieved self sufficiency in cotton production, the area under cotton cultivation is decrease day by day and also the productivity of cotton in India is very low compared to other cotton growing countries. Therefore, it is essential to develop new high yielding cultivars with good fibre quality parameters to improve production level (Jatoi *et al*., 2011; Akhtar *et al*., 2014).

To make the productivity of Indian cotton comparable to other countries like USA and China, there is a need to give more emphasis on the magnitude of heterosis, *per se* performance and stability of genotypes. The concept of combining ability plays an important role in the identification of parents and development of superior lines or hybrids (Sprague and Tatum (1942)). Studies have indicated that the genotypes found good in performance might not necessarily produce desirable progenies when used in hybrid development. It is therefore, necessary to identify promising lines based on combining abilities using appropriate mating design. There is a need to search for the divergent line in the cotton with superior combining abilities. Exploitation of hybrid vigour has become potential tool for the improvement of this crop. However, lot of information is available on heterosis in cotton but still it holds future promise for further utilization. Hybridization is the most potential technique for breaking undesirable linkages and choice of suitable parents for the development of desired hybrid depends on the selection of parents based on combining ability.

This necessitates the study of combining ability effects of crosses for the selection of superior parents and hybrids. To study the extent of heterosis and combining ability of a number of parents, Line x Tester analysis is the most appropriate procedure.The Line x Tester analysis is one of the simplest and efficient methods of evaluating large number of inbreds/parents for their combining ability (Kempthorne, 1957). Based on the information from Line x Tester analysis, production of commercially viable hybrid is possible. 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 (Jatoi *et al*., 2011). Hence combining ability, which is important in the development of breeding procedures, is of notable use in crop hybridization either to exploit heterosis or to combine the favourable fixable genes.

The general purpose of this study were to estimate general combining ability of parents, specific combining ability and heterosis of hybrids in cotton for yield, yield components and fibre quality traits and selecting superior hybrids that can be used in breeding programmes of cotton.

Materials and Methods

The present research work was carried out during winter 2017 in the experimental field of Cotton Research Station, Tamil Nadu Agricultural University, Srivilliputtur, Tamil Nadu, India under irrigated condition.

The genetic populations (50 intra *hirsutum* hybrids) were developed by crossing five female parents *viz.,* CPD 1501, BGDS 1055, TSH 321, CCH 15-1 and SHM 55 with ten male parents *viz.,* TCH 1819, CNH 19, COD 5-1-2, GSHV 177, SCS 1207, Suraj, African I-2, TCH 482-7, TCH 484-4 and TCH 486-2 in a Line x Tester mating fashion. Lines and testers were raised and each of the five lines were crossed with ten testers individually in a Line x Tester model to obtain 50 cross combinations during winter 2016-17. Thus the 50 intra-*hirsutum* crosses were produced using conventional hand emasculation and pollination method developed by Doak (1934). Hybridization programme was continued for twenty days to get sufficient quantity of crossed bolls and they were collected separately and ginned to obtain F_1 seeds. Simultaneously, parental seeds were also produced by selfing selected plants by adopting clay smear method (Ramanatha Iyer, 1936).

The fifty hybrids along with fifteen parents and standard check hybrids (SVPR 1 Cotton Hybrid and Mallika NBt.) were raised during winter 2017-18. Experimental materials were raised in two replications in a randomized block design (RBD) with each cross in double rows of 4.5m length and spacing of 100cm between rows and 45cm between plants so as to maintain 10 plants in each row. Recommended agronomic practices and need based plant protection measures were followed to obtain good crop stand.

Five competitive plants from each genotype were selected in the parents, F_1s and check hybrids at random per replication and were labelled with tags for recording the biometrical observations. The average values of the observations from these five plants represented the mean of that genotype per replication. Thus, a total of 67 genotypes were evaluated for all the 14 characters *viz*., plant height (cm) (PH), number of monopodia per plant (NM/P), number of sympodia per plant (NSy/P), number of bolls per plant (NB/P), boll weight (g) (BW), seed index (SI), lint index (LI), ginning percentage (GP), seed cotton yield per plant (g) (SCY/P), 2.5% span length (mm) (SL), bundle strength (g/tex) (BS), fibre fineness (µ) (FF) , uniformity ratio (%) (UR) and elongation percentage (EP). Observations on five fibre quality traits in each replication were recorded with ten grams of lint sample in High Volume Instrument (HVI) under ICC mode.

The mean data of sixty seven experimental breeding genotypes 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). The estimation of heterosis was done by calculating the superiority of the F_1 over standard check (Mallika NBt.).

Results and Discussion

Analysis of variance showed significant differences due to genotypes for all the traits except elongation percentage indicating the presence of sufficient variability in the experimental materials (Table 1). Parents and hybrids showed significant differences between all the characters studied except elongation percentage. The mean sum of squares of the combining ability variance (Table 2) revealed significant differences in the lines for all the traits studied except number of monopodia per plant, boll weight and elongation percentage showing significant difference. The testers showed significant differences for all the yield and quality traits except plant height, number of sympodia per plant and elongation percentage, 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), Madhuri *et al.*, (2015), Sivia *et al.*, (2017) and Monicashree *et al.*, (2017).
The relative estimates of variances due to additive and dominance components are presented in Table 2. The dominance variance is higher than the additive variance for all the biometric traits and fibre properties indicating the preponderance of dominance gene action. The ratio between additive (δ^2 GCA) and dominance (δ^2 SCA) variance is less than one for fourteen characters studied indicating preponderance of non-additive gene action (dominance and epistasis), which is an important in exploitation of heterosis through hybrid breeding. Several authors Nidagundi *et al.*, (2011) and Pushpam *et al.*, (2015) have reported the predominance of SCA variance in upland cotton for plant morphological, yield and its component characters and Deshpande *et al.*, (2008), Monicashree *et al.*, (2017) for fibre properties.

The proportional contribution of the lines, testers and their interactions are presented in Table 3. The proportional contribution of line was higher for 2.5% span length, whereas line × tester interaction was higher for the remaining characters (Monicashree *et al.*, (2017). The testers showed lowest proportional contribution for all the characters.

Selection of parents for improvement of yield and fibre quality traits is a crucial step in breeding programme for the improvement of yield and other advantageous traits. Parents are selected based on their mean performance and also their general combining ability effects. 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 fifteen parents were evaluated based on *per se* performance and *gca* effects both individually and in combination. Inferiorly significant genotypes were chosen for the traits seed index and fibre fineness.

Parents with good *per se* performance are expected to yield desirable recombinants in the segregating generation and the potentiality of such genotypes will also reflect in the performance of hybrid in most of the occasions. Parents with high mean performance are generally preferred for all the traits except seed index and fibre fineness. Mean performance of the parents are presented in Table 4. The line TSH 321 recorded highest *per se* performance for nine traits namely number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, lint index, seed cotton yield per plant, uniformity ratio, bundle strength, and fibre fineness. The corresponding best parent was GSHV 177 (tester) which registered high mean value for plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, lint index, seed cotton yield per plant, 2.5% span length and bundle strength. Three testers *viz.*, TCH 1819, SCS 1207 and TCH 486-7 were recorded better mean value for five traits each. The parents CPD 1501, BGDS 1055 and CCH 15-1 (lines) and CNH 19, COD 1-5-2, Suraj and TCH 486-2 (testers) recorded high mean performance for four traits each. Finally with respect to seed cotton yield per plant, one line namely TSH 321 (0.07 kg), five testers *viz.*, TCH 486-7 (0.08kg), GSHV 177, SCS 1207, Suraj and TCH 486-2 observed high *per se* performance (0.07kg).

The general combining ability effects (*gca*) of parents give 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 F_2 or later generations. This method has been widely used by several plant breeders for analysing the parents critically for their ability to transmit superior performance to their progenies. The parents with negatively significant *gca* effects were given importance for seed index and fibre fineness while for other traits, parents with positively significant *gca* effects were taken into consideration.

Based on the estimate of *gca* effects (Table 5), the line TSH 321 recorded high significant *gca* effects for number of bolls per plant, 2.5% span length, bundle strength and fiber fineness and significant *gca* effects for boll weight. This was followed by SHM 55 which registered highly significant *gca* effects for plant height, number of sympodia per plant, number of bolls per plant and seed cotton yield per plant. The line BGDS 1055 was recorded highly *gca* effects for lint index, ginning percentage, and uniformity ratio. Among the tester TCH 486-4 had registered high significant *gca* effects for lint index, ginning percentage, bundle strength and significant *gca* effects for number of bolls per plant, 2.5% span length and uniformity ratio. The tester GSHV 177 observed highly significant *gca* effects for five traits namely, number of monopodia per plant, lint index, seed cotton yield per plant, uniformity ratio and bundle strength while African I-2 observed highly significant *gca* effects for boll weight, seed index, 2.5% span length, fibre fineness and significant *gca* effects for plant height and number of bolls per plant.

Evaluation of parents based on mean and *gca* separately might result in identification of different sets of parents as promising ones. 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. 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 knowledge on general combining ability coupled with *per se* performance of parents would be fruitful in selecting suitable parents with good reservoir of superior genes for hybridization programme. In the present study, considering *per se* performance and *gca* effects for seed cotton yield and fibre properties, one line TSH 321 and one tester GSHV 177 were registered significant mean and *gca* effect for four characters each. The former obtained good mean and *gca* effects for number of bolls per plant, boll weight, bundle strength, fibre fineness and the latter have significant value for both mean and *gca* effects for number of monopodia per plant, lint index, seed cotton yield per plant and bundle strength. The parent BDGS 1055 claimed second position for three traits *viz.*, lint index, ginning percentage and uniformity ratio. The parents possessing positive relationship between mean performance and *gca* effects may have more number of additive genes and could contribute for the accumulation of favourable genes in a varietal development programme. The lack of association between mean 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 as reported by Patel *et al*., (2009), Madhuri *et al.*, (2015), Sivia *et al.*, (2017) and Monicashree *et al*., (2017).

The prime objective of hybridization is to congregate the desirable genes present in two or more different parents into a single genetic background and also to create new variability. The hybrids obtained are analyzed for their mean, specific combining ability effects and heterosis over a standard check (Mallika NBt.) in order to suggest them for heterosis and/or recombination breeding procedures. Top performing hybrids for mean performance, *sca* effects and standard heterosis for yield components and fibre quality traits are tabulated in Table 6a, 6b and 6c.

The mean performance of hybrids is the primary criterion for selection of hybrids as it is real value obtained from them. Shima and Ravikesavan (2008) suggested that *per se* of hybrids appeared to be useful index in judging the hybrids. Two hybrids namely BGDS 1055 x GSHV 177 and SHM 55 x TCH 486-7 recorded highest *per se* performance for seven characters each. The former hybrid observed significant mean value for number of monopodia per plant, number of bolls per plant, boll weight, lint index, ginning percentage, seed cotton yield per plant, uniformity ratio and latter for plant height, number of sympodia per plant, number of bolls per plant, seed cotton yield per plant, uniformity ratio, bundle strength and fibre fineness. This was followed by two hybrids namely SHM 55 x Suraj and SHM 55 x African I-2 which registered better *per se* value for six traits each. The former hybrid observed significant mean value for number of monopodia per plant, number of bolls per plant, seed cotton yield per plant, 2.5% span length, uniformity ratio, bundle strength and latter for plant height, number of sympodia per plant, number of bolls per plant, seed index, seed cotton yield per plant and fibre fineness. The crosses TSH 321 x TCH 484-4, TSH 321 x TCH 486-2, CCH 15-1 x CNH 19, CCH 15-1 x GSHV 177 and SHM 55 x TCH 1819 had registered highest mean performance for five traits each.

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 effects 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. Negative *sca* effects were taken into consideration for seed index and fibre fineness.

Based on *sca* effects, the hybrid SHM 55 x TCH 486-7 had recorded significant *sca* effects for fibre properties *viz.*, 2.5% span length, uniformity ratio, bundle strength and fibre fineness. The hybrids namely TSH 321 x African I-2, CCH 15-1 x CNH 19, CCH 15-1 x GSHV 177 and SHM 55 x Suraj had registered significant *sca* effect for three traits. Significant *sca* effects for seed cotton yield per plant was registered by five hybrids namely BGDS 1055 x GSHV 177, TSH 321 x African I-2, TSH 321 x TCH 484-4, CCH 15-1 x GSHV 177, CCH

15-1 x TCH 484-4 and SHM 55 x TCH 1819. 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 Jatoi *et al.,* (2010), Natera *et al.*, (2012), Javaid *et al.*, (2014), Madhuri *et al.*, (2015), Sivia *et al.,* (2017) and Monicashree *et al*., (2017)..

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 NBt. was chosen as the best hybrid in the present study.

Based on standard heterosis, the hybrids SHM 55 x African I-2 had recorded significant heterosis for six traits namely plant height, number of monopodia per plant, number of bolls per plant, seed index, seed cotton yield per plant and fibre fineness. Further three hybrids *viz.,* BGDS 1055 x GSHV 177, TSH 321 x African I-2 and SHM 55 x TCH 486-7 also registered 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), Madhuri *et al.*, (2015), Sivia *et al.*, (2017) and Monicashree *et al*., (2017).

Hybrids for heterosis breeding were selected based on three criteria *viz*., mean performance, *sca* effects and standard heterosis. In this perspective, the hybrids TSH 321 x African I-2, and CCH 15-1 x GSHV 177 for seed cotton yield per plant and fibre properties where as the crosses BGDS 1055 x GSHV 177, TSH 321 x TCH 484-4, SHM 55 x TCH 1819 for seed cotton yield per plant and number of bolls per plant were identified as the best hybrids and these are well suited for exploitation through heterosis breeding for trait as mentioned. 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 *et al.,* (2014); Madhuri *et al.*, (2015); Monicashree *et al*. 2017).

Recombination breeding procedures allow further combination of alleles in segregating generations, so that we could obtain genotypes with favourable combination of alleles for the traits under improvement. Selection of such genotypes will not mislead if such characters and genotypes are under the control of additive genetic effects. Hence, the hybrids suitable for recombination procedures were selected based on the presence of additive genetic effects *i.e.* significant *gca* effects of the parents and absence of non additive genetic effects *i.e.* non significant *sca* effects of the corresponding hybrids. Such hybrids are believed to throw suitable segregants with favourable combination of alleles for the selected traits. Thus the hybrids SHM 55 x CNH 19, SHM 55 x GSHV 177 and SHM 55 x TCH 486-7 could be recommended for recombination breeding as they satisfied for important yield, yield components and fibre quality traits. The TSH 321 × African I-2 for number of bolls per plant and seed index and TSH 321 x COD 5-1-2 for boll weight and 2.5% span length

The results signify the importance of non-additive genetic effects for attaining maximum improvement in quantitative traits. Parents having high *per se* performance and *gca* effects *i.e.*, TSH 321 for number of bolls per plant, boll weight, bundle strength, and fibre fineness, BGDS 1055 for lint index, ginning percentage and uniformity ratio and GSHV 177 for number of monopodia per plant, lint index, seed cotton yield per plant and Bundle strength were detected with higher general combining ability and should be given due consideration in developing superior hybrid or recombinant in the segregating generation. The hybrids TSH 321 x African I-2, and CCH 15-1 x GSHV 177 for seed cotton yield per plant and fibre properties where as the crosses BGDS 1055 x GSHV 177, TSH 321 x TCH 484-4, SHM 55 x TCH 1819 for seed cotton yield per plant and number of bolls per plant were chosen for heterosis breeding as it recorded significant *per se*, *sca* effects and standard heterosis for trait as mentioned. Besides, the hybrids SHM 55 x CNH 19, SHM 55 x GSHV 177 and SHM 55 x TCH 486-7 could be recommended for recombination breeding as they satisfied significant *gca* effects of the parents and non significant *sca* effects of the corresponding hybrids for important yield and fibre quality traits.

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Table 1. Analysis of variance for various yield components and fibre quality traits

Source of Variation	df	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
Replication	1	0.52	0.16	0.02	22.43	0.05	2.07	0.28	3.00	0.00001	0.07	0.09	0.65	0.11	0.001
Genotypes	64	62.04*	0.18*	2.19*	36.00*	0.44*	2.46*	0.79*	9.59*	0.0013*	6.90*	7.30*	12.01*	0.02	0.665*
Parents	14	49.36	0.11*	3.02*	14.40*	0.85*	5.29*	1.18*	18.32*	0.0002*	11.96*	10.88*	21.70*	0.02	0.877*
Crosses	49	50.31*	0.17*	1.37*	34.01*	0.32*	1.67*	0.61*	7.20*	0.0006*	5.79*	6.42*	9.09*	0.02	0.610*
Error	64	26.75	0.03	0.79	4.15	0.15	0.54	0.10	1.72	0.0001*	0.32	0.53	0.23	0.15	0.050

Table 2. Analysis of variance for combining ability for various yield components and fibre quality traits

Source of Variation	df	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
Replication	1	28.30	0.07	0.44	15.21	0.24	2.04	0.27	2.56	0.0000	0.29	0.16	0.88	0.03	0.02
Crosses	49	50.30*	0.20*	1.40*	34.00*	0.30*	1.72*	0.61*	7.20*	0.0006*	5.80*	6.40*	9.11*	0.02	0.61*
Lines	4	217.16*	0.04	2.63*	138.84*	0.36	2.20*	1.68*	35.74*	0.0015*	33.25*	10.89*	38.82*	0.04	0.26*
Testers	9	31.10	0.21*	1.10	28.29*	0.62*	2.69*	0.85*	6.59*	0.0010*	8.49*	7.93*	10.00*	0.02	0.72*
Line × Tester	36	36.57	0.17*	1.29*	23.79*	0.24	1.35*	0.43*	4.18*	0.0004*	2.07*	5.55*	5.66*	0.01	0.62*
Error	49	27.30	0.02	0.68	4.84	0.15	0.55	0.07	1.73	0.0001	0.26	0.52	0.19	0.15	0.05
GCA		0.3046	-0.0001	0.0016	0.2266	0.0017	0.0070	0.0040	0.0669	0.0000	0.0826	0.0193	0.0789	0.0001	-0.0003
SCA		4.6366	0.0734	0.3075	9.4763	0.0470	0.3977	0.1791	1.2291	0.0002	0.9048	2.5174	2.6879	-0.0694	0.2863
GCA/SCA		0.066	-0.001	0.005	0.024	0.036	0.018	0.022	0.054	0.0000	0.091	0.008	0.029	-0.001	-0.001

Table 3. Proportional contribution of lines, testers and their interactions for various yield components and fibre quality traits

Particulars	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
Lines	35.2	2.1	15.7	33.3	9.1	10.8	22.5	40.5	19.4	46.9	13.8	34.9	19.4	3.5
Testers	11.4	23.3	14.7	15.3	35.3	29.7	25.5	16.8	29.5	26.9	22.7	20.2	17.9	21.6
Line × Tester	53.4	74.6	69.6	51.4	55.7	59.5	52.0	42.7	51.1	26.2	63.5	45.0	62.7	74.9

Table 4. Mean performance of parents for yield components and fibre quality traits

Parents	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
Lines														
CPD 1501	95.0	1.4	13.6	18.9	3.8	7.2*	4.6	38.8*	0.06	30.4*	44.1	22.8	5.8	3.9*
BGDS 1055	103.0	1.1	13.6	23.7	5.4*	9.4	6.1*	39.5*	0.06	25.0	50.0*	20.2	5.8	5.2
TSH 321	104.5	1.7*	15.3*	24.7*	5.9*	12.3	6.7*	35.1	0.07*	29.1	49.1*	25.7*	5.8	3.9*
CCH 15-1	107.5	1.2	13.4	21.5	4.0	10.0	5.0	33.2	0.06	33.2*	49.4*	32.5*	6.1	3.4*
SHM 55	110.0*	1.3	13.3	21.3	3.9	9.3	5.2	35.5	0.04	28.2	47.5	20.8	5.8	3.9*
Mean	**104.0**	**1.3**	**13.8**	**22.0**	**4.6**	**9.6**	**5.5**	**36.4**	**0.06**	**29.2**	**48.0**	**24.4**	**5.9**	**4.1**
Testers														
TCH 1819	95.0	1.2	12.4	17.9	5.5*	9.9	5.8*	37.1*	0.05	28.3	48.1	22.4*	5.8	3.1*
CNH 19	107.5	1.3	16.1*	21.6	5.3	12.6	5.5	30.4	0.06	30.1*	48.8*	24.9*	5.8	4.1
COD 5-1-2	105.5	1.7*	13.5	21.5	5.2	11.9	6.8*	36.6	0.06	28.3	50.2*	22.9*	5.9	4.2
GSHV 177	111.0*	1.9*	15.2*	25.7*	5.2	11.0	5.9*	34.7	0.07*	31.1*	46.0	22.1*	5.9	5.6
SCS 1207	107.0	1.2	16.4*	28.2*	4.9	10.5	5.2	33.0	0.07*	26.3	49.4*	20.7*	5.7	4.4
Suraj	99.5	1.4	13.5	24.5*	4.6	9.8	5.3	34.9	0.07*	30.1*	41.9	20.0	5.6	3.3*
African I-2	104.0	1.2	14.7	20.3	4.1	8.4*	4.0	32.3	0.05	31.4*	47.5	25.1*	5.9	4.7
TCH 486-7	98.0	1.4	12.7	22.7	4.9	7.9*	5.1	39.3*	0.08*	26.3	49.8*	21.9*	5.8	4.1
TCH 484-4	101.0	1.2	13.2	21.1	5.3	9.5	6.3*	40.1*	0.05	26.6	48.1	19.8	5.8	4.1
TCH 486-2	104.0	1.2	13.1	20.7	5.1	7.8*	5.1	39.7*	0.07*	26.2	49.2*	20.3	5.8	4.3
Mean	**103.3**	**1.4**	**14.1**	**22.4**	**5.0**	**9.9**	**5.5**	**35.8**	**0.06**	**28.5**	**47.9**	**20.0**	**5.8**	**4.2**
Grand mean	**103.5**	**1.4**	**14.0**	**22.3**	**4.9**	**9.8**	**5.5**	**36.0**	**0.06**	**28.7**	**47.9**	**22.8**	**5.8**	**4.1**
SEd	**5.2**	**0.2**	**0.9**	**2.0**	**0.4**	**0.7**	**0.3**	**1.3**	**0.01**	**0.6**	**0.7**	**0.5**	**0.4**	**0.2**
CD (P=0.05)	**10.2**	**0.3**	**1.8**	**4.0**	**0.8**	**1.5**	**0.6**	**2.6**	**0.02**	**1.1**	**1.4**	**1.0**	**0.8**	**0.4**

Table 5. Estimates of *gca* effects of parents for yield components and fibre quality traits

Parents	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
Lines														
CPD 1501	-2.34	-0.01	-0.40 *	-1.89 **	-0.06	-0.05	0.01	0.15	-0.01 **	-1.84 **	0.49 **	-1.69 **	-0.05	0.04
BGDS 1055	-3.79 **	0.06	-0.32	-1.89 **	-0.09	-0.32	0.38 **	2.24 **	0.00	-0.66 **	1.03 **	-0.62 **	0.00	0.14 **
TSH 321	-0.01	0.02	0.26	1.49 **	0.23 *	0.51 **	0.11	-0.66 *	0.00	0.91 **	-0.28	1.32 **	0.04	-0.15 **
CCH 15-1	1.53	-0.06	0.04	-1.65 **	-0.09	0.11	-0.08	-0.58	-0.01 **	1.40 **	-0.74 **	1.56 **	0.05	-0.08
SHM 55	4.61 **	-0.03	0.44 *	3.96 **	0.01	-0.25	-0.42 **	-1.15 **	0.01 **	0.20	-0.50 **	-0.59 **	-0.03	0.05
SE	**1.17**	**0.03**	**0.18**	**0.49**	**0.09**	**0.17**	**0.06**	**0.29**	**0.002**	**0.11**	**0.16**	**0.10**	**0.09**	**0.05**
Testers														
TCH 1819	-0.34	-0.09	-0.55 *	-1.15	0.22	0.09	-0.01	-0.24	-0.01 **	1.29 **	-1.13 **	0.99 **	0.05	-0.22 **
CNH 19	0.36	0.21 **	0.23	0.79	-0.02	0.32	-0.13	-1.19 **	0.02 **	0.13	0.15	0.17	0.01	0.33 **
COD 5-1-2	0.40	0.01	-0.11	-3.17 **	0.30 *	0.56 *	0.20 *	-0.41	-0.02 **	0.89 **	-1.27 **	0.23	0.01	0.09
GSHV 177	0.52	0.21 **	-0.25	-1.75 *	0.10	0.64 **	0.31 **	-0.20	0.01 **	-0.25	0.71 **	1.25 **	0.03	-0.03
SCS 1207	0.16	-0.17 **	0.13	1.41 *	0.05	0.39	0.12	-0.39	0.00	-0.83 **	1.17 **	-1.07 **	-0.05	0.35 **
Suraj	-1.24	-0.07	0.19	-0.81	-0.19	-0.31	-0.31 **	-0.56	-0.01 **	0.39 *	-0.23	0.81 **	0.03	0.05
African I-2	3.36 *	-0.07	0.43	1.45 *	-0.50 **	-1.08 **	-0.61 **	-0.01	0.01	0.69 **	-1.11 **	-0.59 **	-0.05	-0.59 **
TCH 486-7	1.56	-0.21 **	0.23	1.73 *	-0.01	-0.23	-0.07	0.26	0.01 *	-1.09 **	0.35	-1.33 **	-0.03	-0.01
TCH 484-4	-2.94	0.07	-0.47	1.63 *	-0.20	-0.07	0.30 **	1.26 **	0.00	0.37 *	0.59 *	0.83 **	0.05	-0.05
TCH 486-2	-1.84	0.07	0.21	-0.09	0.28 *	-0.34	0.18 *	1.46 **	0.01	-1.57 **	0.77 **	-1.33 **	-0.03	0.07
SE	**1.65**	**0.05**	**0.26**	**0.70**	**0.12**	**0.24**	**0.09**	**0.42**	**0.003**	**0.16**	**0.23**	**0.14**	**0.12**	**0.07**

Table 6a. Mean performance of top performing crosses for yield and fibre quality traits

Crosses	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
CPD 1501 x CNH 19	107.0	2.3*	14.7	27.4	5.1	9.9	5.6	35.9	0.12*	27.1	48.3	21.9	5.8	5.0
BGDS 1055 x CNH 19	111.0	2.3*	15.2	24.2	5.1	11.1	6.5*	36.9	0.12*	29.0	47.9	23.4	5.9	5.2
BGDS 1055 x GSHV 177	107.5	2.1*	15.3	30.5*	5.4*	10.6	6.8*	39.1*	0.12*	28.1	49.8*	23.6	5.8	4.4
BGDS 1055 x TCH 484-4	104.5	1.4	15.0	26.6	5.2	9.1*	6.3*	41.2*	0.12*	27.3	47.3	21.1	5.8	4.2
TSH 321 x SCS 1207	112.0	1.7	15.8	33.0*	5.7*	10.8	5.8	35.1	0.12*	29.1	48.1	23.1	5.8	4.5
TSH 321 x African I-2	110.5	1.3	14.8	30.5*	4.9	10.4	6.1*	37.0	0.13*	32.2*	46.0	23.9	5.9	4.5
TSH 321 x TCH 486-7	107.5	1.7	15.9	28.5	5.4*	10.2	6.2*	37.6	0.12*	28.0	47.5	21.9	5.8	4.4
TSH 321 x TCH 484-4	102.5	1.6	13.8	36.0*	4.8	10.3	6.2*	37.5	0.12*	29.1	49.1*	25.8*	5.9	4.3
TSH 321 x TCH 486-2	111.0	1.4	16.5*	31.3*	5.0	9.3*	5.3	36.2	0.13*	28.3	47.7	23.6	5.8	3.8*
CCH 15-1 x CNH 19	106.5	1.4	15.6	24.7	4.5	8.9*	5.3	37.3	0.12*	29.8*	48.0	24.5*	5.8	3.9*
CCH 15-1 x GSHV 177	115.5*	1.4	15.2	24.0	5.0	11.5	6.2*	35.1	0.13*	29.6	45.3	27.5*	5.9	3.3*
CCH 15-1 x TCH 484-4	108.5	1.5	15.0	26.5	4.6	9.6	5.6	36.8	0.12*	31.2	48.1	25.5*	5.9	4.5
SHM 55 x TCH 1819	114.5	1.7	15.6	39.0*	5.4*	9.9	5.3	35.1	0.13*	30.0*	45.0	22.9	5.8	4.0*
SHM 55 x CNH 19	114.0	1.5	15.7	35.0*	5.2	10.4	5.5	34.4	0.14*	28.6	49.0*	22.8	5.9	5.4
SHM 55 x GSHV 177	110.5	1.7	14.9	25.5	4.7	10.2	5.8	36.2	0.13*	31.4*	48.7*	26.2*	6.0	4.8
SHM 55 x SCS 1207	113.5	1.4	15.2	30.5*	4.6	9.1*	5.3	36.9	0.13*	27.5	48.4	20.9	5.7	4.5
SHM 55 x Suraj	111.5	1.9*	15.2	31.8*	5.0	10.4	5.4	34.1	0.12*	29.8*	48.7*	24.6*	5.9	4.5
SHM 55 x African I-2	123.0*	1.7	16.2*	30.3*	4.3	7.8*	4.1	34.3	0.13*	28.9	46.0	21.3	5.7	3.5*
SHM 55 x TCH 486-7	116.5*	1.4	16.2*	32.5*	4.9	10.8	5.7	34.5	0.13*	29.0	49.0*	24.7*	5.8	3.6*
SHM 55 x TCH 486-2	116.0*	1.7	15.9	27.3	5.8*	10.2	5.6	35.6	0.12*	28.3	50.2*	22.9	5.9	4.9
Mean	**109.4**	**1.7**	**15.2**	**26.6**	**5.0**	**10.1**	**5.8**	**36.4**	**0.11**	**29.2**	**47.8**	**23.7**	**5.9**	**4.3**
SEd	**5.2**	**0.2**	**0.8**	**2.2**	**0.4**	**0.7**	**0.3**	**1.3**	**0.01**	**0.5**	**0.7**	**0.4**	**0.4**	**0.2**
CD (P=0.05)	**10.5**	**0.3**	**1.7**	**4.4**	**0.8**	**1.5**	**0.5**	**2.6**	**0.02**	**1.0**	**1.5**	**0.9**	**0.8**	**0.5**
Range	**98** **to** **123**	**1.3** **to** **2.5**	**12.4** **to** **17.0**	**20.0** **to** **39.0**	**4.0** **to** **5.8**	**7.8** **to** **12.0**	**4.1** **to** **7.1**	**31.8** **to** **41.2**	**0.8** **to** **14.0**	**26.3** **to** **32.6**	**45.0** **to** **52.1**	**20.6** **to** **29.2**	**5.7** **to** **6.1**	**3.3** **to** **5.4**

Table 6b. *sca* effects of top performing crosses for yield and fibre quality traits

Crosses	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
CPD 1501 x CNH 19	-0.46	0.43 **	-0.28	1.87	0.18	-0.48	-0.11	0.53	0.01	-0.34	-0.17	-0.31	-0.01	0.36 *
BGDS 1055 x CNH 19	4.99	0.36 **	0.14	-1.33	0.21	0.94	0.42 *	-0.61	-0.00	0.38	-1.11 *	0.12	0.04	0.46 **
BGDS 1055 x GSHV 177	1.33	0.16	0.72	7.51 **	0.34	0.17	0.33	0.65	0.01 *	-0.14	0.23	-0.76 *	-0.08	0.02
BGDS 1055 x TCH 484-4	-2.71	-0.12	-0.06	0.13	0.25	-0.51	0.21	2.29 *	0.01	-0.10	-1.91 **	-0.68 *	-0.02	-0.20
TSH 321 x SCS 1207	2.41	0.18	0.26	3.47 *	0.37	-0.26	-0.21	-0.31	0.01	-0.13	-0.62	-0.88 **	-0.04	0.03
TSH 321 x African I-2	-2.29	-0.32 **	-1.04	0.93	0.12	0.86	0.82 **	1.21	0.01 *	1.45 **	-0.44	-0.56	0.06	0.97 **
TSH 321 x TCH 486-7	-3.49	0.22 *	0.26	-1.35	0.13	-0.19	0.33	1.59	0.01	-0.97 **	-0.40	-1.82 **	-0.06	0.29
TSH 321 x TCH 484-4	-3.99	-0.16	-1.14	6.25 **	-0.28	-0.25	-0.04	0.44	0.02 *	-1.33 **	0.96	-0.08	-0.04	0.23
TSH 321 x TCH 486-2	3.41	-0.36 **	0.88	3.27 *	-0.51	-1.03	-0.82 **	-1.01	0.01	-0.19	-0.62	-0.12	-0.06	-0.39 *
CCH 15-1 x CNH 19	-4.83	-0.42 **	0.18	-1.07	-0.44	-1.69 **	-0.32	2.61 **	0.00	-0.88 *	0.76	-0.96 **	-0.11	-0.62 **
CCH 15-1 x GSHV 177	4.01	-0.42 **	0.26	0.77	-0.01	0.64	0.19	-0.58	0.02 **	-0.70	-2.50 **	0.96 **	-0.03	-0.86 **
CCH 15-1 x TCH 484-4	0.47	-0.18	0.28	-0.11	-0.16	-0.60	-0.45 *	-0.34	0.02 **	0.28	0.42	-0.62 *	-0.05	0.36 *
SHM 55 x TCH 1819	0.79	0.15	0.56	9.56 **	0.12	-0.10	-0.05	0.08	0.03 **	-0.64	-1.20 *	-1.23 **	-0.07	-0.10
SHM 55 x CNH 19	-0.41	-0.35 **	-0.12	3.62 *	0.21	0.22	0.22	0.28	0.01	-0.88 *	1.52 **	-0.51	0.07	0.75 **
SHM 55 x GSHV 177	-4.07	-0.15	-0.44	-3.34 *	-0.41	-0.30	0.08	1.14	-0.00	2.30 **	0.66	1.81 **	0.15	0.51 **
SHM 55 x SCS 1207	-0.71	-0.07	-0.52	-1.50	-0.46	-1.15 *	-0.18	1.98 *	0.00	-1.02 **	-0.10	-1.17 **	-0.07	-0.17
SHM 55 x Suraj	-1.31	0.33 **	-0.58	2.02	0.18	0.80	0.30	-0.65	0.01	0.06	1.60 **	0.65 *	0.05	0.13
SHM 55 x African I-2	5.59	0.13	0.18	-1.74	-0.21	-0.98	-0.70 **	-0.95	0.01	-1.14 **	-0.22	-1.25 **	-0.07	-0.23
SHM 55 x TCH 486-7	0.89	-0.03	0.38	0.18	-0.10	1.12 *	0.36	-1.07	0.01	0.74 *	1.32 *	2.89 **	0.01	-0.71 **
SHM 55 x TCH 486-2	3.79	-0.01	0.10	-3.20 *	0.46	0.63	0.06	-1.17	-0.01	0.52	2.10 **	1.09 **	0.11	0.51 **
SE	**3.70**	**0.10**	**0.58**	**0.56**	**0.27**	**0.53**	**0.19**	**0.93**	**0.006**	**0.36**	**0.51**	**0.31**	**0.28**	**0.16**
Range	**-7.31 to 9.33**	**-0.42 to 0.60**	**-1.88 to 1.74**	**-4.02 to 9.56**	**-0.88 to 0.46**	**-1.69 to 1.33**	**-1.10 to 0.59**	**-2.81 to 2.61**	**-0.03 to 0.30**	**-1.48 to 2.30**	**-2.86 to 3.19**	**-2.94 to 3.23**	**-0.12 to 0.16**	**-0.95 to 0.97**

Table 6c. Standard heterosis of top performing crosses for yield and fibre quality traits

Crosses	PH	NM/P	NSy/P	NB/P	BW	SI	LI	GP	SCY/P	SL	UR	BS	EP	FF
CPD 1501 x CNH 19	1.23	64.29**	-9.26	11.38	2.82	7.03	1.82	-3.70	19.05*	-11.15**	-0.41	-10.25**	-1.69	15.74**
BGDS 1055 x CNH 19	5.01	64.29**	-6.17	-1.63	2.82	20.00*	18.18**	-1.02	14.29	-4.92**	-1.24	-4.10*	0.00	20.37**
BGDS 1055 x GSHV 177	1.70	50.00**	-5.56	23.98**	8.87	14.59	23.64**	4.88	19.05*	-7.87**	2.68	-3.28	-1.69	1.85
BGDS 1055 x TCH 484-4	-1.14	0.00	-7.41	8.13	4.84	-1.62	14.55**	10.52**	14.29	-10.49**	-2.47	-13.52**	-1.69	-2.78
TSH 321 x SCS 1207	5.96	21.43*	-2.47	34.15**	14.92	16.76*	5.45	-5.85	14.29	-4.59**	-0.82	-5.33**	-1.69	4.17
TSH 321 x African I-2	4.54	-7.14	-8.64	23.98**	-1.21	12.43	10.91*	-0.75	23.81**	5.57**	-5.15**	-2.05	0.00	4.17
TSH 321 x TCH 486-7	1.70	21.43*	-1.85	15.85	8.87	10.27	12.73*	0.86	19.05*	-8.20**	-2.06	-10.25**	-1.69	1.85
TSH 321 x TCH 484-4	-3.03	14.29	-14.81**	46.34**	-3.23	11.35	12.73*	0.59	19.05*	-4.59**	1.24	5.74**	0.00	-0.46
TSH 321 x TCH 486-2	5.01	0.00	1.85	27.24**	0.81	0.54	-3.64	-2.90	19.05*	-7.21**	-1.65	-3.28	-1.69	-12.04**
CCH 15-1 x CNH 19	0.76	0.00	-3.70	0.41	-9.27	-3.78	-3.64	0.05	14.29	-2.30	-1.03	0.41	-1.69	-9.72
CCH 15-1 x GSHV 177	9.27	0.00	-6.17	-2.44	0.81	24.32*	12.73*	-5.85	23.81**	-2.95	-6.60**	12.70**	0.00	-23.61**
CCH 15-1 x TCH 484-4	2.65	7.14	-7.41	7.72	-7.26	3.78	1.82	-1.29	14.29	2.30	-0.82	4.51*	0.00	4.17
SHM 55 x TCH 1819	8.33	21.43*	-3.70	58.54**	8.87	7.03	-3.64	-5.85	28.57**	-1.64	-7.22**	-6.15**	-1.69	-7.41
SHM 55 x CNH 19	7.85	7.14	-3.09	42.28**	4.84	12.43	0.00	-7.73*	38.10**	-6.23**	1.03	-6.56**	0.00	25.00**
SHM 55 x GSHV 177	4.54	21.43*	-8.02	3.66	-5.24	10.27	5.45	-2.90	19.05*	2.95	0.41	7.38**	1.69	11.11
SHM 55 x SCS 1207	7.38	0.00	-6.17	23.98**	-7.26	-1.62	-3.64	-1.02	19.05*	-9.84**	-0.21	-14.34**	-3.39	4.17
SHM 55 x Suraj	5.49	35.71**	-6.17	29.27**	0.81	12.43	-1.82	-8.53*	19.05*	-2.30	0.41	0.82	0.00	4.17
SHM 55 x African I-2	16.37**	21.43*	0.00	23.17**	-13.31	-15.68*	-25.45**	-7.99*	23.81*	-5.25**	-5.15**	-12.70**	-3.39	-18.98**
SHM 55 x TCH 486-7	10.22*	0.00	0.00	32.11**	-1.21	16.76*	3.64	-7.46*	28.57*	-4.92**	1.03	1.23	-1.69	-16.67**
SHM 55 x TCH 486-2	9.74*	21.43*	-1.85	10.98	16.94	10.27	1.82	-4.51	14.29	-7.21**	3.51**	-6.15**	0.00	13.43**
SE	**3.64**	**0.11**	**0.58**	**1.52**	**0.23**	**0.52**	**0.19**	**0.92**	**0.01**	**0.35**	**0.51**	**0.30**	**0.27**	**0.16**
Range	**-7.28 to 16.37**	**-7.14 to 64.29**	**-23.46 to 4.90**	**-18.7 to 28.54**	**-21.00 to 16.00**	**-15.68 to 29.19**	**-26.36 to 28.18**	**-14.88 to 10.46**	**-28.57 to 28.57**	**-20.98 to 6.89**	**-10.93 to 7.84**	**-15.57 to 16.67**	**-3.39 to 3.39**	**-23.26 to 25.58**