

Research Article

Combining ability and heterosis for seed cotton yield, its components and fibre quality traits in upland cotton (*Gossypium hirsutum* L.)

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Abstract

The investigation was carried out to estimate combining ability, heterosis and hybrids suitable for recombination breeding for seed cotton yield, yield components and fibre quality traits designed among 13 parents and 40 hybrids developed through line \times tester method. The analysis of variance indicated substantial variability among the experimental material for yield, its components and fibre quality traits. All the characters were predominantly controlled by non-additive gene action. Four parents namely TCH 1819, TSH 0499, SVPR 2 and SVPR 5 were identified as very good general combiners for most of the yield and fibre quality traits. The cross combinations, TCH 1819 \times TSH 0499, TCH 1819 \times MCU 7, KC 2 \times SVPR 4, TCH 1818 \times SVPR 5, TCH 1818 \times SVPR 2 and TCH 1818 \times CO 14 were identified as the best hybrids and these are well suited for exploitation through heterosis breeding as it recorded highest *per se* performance, significant *sca* effects and standard heterosis for important yield components and fibre quality traits. Besides, the crosses *viz.*, TCH 1819 \times SVPR 5 and TCH 1819 \times SVPR 4 could be recommended for recombination breeding as they satisfied the presence of significant *gca* effects of the parents and non significant *sca* effects.

Key words

Combining ability, heterosis breeding, recombination breeding, cotton

Introduction

Cotton (*Gossypium hirsutum* L.) is an important natural fibre crop and plays a vital role as a cash crop in commerce of many countries *viz.*, USA, China, India, Pakistan, Uzbekistan, Australia and Africa. It resides a distinctive position in the global trade because it is a very important agricultural and industrial crop. 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 124.29 lakh ha producing 370 lakh bales (170 kgs) with a productivity of 506 kg/ha whereas, Tamil Nadu, cotton is cultivated in 1.85 lakh ha producing 5.50 lakh bales (170 kgs) and 505 kg/ha as productivity during 2017–18 (AICCIP Annual Report 2018-19). The use of low yielding cultivars and poor quality seed are the primary reasons for lowering the yield per acre in all cotton growing areas of India. 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).

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 as well as influenced by environment. 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 \times Tester (L \times T) 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 both in self and cross pollinated crop species (Shakeel *et al.*, 2012; Ali *et al.*, 2013; Ahsan *et al.*, 2013; Ali *et al.*, 2014). 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. The concept of combining ability was introduced by Sparague and Tautum (1942). 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 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. Hence, the objectives fixed to evaluate 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 recombination breeding programmes of cotton.

Materials and Methods

The experiment was carried out during winter 2017 in the experimental field at Cotton Research Station, Srivilliputtur, Tamil Nadu, India under irrigated conditions.

The experimental material used for the study comprised of 13 parents *viz.*, five lines, TCH 1818, KC 2, TCH 1819, TCH 1705 and KC 3 and eight testers, MCU 5, CO 14, TSH 0499, SVPR 2, SVPR 3, SVPR 4, MCU 7 and SVPR 5 and the resulting 40 crosses along with two check hybrids *viz.* SVPR 1 Cotton hybrid and RCH 2 NBt. Genotypes of lines and testers were raised and each of the five lines was crossed with eight testers individually in a line \times tester model (Kempthorne, 1957) and obtained 40 cross combinations during winter 2016-17. The intra-specific crosses among the *G. hirsutum* genotypes were produced using conventional hand emasculation and pollination method developed by Doak (1934). Hybridization programme was continued for 30 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 F_1 seed of 40 hybrids along with 13 parents and standard check hybrids (SVPR 1 Cotton hybrid and RCH 2 NBt) were raised during winter 2017-18. Forty crosses 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. The parents were also raised in the adjacent block with double row for each entry and spacing of 100 \times 45cm

along with standard check hybrids for evaluating their combining ability. Recommended agronomic practices and need based plant protection measures were followed under irrigated condition to obtain good crop stand.

Five competitive plants for each genotype from parents, F_1 s and check hybrids were selected at random per replication and were labelled with tags for recording the biometrical observations of nine yield attributes (plant height (cm) (PH), number of monopodial branches per plant (NMP), number of sympodial branches per plant (NSyP), number of bolls per plant (NB), boll weight (g) (BW), seed index (SI), lint index (LI), ginning percentage (%) (GP), seed cotton yield per plant (g) (SCYP)) and five fibre quality traits (upper half mean length (mm) (UHML), bundle strength (g/tex) (BS), fibre fineness (mic.) (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 HVI mode.

At crop maturity, the mean data of 40 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 \times Tester analysis for 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 (RCH 2 NBt).

Results and Discussion

Analysis of variance (Table 1) showed significant differences due to genotypes for all the traits except number of symbodia per plant and elongation percentage indicating the presence of sufficient variability in the experimental materials. The mean sum of squares for combining ability variance (Table 2) revealed significant differences in the lines and testers for important yield and fibre quality traits. The interaction between lines and testers had significant differences for majority of the traits under study which was in accordance with the findings made by Deshpande *et al.*, (2008), Punitha *et al.*, (2008), Madhuri *et al.*, (2015). The relative estimates of variances due to additive and dominance components revealed that the dominance variance is higher than the additive variance for all the biometric traits indicating the preponderance of dominance gene action. The ratio between additive and dominance variance is less than one for fourteen characters studied. Similar

findings have been reported by Deshpande *et al.*, (2008). The proportional contribution (Table 3) of tester was higher for boll weight, seed index, lint index and upper half mean length, whereas line \times tester interaction was higher for the remaining characters. The lines showed lowest proportional contribution for all the characters.

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 non-fixable results from dominance, epistasis and various other interactions. Further, heterosis breeding procedures are effective in harnessing dominance gene action to the full extent.

Selection of parents for improvement of yield and fibre quality traits is a crucial step in breeding programme. Parents with high mean performance and positive significant *gca* effects are generally preferred for all the traits except 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. Among the parents, TCH 1819, TSH 0499, SVPR 2 and SVPR 5 had registered highest *per se* performance (Table 4) for most of the yield, its contributing characters and fibre quality traits.

Singh and Hari Singh (1985) suggested that parents with high *gca* would produce transgressive segregants in F_2 or later generations. The genotypes, TCH 1819 and SVPR 5 had registered significant *gca* effects (Table 5) for eight traits, TSH 0499 and SVPR 2 for seven traits, KC 2 for six traits and SVPR 4 for five traits of the important yield components and fibre quality traits. 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 (Singh *et al.*, 1983, Arumugampillai and Amirthadevarathinam (1998)). On overall consideration of parents for *per se* performance and *gca* effects, the parents TCH 1819, TSH 0499, SVPR 2 and SVPR 5 could be the best ones for developing both yield and fibre quality traits. The results of the present study also indicated that it would be desirable to develop multiple cross to select desirable segregants for yield and fibre quality traits in the advanced generations, as no parent was a good general combiner for all the

traits as reported by Punitha *et al.*, (2008) and Patel *et al.*, (2009).

The prime objective of hybridization is to converge 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 (RCH 2 NBt) in order to suggest them for heterosis and / or recombination breeding procedures (Monicashree *et al.*, 2017). Crosses with high *per se* performance and positive significant are generally preferred for all the traits except seed index and fibre fineness. Top performing crosses for mean performance, *gca* 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. Shimna and Ravikesavan (2008) suggested that *per se* of hybrids appeared to be useful index in judging the hybrids. The cross, KC 2 \times SVPR 4 recorded highest *per se* performance for six characters, whereas the crosses TCH 1819 \times TSH 0499, TCH 1819 \times SVPR 4 and TCH 1819 \times SVPR 5 had registered for five yield and fibre quality traits. The other high performing hybrids namely TCH 1818 \times SVPR 5, TCH 1819 \times MCU 7 and TCH 1705 \times SVPR 2 had registered high mean performance for four traits. Hence, these hybrids had high mean performance for important yield and fibre quality traits.

The second important criterion for judging the hybrids is the specific combining ability which is the deviation from the mean performance, predicted on the basis of general combining ability and it is due to non additive genetic interaction (Allard, 1960). Narendra Kumar and Hari Har Ram (1987) suggested that when non allelic interactions are prevalent, the specific combining ability estimate is considered to be the best criterion for choice of hybrids. Based on *sca* effects, the hybrid TCH 1819 \times MCU 7 recorded significant *sca* effects for number of bolls per plant, boll weight, seed cotton yield per plant, uniformity ratio and bundle strength. The other hybrids namely TCH 1818 \times SVPR 2, KC 2 \times SVPR 4, TCH 1819 \times TSH 0499 and KC 3 \times MCU 5 had registered significant *sca* effect for four traits whereas TCH 1818 \times SVPR 5 and TCH 1818 \times CO 14 for three important characters.

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). Rather than mid parent heterosis and heterobeltiosis, the standard, useful or economic heterosis reflecting the actual superiority over the best existing cultivar to be more relevant and practical (Basu *et al.*, 1995). Therefore heterosis over standard hybrid RCH 2 NBt was chosen as the third criterion for selecting the hybrids. The hybrid TCH 1819 \times MCU 7 had recorded significant heterosis for six traits, TCH 1818 \times CO 14 and TCH 1819 \times TSH 0499 for five traits and TCH 1818 \times SVPR 2, KC 2 \times SVPR 5, TCH 1819 \times SVPR 4 and KC 3 \times SVPR 3 for four important yield components and fibre quality traits.

On overall, the hybrids TCH 1819 \times TSH 0499, TCH 1819 \times MCU 7, KC 2 \times SVPR 4, TCH 1818 \times SVPR 5, TCH 1818 \times SVPR 2 and TCH 1818 \times CO 14 were chosen for heterosis breeding. Since cotton is an often cross pollinating crop, varietal crosses are easy by hand emasculation. Therefore, these hybrids could be utilized for heterosis breeding.

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.

On overall, the hybrids TCH 1819 \times SVPR 5 and TCH 1819 \times SVPR 4 could be recommended for recombination breeding as they satisfied for important yield components and fibre quality traits. The TCH 1819 \times SVPR 5 hybrid satisfied four yield and fibre quality traits namely seed cotton yield per plant, number of bolls per plant, UHML and bundle strength whereas, the TCH 1819 \times SVPR 4 hybrid satisfied the criteria of seed cotton yield per plant and number of bolls per plant.

Based on the *per se* performance and *gca* effects, the parents TCH 1819, TSH 0499, SVPR 2 and SVPR 5 could be the best combiners for developing a good hybrid or recombinant in the segregating generation for yield components and fibre quality traits. The cross combinations namely TCH 1819 \times TSH 0499, TCH 1819 \times MCU 7, KC 2 \times SVPR 4,

TCH 1818 \times SVPR 5, TCH 1818 \times SVPR 2 and TCH 1818 \times CO 14 were chosen for heterosis breeding as it satisfied mean performance, *sca* effects and standard heterosis for important yield and fibre quality traits. Besides, the crosses TCH 1819 \times SVPR 5 and TCH 1819 \times SVPR 4 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 components 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	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
Replication	1	54.20	0.05	0.34	0.18	0.11	1.00	0.01	6.93	0.0000	0.17	0.70	0.49	0.08	0.00
Genotypes	52	103.62*	0.09*	1.30	48.59*	0.52*	1.83*	0.77*	9.04*	0.0016*	10.56*	8.56*	8.77*	0.02	0.79*
Parents	12	251.63*	0.09*	1.71	19.55*	0.55*	1.55*	0.90*	15.11*	0.0002*	16.95*	8.90*	9.64*	0.01	1.39*
Crosses	39	60.39*	0.07*	0.89	53.55*	0.52*	1.91*	0.75*	6.62*	0.0006*	8.85*	7.99*	8.10*	0.01	0.53*
Error	52	27.67	0.04	0.90	4.08	0.10	0.72	0.31	1.80	0.0001	0.33	0.53	0.24	0.11	0.04

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

Source of Variation	df	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
Replication	1	150.70	0.06	0.72	1.46	0.08	2.18	0.29	4.05	0.0000	0.06	1.20	0.48	0.22	0.01
Lines	4	67.05	0.03	1.21	124.54*	1.04*	1.02	1.12	21.80*	0.0008*	5.43*	5.75*	9.38*	0.05	1.05*
Testers	7	111.76*	0.06	1.40	46.34*	1.25*	5.76*	2.23*	10.34*	0.0008*	24.27*	10.41*	18.28*	0.01	0.31*
Line × Tester	28	46.59*	0.08*	0.71	45.21*	0.26*	1.07	0.33*	3.52	0.0005*	5.49*	7.70*	5.37*	0.01	0.51*
Error	39	29.55	0.04	0.86	4.15	0.11	0.69	0.27	1.99	0.0001	0.27	0.56	0.25	0.11	0.04
GCA		0.37	-0.0002	0.005	0.22	0.01	0.02	0.01	0.08	0.0000	0.09	0.01	0.07	0.0001	0.001
SCA		8.52	0.0189	-0.073	20.53	0.08	0.19	0.03	0.77	0.0002	2.61	3.57	2.56	-0.0511	0.232
GCA/SCA		0.043	0.011	0.068	0.011	0.125	0.105	0.330	0.104	-	0.034	0.003	0.027	0.002	0.004

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

Particulars	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
Lines	11.39	4.57	13.94	23.85	20.64	5.50	15.24	33.78	13.79	6.29	7.38	11.87	34.59	20.44
Testers	33.22	15.09	28.42	15.53	43.41	54.13	53.31	28.04	26.10	49.19	23.39	40.50	16.85	10.58
Line × Tester	55.39	80.34	57.64	60.62	35.95	40.37	31.44	38.18	60.11	44.51	69.22	47.62	48.57	68.99



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

Parents	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
TCH 1818	92.5	1.0	13.7	19.0	3.8	8.9	5.8	39.4*	0.07*	27.2	48.5	20.7	5.8	4.2
KC 2	109.0	1.4	14.3	23.5	4.1	9.1	5.2	36.3	0.05	26.6	47.4	20.1	5.7	4.4
TCH 1819	107.0	1.3	15.1	24.2	5.4*	8.8	5.7	39.2*	0.06	27.5	49.1*	22.5*	5.8	3.1*
TCH 1705	96.0	1.1	14.3	22.3	4.3	8.6	5.1	36.9	0.05	29.9*	46.8	23.7*	5.8	3.0*
KC 3	105.0	1.2	14.7	26.6	3.9	7.6	4.4	36.9	0.05	25.2	49.6*	19.1	5.7	5.4
Mean	101.9	1.2	14.4	23.1	4.3	8.6	5.2	37.7	0.06	27.3	48.3	21.2	5.8	4.0
MCU 5	107.0	1.1	14.3	25.6	3.8	8.3	4.3	34.1	0.05	30.2*	43.0	20.5	5.7	4.1
CO 14	109.0	1.5	13.1	23.0	4.6	10.6	5.8	35.2	0.05	33.6*	44.9	25.2*	5.8	3.4*
TSH 0499	121.0*	1.4	14.9	29.2*	4.4	9.9	5.9	37.2	0.07*	23.7	50.6*	19.1	5.6	4.6
SVPR 2	127.5*	1.7*	16.3	28.6	4.9*	9.9	5.2	34.5	0.05	26.1	49.4*	19.7	5.7	4.8
SVPR 3	98.5	1.0	14.3	28.8	3.4	8.4	3.9	31.3	0.04	24.1	48.5	18.2	5.6	3.7
SVPR 4	119.0*	1.1	16.0	27.5	4.3	10.4	5.5	34.2	0.05	28.8	48.3	21.0	5.7	4.8
MCU 7	91.5	1.2	13.6	21.8	4.0	9.7	4.1	29.8	0.04	29.0	46.2	22.5*	5.7	2.8*
SVPR 5	117.0	1.0	15.4	26.7	4.0	9.1	4.9	35.1	0.06	31.5*	46.3	24.4*	5.8	3.0*
Mean	111.3	1.3	14.7	26.4	4.2	9.5	4.9	33.9	0.05	28.4	47.2	21.3	5.7	3.9
Grand mean	107.7	1.2	14.6	25.1	4.2	9.2	5.0	35.4	0.05	28.0	47.6	21.3	5.7	3.9
SEd	5.26	0.19	0.95	2.02	0.32	0.85	0.56	1.34	0.01	0.58	0.73	0.49	0.33	0.20
CD (P=0.05)	10.42	0.37	1.87	4.00	0.63	1.68	1.11	2.66	0.02	1.15	1.44	0.97	0.65	0.40



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

Parents	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
TCH 1818	-1.96	-0.03	-0.37	2.22 **	0.05	-0.10	0.14	0.97 **	0.00	-0.59 **	0.52 **	-0.03	0.01	-0.24 **
KC 2	2.66	0.01	0.29	1.98 **	-0.01	0.15	0.37 **	1.26 **	0.00	0.01	0.30	0.07	0.02	0.21 **
TCH 1819	0.98	-0.05	0.13	1.91 **	0.36 **	-0.15	-0.06	0.03	0.01 **	0.80 **	0.48 *	1.08 **	0.07	0.29 **
TCH 1705	-2.15	0.06	-0.20	-3.04 **	-0.05	0.36	-0.15	-1.56 **	-0.01 **	0.31 *	-0.68 **	-0.03	-0.02	-0.28 **
KC 3	0.47	0.00	0.15	-3.07 **	-0.35 **	-0.27	-0.31 *	-0.71	0.00	-0.53 **	-0.62 **	-1.08 **	-0.08	0.02
SE	1.92	0.07	0.33	0.72	0.11	0.29	0.18	0.50	0.003	0.18	0.26	0.18	0.12	0.07
MCU 5	-3.13	0.02	-0.57	-4.16 **	-0.28 *	-0.24	0.03	0.85	-0.01 **	1.98 **	-1.23 **	1.64 **	0.01	0.22 **
CO 14	-3.83 *	0.02	-0.39	-0.60	0.25 *	0.61 *	0.00	-1.66 **	0.00	1.60 **	-1.73 **	0.77 **	0.01	0.06
TSH 0499	0.57	0.10	-0.25	-1.02	0.70 **	1.50 **	0.92 **	0.25	-0.01 *	0.46 **	-0.13	0.43 **	0.02	0.00
SVPR 2	4.47 *	0.06	0.43	0.66	-0.12	-0.41	-0.09	0.67	0.00	-1.46 **	1.11 **	-0.62 **	0.00	-0.23 **
SVPR 3	-0.01	0.00	0.13	0.96	-0.21	-0.61 *	-0.23	0.74	0.00	-2.70 **	1.09 **	-2.48 **	-0.08	-0.13
SVPR 4	5.27 **	0.02	0.41	1.58 *	0.08	-0.21	0.04	0.62	0.01 **	0.22	0.11	-0.36 *	0.00	0.17 *
MCU 7	-1.83	-0.04	-0.03	-0.52	-0.42 **	-0.85 **	-0.79 **	-1.51 **	-0.01 **	-0.70 **	0.27	-0.81 **	0.04	0.12
SVPR 5	-1.53	-0.16 *	0.27	3.10 **	0.00	0.21	0.12	0.05	0.01 **	0.58 **	0.51 *	1.42 **	0.02	-0.23 **
SE	2.43	0.09	0.41	0.91	0.15	0.37	0.23	0.63	0.004	0.23	0.33	0.22	0.15	0.09



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

Crosses	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
TCH 1818 × CO 14	105.0	1.5	14.8	34.6*	4.9	10.0	5.6	36.0	0.11	30.5*	47.9	27.0*	5.9	4.0
TCH 1818 × SVPR 2	115.5	1.3	16.0	34.9*	4.1	7.8	4.8	38.0	0.11	27.2	50.7*	23.2	5.8	3.2*
TCH 1818 × SVPR 3	106.0	1.3	14.7	32.6*	4.1	7.5	4.9	39.6*	0.12	24.7	49.8	19.3	5.7	4.2
TCH 1818 × SVPR 5	104.5	1.3	15.7	38.2*	4.8	9.1	5.4	37.3	0.14*	28.9*	46.4	22.7	5.8	4.2
KC 2 × SVPR 3	113.5	1.6	15.6	33.4*	4.2	9.7	5.9	37.7	0.12	25.5	50.2	19.8	5.8	4.4
KC 2 × SVPR 4	120.5*	1.5	16.3	37.1*	4.4	8.4	5.5	39.7*	0.14*	29.4*	49.3	24.1*	5.9	5.1
KC 2 × SVPR 5	107.5	0.8	15.7	36.1*	4.9	9.0	5.3	36.9	0.12	27.4	50.0	23.9*	5.8	4.5
TCH 1819 × TSH 0499	110.5	1.4	15.5	34.1*	5.3*	10.2	6.0	37.1	0.12	30.6*	46.7	26.3*	5.9	3.9*
TCH 1819 × SVPR 4	112.0	1.6	15.9	37.6*	5.2*	8.6	5.3	38.1	0.14*	30.0*	49.3	23.8*	6.0	5.1
TCH 1819 × MCU 7	108.5	1.1	15.1	34.7*	4.9	7.5	4.0	34.6	0.13*	26.5	54.0*	23.9*	5.9	5.0
TCH 1819 × SVPR 5	110.5	1.4	15.9	34.8*	4.4	8.2	5.6	40.3*	0.14*	29.5*	50.2	25.4*	5.9	4.4
TCH 1705 × SVPR 2	105.5	1.5	15.4	34.0*	4.2	8.8	5.1	36.5	0.13*	24.3	49.8	20.3	5.7	3.6*
KC 3 × MCU 5	102.0	1.4	15.2	22.5	3.3	7.2	4.5	38.5	0.11	29.0*	48.6	23.9*	5.8	4.6
KC 3 × SVPR 2	114.0	1.5	15.8	24.7	4.2	8.6	5.0	36.5	0.12	26.1	47.9	20.9	5.7	4.2
KC 3 × SVPR 3	111.5	1.4	16.5	27.4	4.4	7.8	4.5	36.8	0.12	25.1	47.8	19.8	5.6	3.6*
Mean	108.5	1.4	15.4	28.4	4.4	8.8	5.1	36.6	0.11	27.8	48.8	22.4	5.8	4.3
SEd	5.44	0.21	0.93	2.04	0.33	0.83	0.52	1.41	0.01	0.52	0.75	0.50	0.33	0.21
CD (P=0.05)	10.93	0.41	1.86	4.09	0.65	1.67	1.05	2.83	0.02	1.04	1.51	1.00	0.67	0.42



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

Crosses	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
TCH 1818 × CO 14	2.26	0.09	0.15	4.63 **	0.20	0.65	0.34	0.06	0.00	1.71 **	0.36	3.87 **	0.07	-0.21
TCH 1818 × SVPR 2	4.47	-0.14	0.53	3.67 *	-0.19	-0.53	-0.42	-0.32	0.00	1.47 **	0.32	1.45 **	-0.01	-0.72 **
TCH 1818 × SVPR 3	-0.55	-0.09	-0.47	1.07	-0.15	-0.68	-0.18	1.27	0.01	0.21	-0.57	-0.59	-0.03	0.18
TCH 1818 × SVPR 5	-0.54	0.07	0.39	4.53 **	0.40	0.10	-0.02	-0.40	0.02 *	1.13 **	-3.39 **	-1.09 **	-0.03	0.33 *
KC 2 × SVPR 3	2.32	0.17	-0.23	2.10	0.06	1.32 *	0.59	-0.97	0.01	0.41	0.06	-0.19	0.06	-0.07
KC 2 × SVPR 4	4.04	0.04	0.19	5.18 **	-0.07	-0.43	-0.07	1.15	0.02 **	1.39 **	0.14	1.99 **	0.08	0.33 *
KC 2 × SVPR 5	-2.16	-0.47 **	-0.27	2.66	0.51 *	-0.20	-0.35	-1.08	0.01	-0.97 *	0.44	0.01	-0.04	0.18
TCH 1819 × TSH 0499	0.42	-0.07	0.21	4.85 **	-0.12	-0.04	0.02	0.19	0.01	1.56 **	-2.39 **	2.40 **	0.01	-0.73 **
TCH 1819 × SVPR 4	-2.78	0.21	-0.05	5.75 **	0.36	0.07	0.21	0.78	0.01	1.20 **	-0.04	0.68	0.13	0.25
TCH 1819 × MCU 7	0.82	-0.23	-0.41	4.94 **	0.61 *	-0.34	-0.31	-0.59	0.02 **	-1.38 **	4.51 **	1.24 **	-0.01	0.25
TCH 1819 × SVPR 5	2.52	0.19	0.09	1.42	-0.31	-0.70	0.38	3.55 **	0.00	0.34	0.47	0.50	0.01	-0.05
TCH 1705 × SVPR 2	-5.35	-0.04	-0.24	8.01 **	-0.04	0.01	0.22	0.76	0.02 **	-2.33 **	0.61	-1.45 **	-0.08	-0.28
KC 3 × MCU 5	-3.87	-0.04	0.21	1.37	-0.43	-1.18 *	-0.38	1.68	0.02 *	-0.23	1.71 **	0.94 *	0.06	0.02
KC 3 × SVPR 2	0.53	0.02	-0.19	-1.25	0.31	0.38	0.23	-0.09	0.02 *	0.31	-1.33 *	0.20	-0.02	0.07
KC 3 × SVPR 3	2.51	-0.02	0.81	1.15	0.55 *	-0.16	-0.08	0.10	0.01 *	0.55	-1.42 *	0.96 **	-0.04	-0.63 **
SE	5.44	0.21	0.93	2.04	0.32	0.83	0.52	1.41	0.009	0.52	0.75	0.50	0.33	0.21



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

Crosses	PH	NMP	NSyP	NB	BW	SI	LI	GP	SCYP	SL	UR	BS	EP	FF
TCH 1818 × CO 14	-9.87 *	-21.05	1.37	47.23 **	18.29 *	4.17	-4.27	-4.51	25.82 **	0.33	-4.96 **	21.62 **	0.00	-10.23 *
TCH 1818 × SVPR 2	-0.86	-31.58 **	9.59	48.51 **	0.00	-18.75 *	-18.80 *	0.66	25.82 **	-10.53 **	0.60	4.50	-1.69	-28.41 **
TCH 1818 × SVPR 3	-9.01	-31.58 **	0.68	38.72 **	-1.22	-22.40 *	-17.09	5.04	29.12 **	-18.75 **	-1.19	-13.06 **	-3.39	-5.68
TCH 1818 × SVPR 5	-10.30 *	-31.58 **	7.53	62.55 **	17.07 *	-5.73	-8.55	-1.19	53.85 **	-4.93 **	-7.94 **	2.25	-1.69	-4.55
KC 2 × SVPR 3	-2.58	-15.79	6.85	42.13 **	2.44	1.04	0.00	-0.13	26.92 **	-16.12 **	-0.40	-10.81 **	-1.69	-1.14
KC 2 × SVPR 4	3.43	-21.05	11.64	57.87 **	6.10	-13.02	-6.84	5.17	51.65 **	-3.29	-2.18	8.56 **	0.00	14.77 **
KC 2 × SVPR 5	-7.73	-57.89 **	7.53	53.62 **	18.29 *	-6.25	-10.26	-2.25	35.71 **	-9.87 **	-0.79	7.66 **	-1.69	2.27
TCH 1819 × TSH 0499	-5.15	-26.32 *	6.16	45.11 **	29.27 **	5.73	2.56	-1.59	29.12 **	0.66	-7.34 **	18.47 **	0.00	-11.36 *
TCH 1819 × SVPR 4	-3.86	-15.79	8.90	60.00 **	25.61 **	-10.94	-9.40	0.93	51.10 **	-1.32	-2.18	7.21 **	1.69	14.77 **
TCH 1819 × MCU 7	-6.87	-42.11 **	3.42	47.66 **	19.51 *	-21.87 *	-32.48 **	-8.36 *	38.46 **	-12.83 **	7.14 **	7.66 **	0.00	13.64 **
TCH 1819 × SVPR 5	-5.15	-26.32 *	8.90	48.09 **	7.32	-14.58	-5.13	6.76	49.45 **	-2.96	-0.40	14.41 **	0.00	-1.14
TCH 1705 × SVPR 2	-9.44 *	-21.05	5.48	44.68 **	1.22	-8.33	-12.82	-3.18	38.46 **	-20.07 **	-1.19	-8.56 **	-3.39	-19.32 **
KC 3 × MCU 5	-12.45 *	-26.32 *	4.11	-4.26	-19.51 *	-25.52 **	-23.93 **	1.99	17.03	-4.61 **	-3.57 *	7.66 **	-1.69	4.55
KC 3 × SVPR 2	-2.15	-21.05	8.22	5.11	2.44	-10.94	-15.38	-3.18	35.71 **	-14.14 **	-4.96 **	-5.86 *	-3.39	-4.55
KC 3 × SVPR 3	-4.29	-26.32 *	13.01 *	16.60	6.10	-18.75 *	-23.08 *	-2.52	29.12 **	-17.43 **	-5.16 **	-10.81 **	-5.08	-18.18 **
SE	3.87	0.14	0.65	1.41	0.22	0.57	0.36	0.99	0.01	0.37	0.54	0.36	0.23	0.15