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Combining ability studies in cotton (*Gossypium barbadense* L.)

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Abstract
A study was carried out to estimate the GCA of the parents and SCA of the hybrids towards identifying high yielding and better quality cultivars. Eight genotypes and 28 F_1 hybrids derived by crossing the eight parental genotypes in half diallel mating system were sown in randomized complete block design. Half diallel analysis revealed significant GCA and SCA mean squares for all the traits except for number of reproductive points per plant, 2.5 percent span length. However GCA variance showed significant mean squares for all the traits except boll weight and uniformity ratio, and SCA showed significant mean squares for all the traits except sympodia per plant, micronaire and fibre strength. Among the parents: GSB 40, RHCB 011 and DB 16 were found to be best general combiners for seed cotton yield. Parent TCB 37 and GSB 21 are good combiners for fibre quality traits.

Keywords: Cotton, fibre quality traits, general (GCA) combining ability, half diallel and specific (SCA) combining ability

Introduction
Plant breeders are always in pursuit of desirable genes and gene complex identification of promising individuals is very important in any breeding program. Diallel mating design is one of the tools which help the breeder to identify the potential genotypes and the promising recombinants produced by combining the parental individuals through GCA and SCA. In halfdiallel mating, all possible crosses among selected parents are made in one direction only *i.e.*, direct crosses to identify parents as best/poor general combiners through GCA and the specific cross combinations through SCA.
In combining ability, the entire genetic variability of each trait can be partitioned into GCA and SCA (Sprague & Tatum 1942) [12]. GCA effects administer the additive type of gene action whereas SCA effects are shown due to genes which are non-additive (dominant or epistatic) in nature. Importance of non-additive type of gene action is observed for different cotton traits, however, their exists the appreciable degree of variance due to GCA for morpho-yield traits (Khan 2010) [3]. The mean squares dueto GCA and SCA were highly significant; however, the genetic variances due to SCA were greater than GCA for the yield related traits, showing the predominance of non-additive gene action (Makhdoom, 2011) [10].
Many cotton cultivars despite their high/low agronomic performance combine in a better way/poorly when used as a parental cultivars in cross combinations (Batool *et al*. 2010) [3]. Therefore, the said research work was conducted to analyze some important seaisl and cotton genotypes and their 8 × 8 F_1diallel hybrids to ascertain their relative performance regarding their genetic potential through combining ability effects and variances of seed cotton yield with yield and fibre quality related traits.

Material and Methods
Plant material and field procedure
The research work pertaining to study the genetic potential of genotypes and combining ability in F_1 hybrids of cotton (*Gossypium barbadense* L.) was carried out at Main Agricultural Research Station, Raichur, University of Agricultural Sciences, Raichur, Karnataka, India. Eight diverse genotypes **(**GSB 40, RAB 8, RHCB 011, TCB 37, DB 16, GSB 21, DB 39 and CCB 30) of island cotton handpicked from the All India Coordinated Research Project on Cotton and 28 F_1s were hand sown during July 2014 in a RCB design. Parents and F_1s were planted in four rows measuring six meter with two replications. The row and plant spacings were 90 and 60 cm, respectively. Recommended cultural practices were carried out and the crop was grown under uniform field conditions to minimize environmental variations to the maximum possible extent. Picking was made during the month of December and ginning was performed.

Traits measurement and statistical analyses

Data were recorded for fifteen traits like Seed cotton yield (kg/ha), lint yield (kg/ha), boll weight (g), ginning out turn (%), seed index (g), lint index, plant height (cm), number of monopodia per plant, number of sympodia per plant, sympodial length at 50 percent plant height (cm), number of reproductive points per plant, 2.5% span length (mm), fibre uniformity ratio (%), micronaire value (g/inch) and fibre strength (g/tex). Analysis of variance for individual characters was carried out on the basis of mean value per entry per replication as suggested by Panse and Sukhatme (1967) [11]. Least Significant Difference test was also used for meansseparation and comparison after significance. The data of allthe parameters on 28 F_1s and eight parental genotypes were further subjected to the combining ability analysis accordingto Griffing's (1956) Method-II based on Model-II.

Results and Discussion

The mean squares of the analysis of variance of genotypes for combining ability (Table 1) showed significant mean squares for 11 traits revealing presence of diversity among them. No significant mean squares existed for traits like number of reproductive points per plant, 2.5 percent span length, micronaire and fibre strength. Parents could not establish significant mean squares for boll weight, lint index and number of reproductive points per plant, 2.5 percent span length, micronaire and fibre strength, while croses could not establish significant mean squares for traits like number of reproductive points per plant, 2.5 percent span length, micronaire and ginning out turn, number of reproductive points per plant, 2.5 percent span length and micronaire. Variances for GCA and SCA both appeared significant and important in determining the genetic control of most of the traits investigated. While significant GCA indicates preponderance of additive gene action, significant SCA indicates preponderance of non- additive gene action which was evident for most of the traits except fibre quality traits. The GCA variances were lower than SCA variances for traits like seed cotton yield, lint yield, boll weight and uniformity ratio as indicated by their lower ratios indicating predominance of non-additive gene action (dominant or epistasis) in inheritance of all these traits (Sprague & Tatum 1942) [12]. Genotypes GSB 40, RHCB 011 and DB 16 proved to be potential by exhibiting significant positive GCA effects for most of the yield and other yield related traits (Table 2). Crossing these parents therefore will likely produce high yielding hybrids. Similarly TCB 37 and GSB 21 are good general combiners for fibre quality traits, but recorded negative gca effects for seed cotton yield and hence if these parents are crossed with GSB 40, RHCB 011 and DB 16 can produce hybrids that would be high yielding coupled with favourable fibre quality traits. Similar results were reported by Ahuja Dhayal (2007) [1] and Kaushik and Kapoor (2007) [8]. Most of the parents recorded negative gca effect for plant height, boll weight, monopodia per plant and sympodial length at 50 percent plant height and hence selection of these traits would lead to decreased seed cotton yield. Results were in line as those of Tariq Manzoor Khan and Uzair Qasim (2012) [3]. Alabi *et al*. (1987) [2] who suggested that parents found to be good general combiners for different characters should be extensively used in hybridization programme. Echekwu and Alabi (1994) [4] also suggested that parents with positive GCA effects should contribute positive additive effects to their progeny, other lines which show average to high GCA for yield and are components may possess favourable genes for these traits and could be exploited in breeding programmes. The specific combining ability effects are usually used to identify the best cross combinations for hybrid production. This study revealed that hybrids with high sca effects involved at least one or both high general combiners as parents (Table 3) In other words, most crosses with high sca effects involved at least one of the high general combiners. Crosses likeGSB40 x RHCB 011, GSB 40 x CCB 30, GSB 40 x TCB 37and RAB 8 x DB 16 proved good hybrids for seed cotton yield, while crosses like RHCB 011 x TCB 37, RAB 8 x GSB 21, RAB 8 x TCB 37 and TCB 37 x CCB 30 for good fibre quality traits. The best hybrid for yield as well as fibre quality traits is RHCB 011 x CCB 30, hence from these crosses it is evident that GSB 40 is the best combiner for yield and TCB 37 for fibre quality traits. Kadams *et al*. (1999) [7] reported similar results where a hybrid with high sca effects involved one or both of the good general combiners as parents while sca effects are brought about the action of non-additive genes. It should be noted that if there are inconsistencies in sca effects, it is due to environmental effects and therefore it is advisable to try the material in several locations before selection is carried out. The low levels of SCA effects imply that dominance gene action was not appreciable. The high and low levels of GCA and SCA effects in this analysis agrees with the results of Elden *et al*. (1986) [5]. These good materials identified could be bulked together to generate population for the improvement of important yield and yield traits in cotton.

Table 1: ANOVA for different quantitative traits in 8 x 8 half diallel set of cross at MARS Raichur during *kharif* 2014-15

Source of variation	Df	Seed cotton yield (kg/ha)	Lint yield (kg/ha)	Boll weight (g)	Ginning out turn (%)	Seed index (g)	Lint index	Plant height (cm)	Sympodia per plant	Monopodia per plant	Sympodial length at 50% plant height	Number of Reproductive parts per plant	2.5% span length (mm)	Uniformity ratio (%)	Micronaire (µg/inch)	Fibre strength (g/tex)
Replicates	1	28322.00	2429.51	0.19	1.28	0.23	0.15	1850.34	6.72	0.10	1.22	0.34	2.68	23.34	0.23	21.01
Treatments	35	74273.72**	10556.01**	0.16*	3.39**	1.56**	0.28*	1088.90**	30.14**	0.54**	53.58**	1.96	3.88	1.67*	0.11	1.50
Parents	7	54403.57**	5636.00**	0.16	5.35**	2.96**	0.19	2852.53**	37.63*	0.49*	53.47**	2.90	4.16	0.70	0.16*	1.05
Hybrids	27	81438.66**	12150.57**	0.16*	3.00	1.25**	0.26*	668.87**	29.18*	0.56**	54.79**	1.75	3.94	1.98**	0.09	1.66*
Parent Vs Hybrids	1	19911.11*	1942.75*	0.13	0.15	0.13	1.42**	84.58	3.45	0.16	21.61**	1.12	0.29	0.04	0.17	0.48
Error	35	3142.94	274.65	0.08	0.45	0.03	0.14	134.17	12.92	0.20	1.53	1.32	2.65	0.80	0.06	0.91
Total	71	38562.04	5373.27	0.12	1.91	0.79	0.21	628.99	21.32	0.37	27.18	1.62	3.25	1.54	0.09	1.49
GCA	7	27328.51**	5006.36**	0.05	3.35**	1.83**	0.29**	1513.44**	42.11**	0.47**	52.40**	1.40	2.94	0.70	0.10*	1.56**
SCA	28	39588.95**	5345.91**	0.09*	1.28**	0.52**	0.10	302.20***	8.31	0.21*	20.38**	0.87	1.68	0.86*	0.04	0.55
GCA/SCA		0.69	0.94	0.56	2.61	3.52	2.88	5.00	5.06	2.24	2.57	1.61	1.75	0.81	2.5	2.84
Error	35	1571.47	137.32	0.04	0.22	001	0.07	67.08	6.46	0.10	0.76	0.66	1.32	0.40	0.03	045

*, ** Significant at 5% and 1% levels, respectively

Table 2: Estimates of gca effects of different quantitative traits in 8x 8 half diallel set of crosses

Parents (F_1 crosses)	Seed cotton yield (kg/ha)	Lint yield (kg/ha)	Boll weight (g)	Ginning out turn (%)	Seed index (g)	Lint index	Plant height (cm)	Sympodia per plant	Monopdia per plant	Sympodial length at 50% plant height	Number of Reproductive points per plant	2.5% span length	Uniformity ratio (%)	Micronaire (µg/inch)	Fibre strength (g/t)
GSB 40	57.25**	29.52**	0.08	0.52**	-0.98**	-0.34**	28.33**	4.02**	0.32**	4.36**	0.57	-1.16*	-0.23	-0.20**	-0.60*
RAB 8	-102.60**	-43.18**	-0.05	-0.92**	0.08	-0.14	1.83	0.52	-0.28*	1.52**	0.24	0.27	-0.43	-0.06	-0.13
RHCB 011	40.20*	14.71**	0.11	0.72**	0.07	-0.01	-0.26	1.02	0.19	-0.36	0.28	-0.38	-0.03	0.03	-0.14
TCB 37	-19.15	-6.33	-0.01	0.49**	0.01	0.12	-4.91	0.12	-0.07	-1.40**	-0.05	0.32	0.36	0.11	0.49
DB 16	52.35**	20.39**	-0.08	0.13	0.25**	0.04	-2.66	-1.77*	-0.06	-0.28	-0.49	-0.07	0.21	-0.01	0.34
GSB 21	-7.15	-4.08	-0.02	-0.40	0.10	0.01	-12.91**	-2.62**	0.21	-1.43**	-0.15	0.39	0.21	0.03	0.27
DB 39	-23.35	-8.53*	0.04	-0.50**	0.47**	0.18	-7.01	-1.37	-0.15	-3.22**	-0.48	0.29	-0.13	0.11	-0.44
CCB 30	2.45	-2.50	-0.06	-0.05	-0.02	0.13	-2.41	0.07	-0.16	0.81*	0.06	0.34	0.06	-0.01	0.20
$CD_{(gi)}$ @ 5%	35.1	3.77	0.49	0.75	0.35	0.52	3.14	1.74	0.60	1.01	0.97	1.17	0.85	0.44	0.89
CD gi – gj @ 5%	52.16	10.63	0.18	0.43	0.11	0.24	7.43	2.30	0.29	0.79	0.73	1.04	0.57	0.16	0.60

*, ** Significant at 5% and 1% levels, respectively

Table 3: Estimates of sca effects for different characters in 8 x 8 half diallel set of crosses

Character / Crosses	Seed cotton yield (kg/ha)	Lint yield (kg/ha)	Boll weight (g)	Ginning out turn (%)	Seed index (g)	Lint index	Plant height (cm)	Sympodia per plant	Monopdia per plant	Sympodial length at 50% plant height	Number of Reproductive points per plant	2.5% span length	Uniformity ratio (%)	Micronaire (µg/inch)	Fibre strength (g/t)
GSB 40x RAB 8	57.73	20.34	0.01	-0.01	-1.16**	0.31	-20.02	3.97	0.70	-1.22	-0.51	-0.39	-0.58	0.23	-0.60
GSB 40x RHCB 011	442.93**	159.94**	0.43	0.08	-0.45**	-0.41	23.07*	3.47	0.12	1.97	0.54	-0.83	0.51	0.03	-0.03
GSB 40x TCB 37	95.78	32.14*	-0.28	1.68**	0.65**	-0.40	-10.92	-0.52	0.14	0.21	-0.22	0.62	-0.28	-0.30	0.83
GSB 40x DB 16	322.28**	113.99**	0.08	0.25	0.11	-0.60	8.72	-0.62	0.01	0.01	-1.21	-1.60	0.61	-0.34	-0.22
GSB 40x GSB 21	118.63*	33.19*	0.36	0.97	-0.03	0.01	-5.27	-1.62	0.26	-0.65	0.91	-0.94	-0.68	-0.03	-1.50
GSB 40x DB 39	-131.66*	-42.69**	-0.24	0.61	-0.67**	-0.32	-4.17	2.37	-0.06	2.24*	-0.02	-0.13	0.91	-0.08	-0.13
GSB 40 x CCB 30	262.28**	91.79**	0.28	0.78	0.22	-0.27	3.97	3.77	0.18	11.59**	-1.07	-1.15	0.26	-0.01	-0.18
RAB 8x RHCB 011	-228.36**	-87.74**	-0.24	-1.12	0.54**	-0.27	3.97	-3.22	-0.59	-0.31	-1.24	1.25	0.46	-0.25	0.59
RAB 8x TCB 37	-258.16**	-88.42**	-0.22	-0.76	0.18	0.14	8.07	-1.72	0.01	-7.67**	-1.08	1.11	0.06	-0.05	0.90
RAB 8x DB 16	161.18**	72.12**	-0.36	1.38*	-0.73**	0.25	-9.27	-2.82	0.29	-2.23	-0.24	-0.99	-0.33	0.01	-0.33
RAB 8x GSB 21	-64.21	-32.24*	-0.23	-0.52	0.27	0.16	-34.77**	-5.87	0.11	-2.36*	-0.81	-0.07	0.76	0.18	1.13
RAB 8x DB 39	-168.36**	-61.10**	-0.49	-0.72	-0.11	-0.28	18.22	2.12	-0.97**	4.98**	0.11	1.73	-1.03	0.19	-0.73
RAB 8x CCB 30	-3.16	-17.94	0.35	-0.68	-1.68**	-0.26	-4.17	-1.87	0.44	-1.23	0.27	-0.20	-0.93	-0.01	-0.42
RHCB 011x TCB 37	16.18	-0.89	-0.16	0.30	-0.23	-0.05	20.47	1.52	-0.28	3.71**	0.71	-0.01	2.66**	-0.23	1.73*
CD (Sij-Sik) at 5%	107.97	31.91	0.55	1.29	0.34	0.73	22.30	6.92	0.87	2.38	2.21	3.13	1.72	0.50	1.84
CD (Sij-Skm) at 5%	101.79	30.09	0.52	1.22	0.32	0.69	21.03	6.52	0.82	2.24	2.08	2.95	1.62	0.47	1.73
RHCB 011 x DB 16	-112.81*	-36.62*	0.15	0.66	0.39*	0.07	2.72	-1.07	-0.49	-0.01	-0.24	1.43	-0.68	-0.20	0.38
RHCB 011 x GSB 21	-155.51**	-59.80**	-0.04	-1.90**	0.69**	-0.26	-3.17	-1.12	0.07	-0.67	-0.08	0.33	0.11	-0.13	0.36
RHCB 011 x DB 39	-99.16	-29.60	0.09	0.51	0.44**	-0.01	22.32*	-2.12	-0.20	-4.43**	0.84	0.09	-0.18	-0.07	-0.16
RHCB 011 x CCB 30	23.53	12.50	-0.36	-1.33*	0.04	0.35	-18.57	-1.62	0.40	4.16**	0.20	0.01	0.41	0.17	-0.04
TCB 37 x DB 16	-71.61	-29.94	-0.31	-1.30*	-1.10**	-0.38	18.57	5.77	-0.31	6.20**	1.44	0.68	-0.48	-0.15	0.91
TCB 37 x GSB 21	-31.11	-26.67	0.07	-0.94	-0.15	0.09	-6.17	2.67	0.46	2.08	0.38	-2.96*	0.66	0.47	-1.29
TCB 37 x DB 39	-30.61	-2.19	0.28	-0.92	0.49**	0.13	-3.92	-0.47	-0.20	-4.87**	-1.75	0.96	-1.33	-0.02	-0.37
TCB 37 x CCB 30	-12.31	-23.82	0.13	0.62	1.31**	0.13	-37.77**	-1.57	-0.20	0.39	-0.33	2.22	-1.08	0.19	0.10
DB 16 x GSB 21	-185.46**	-59.33**	-0.30	0.32	0.14	0.09	2.728	-1.57	-0.29	4.78**	1.09	-1.41	0.11	-0.24	0.53
DB 16 x DB 39	-5.26	-16.02	-0.06	-0.18	0.03	-0.33	-21.67*	-3.07	0.82*	-9.47**	0.05	-0.15	-1.28	-0.04	-0.70
DB 16 x CCB 30	-62.41	-12.47	0.01	0.17	0.45**	0.22	2.97	-0.17	-0.10	-0.83	-0.60	-1.31	0.31	0.17	-0.19
GSB 21 x DB 39	79.58	44.79**	0.40	1.15	-0.64**	-0.30	7.72	4.22	0.38	-2.35*	1.33	-0.81	0.96	-0.04	0.80
GSB 21 x CCB 30	328.58**	147.27**	0.28	0.98	0.01	0.18	10.47	4.07	0.35	0.69	0.69	0.41	-0.03	0.01	-0.32
DB 39 x CCB 30	-39.71	-22.77	-0.25	0.59	0.30	-0.14	9.57	0.32	-0.32	3.48**	-0.97	1.11	-0.18	-0.12	0.19
CD (Sij-Sik) at 5%	107.97	31.91	0.55	1.29	0.34	0.73	22.30	6.92	0.87	2.38	2.21	3.13	1.72	0.50	1.84
CD (Sij-Skm) at 5%	101.79	30.09	0.52	1.22	0.32	0.69	21.03	6.52	0.82	2.24	2.08	2.95	1.62	0.47	1.73

*, ** Significant at 5% and 1% levels, respectively

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