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Combining ability studies in cotton (*Gossypium hirsutum* L.) for yield and fibre quality parameters

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Abstract

Combining ability is mostly used by breeders to identify and select appropriate parental genotypes to produce the larger progeny of new combinations through their hybridization. The objective of this research was to estimate general combining ability of parents and specific combining abilities of F_1 hybrids, to identify suitable parents and hybrids for yield and its contributing traits, fibre quality parameters. Nine genotypes and 20 F_1 hybrids derived by crossing the parental genotypes in $L \times T$ design were sown in randomized complete block design. The ratio of $\sigma^2 GCA/\sigma^2 SCA$ was smaller than zero for all the characters indicating predominance of non-additive gene action (dominant or epistasis) in the inheritance of investigated traits except lint index. The line $\times$ tester interactions made greater contribution to the total variance for most of the traits i.e. boll number per plant, boll weight, lint index, lint yield, micronaire, elongation per cent and seed cotton yield. From this study, it is evident that the genotypes TCH 1716 and L 765 were found to be the potential combiners for yield and most of the fibre quality parameters as well. Further, the cross combination GSHV 179 $\times$ L 765 was found to be the best for commercial exploitation.

Keywords: cotton, Combining ability, yield contributing and quality traits

Introduction

Selection of superior parents with good combining ability for most of the yield contributing and quality parameters is the prime objective of any crop improvement programmes. Hence, identification of parents based on their combining ability is an important step to proceed further for hybridization and selection of superior segregants or to identify good hybrids for commercial exploitation. Line $\times$ Tester design of crossing the genotypes is one of the tools which facilitates the plant breeder to identify superior genotypes and promising recombinants produced through estimation of General Combining Ability (GCA) and Specific Combining Ability (SCA). To choose appropriate parents and hybrids based on their combining ability estimates, the Line $\times$ Tester method has been widely used by plant breeders in both self and cross pollinated crops (Konak *et al.*, 1999; Mert *et al.*, 2003; Basbag *et al.*, 2007; Ahuja & Dhayal, 2007; Basal *et al.*, 2009) [20, 24, 7, 2, 19]. Sprague and Tatum (1942) [26] used the term GCA to designate the average performance of a genotype in hybrid combinations and used the term SCA to define those cases in which, combinations do relatively better or worse than the expected on the basis of average performance of the genotypes involved.

In combining ability, the genetic variability of each trait can be partitioned into GCA and SCA (Sprague and Tatum 1942) [26]. GCA effects explain about the additive type of gene action, whereas, SCA effects estimate the non-additive (Dominant or epistasis) gene action. Importance of non-additive gene action is observed for different yield contributing traits. However, appreciable degree of variance due to GCA was observed for morphological and yield traits (Khan, 2010) [15]. 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) [8]. Hence, the present study was conducted to analyse nine genotypes (4 Lines & 5 Testers) of cotton (*G. hirsutum* L.) and their 20 F_1 s crossed in $L \times T$ manner to ascertain their relative performance regarding their genetic potential through combining ability effects and variances of cotton yield with yield contributing & fibre quality parameters as well.

Material and Methods

The present study of estimation of combining ability of *G. hirsutum* L. genotypes and F₁ hybrids of cotton was carried out at RARS, Lam, Guntur, ANGRAU during 2017-18 and 2018-19. Out of nine genotypes chosen for the study, four were designated as lines (Females) and five as testers (Males) and 20 F₁s were derived by crossing them in L x T design. The nine parents and 20 hybrids were sown in four rows measuring six meters in a RCB design with two replications. The row and plant spacings adapted were 105 and 60 cm, respectively. Recommended cultural practices were carried out and the crop was grown under uniform field condition to minimize environmental variations to the maximum possible extent. Data were recorded from 10 plants /entry / replication for the traits viz., Seed cotton yield (kg/ha) (SCY), lint yield (kg/ha), number of bolls per plant, boll weight (g), ginning out turn (%) (GOT), seed index (g), lint index (g), plant height (cm) (PH), number of monopodia per plant, number of sympodia per plant, days to 50 per cent flowering (DFF), upper half mean length(mm) (UHML), mean length (mm) (ML), fibre uniformity index (%) (UI), micronaire value (g/inch) and fibre strength (g/tex). Forty well developed open bolls were randomly hand harvested from each row of parents and F₁'s. The bulked bolls from each genotype were ginned. The seed cotton weight per boll (SCW/B) and lint per cent (LP) were obtained from each boll sample. A high volume instrument (HVI) was used to measure fibre length (UHML), fibre strength (Str.), fibre uniformity (UI), micronaire (Mic.) and fibre elongation (%). All the recorded data were subjected to analysis of variance (ANOVA) technique for a RCB design as outlined by Steel & Torrie (1980) through Mstatc computer programme for all the traits to test the null hypothesis of no differences among the cotton genotypes. The genotypes means for each parameter were further separated and compared by using the least significant difference (LSD) test at 5% level of probability. The GCA and SCA variance effects of parents and F₁ hybrids, respectively were estimated by using line x tester analysis method as described by Kempthorne (1957) [14].

Results and discussion

Significant differences were detected among parents and F₁ hybrids for yield & yield components and fibre quality traits indicating the presence of sufficient genetic variability among them (Table 1). The data showed that the parents as well as crosses didn't follow the same pattern for investigated traits. The ratio of σ^2 GCA/ σ^2 SCA was smaller than zero for all the characters indicating predominance of non-additive gene action (dominant or epistasis) in the inheritance of investigated traits except lint index. However, Karademir and Gençer (2010) [13] reported that GCA effects were higher than SCA effects for the ginning percentage, fiber length, fiber fineness and fiber elongation. They also found that the mean squares of the SCA were highly significant for seed cotton yield, fibre strength and fibre uniformity. The contrasting study of Ashokkumar (2010) indicated that GCA variances were lower than SCA variances for all the characters studied (Seed cotton yield, plant traits, fibre quality), as indicated by their lower ratios indicating predominance of non-additive gene action (Dominant or epistasis). The differences in the findings might have resulted due to different breeding material tested under each particular environmental condition. Several studies have been conducted to estimate the gene action for yield and yield contributing traits and fibre quality parameters. However, inconsistent results were reported

including non-additive (Shakeel *et al.*, 2001; Ahuja & Dhayal, 2007; Khan *et al.*, 2009) [25, 2, 19], additive as well as non-additive (Kumaresan *et al.*, 1999; Basal & Turgut, 2005; Basal *et al.*, 2009) [21, 5, 6] and additive gene action (Chinchane *et al.*, 2002; Khan *et al.*, 2005; Aguiar *et al.*, 2007; Lukonge *et al.*, 2007) [9, 17, 1] for the yield components and fibre quality traits. Contradictions may be due to different genetic backgrounds of cultivars used and environmental conditions under which the studies were conducted.

The proportional contributions of lines and testers and their interactions (Line x Tester) to the total variance were varied among the investigated characters (Table 1). Results revealed that line x tester interactions made greater contribution to the total variance for most of the yield contributing and fibre quality traits viz., boll number per plant, boll weight, lint index, lint yield, micronaire fibre elongation per cent and seed cotton yield. Proportional contribution of lines to total variance was very low for all the traits except days to 50 per cent flowering, while testers also followed similar pattern and contributed a minimum to the total variance. However, maximum variance was extended by line x tester interaction for all the traits studied except seed index, ginning per cent and upper half mean length.

Significant GCA effects were detected for yield components and seed cotton yield and fibre quality parameters (Table 2). Out of four lines the entry, TCH1716 exhibited significant positive GCA for most of the tested traits viz., seed cotton yield, plant height, number of monopods, number of sympodia, number of bolls per plant, boll weight, seed index, upper half mean length and mean length and found to be the best combiner among the genotypes used for the study. However, the general combining ability in negative direction for the traits GOT and micronaire values indicated its inability of this genotype to contribute for further improvement in the breeding programmes. Similarly, GSHV 179 expressed significant GCA in negative direction for number of monopods and showed significant positive GCA for days to 50 per cent flowering. It showed negative GCA for most of the yield and quality traits viz., number of sympodia, number of bolls per plant, boll weight, lint index, seed index and GOT. While BGDS 1033 recorded significant negative GCA for days to 50 per cent flowering, number of sympodia and boll weight. Similarly, the line F2453 exhibited significant negative GCA for most of the traits tested viz., seed cotton yield, lint yield, UHML, ML and fibre strength indicating the lesser chances of further improvement of these traits by using these parents.

Among the testers, the entry L765 was found to be potential general combiner for number of monopods, number of sympodia, number of bolls per plant and boll weight. However, GISV 164 found to be good combiner for micronaire value. Hence, it can be concluded that among the parents, TCH 1716 and GSHV 179 were found to be the good source of favourable genes for improving the seed cotton yield besides quality parameters like micronaire value, UHML, mean fibre length and BGDS 1033 & L766 for micronaire value & F 2453 for mean fibre length improvement.

Further, the general combiners among lines and testers exhibited better mean performance as reflected by positive association between them indicating that the parent may be selected either on the basis of GCA or mean performance or in combination. The positive GCA effects indicated the scope for further improvement of yield and fibre quality traits by utilizing these parents. Similar conclusions were also made by

Tang *et al.*, (1993) ^[27], Meredith & Brown (1998) ^[23] and Ahuja and Dhayal (2007) ^[2]. These findings were inconsistent with some previous studies of Khan *et al.*, (1991) ^[16], Coyle & Smith (1997) ^[10], Shakeel *et al.*, (2001) ^[25], Basal & Turgut (2003) ^[4]. However, Khan *et al.*, (2007) ^[18] and Basal *et al.*, (2009) ^[6] reported that higher GCA of parents does not necessarily confer higher SCA, thus GCA and SCA were independent.

Specific combining ability effects represent the deviation of hybrid performance from the estimated GCA effects for each parent. The GCA effects of parents did not confer high and significant SCA effects for hybrids. 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. Out of 20 hybrids evaluated, the hybrid combination GSHV 179 x L 765 was found to be the

best cross combination as it exhibited the significant positive SCA for plant height, number of sympodia, number of bolls per plant, lint index, seed cotton yield per hectare. However, the other potential cross combinations identified were BGDS 1033 x L 765 for boll weight, GSHV 179 x L 766 and BGDS 1033 x HYPS 152 for mean length of the fibre and F2453 x GISV 164 for boll weight. Results also revealed that good SCA effects didn't necessarily indicate superior trait performance. Kadams *et al.* (1999) ^[12] 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 at all, there are inconsistencies in SCA effects, it must be 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) ^[11].

Table 1: Analysis of variance (mean squares) for combining ability for yield, yield components and quality parameters in cotton

Source of variation	DF	DF	PH(cm)	No. of monopods	No. of Sympodia	No. of Bolls/Plant	Boll wt (g)	Lint Index(g)	Seed index(g)	GOT (%)	SCY (Kg/ha)	Lint yield (Kg/ha)	UHML (mm)	ML(mm)	UI (%)	Mic (ug/inch)	Bundle strength (g tex)	E (%)
Replications	1	0.27	177.25	0.12	2.16	0.01	0.62*	0.3	0.58	8.55	4027.3	7473.2	10.09	20.52**	11963.6**	0.00017	18.77*	7.96**
Treatments	2.8	9.59**	779.66**	0.51**	7.04**	135.73**	0.36**	0.87**	1.43	10.22*	226740.9**	40968.2**	8.83**	8.91**	912.95	0.206**	7.2*	0.32
Parents	8	7.37**	153.68	0.59**	6.66	54.05	0.23*	0.92**	0.41	12.33*	150653.2*	33041.9*	12.99**	13.5**	2.12	0.278**	6.17	0.13
Parents vs Crosses	1	13.04*	2568.37**	0.06	1.12	188.73*	1.98**	1.02	1.12	37.56**	1100797**	254300.1**	11.88*	20.22**	25511.72**	0.42**	3.93*	0.98
Crosses	19	10.34**	949.09**	0.5**	9.78**	167.34**	0.32**	0.84**	1.87	7.89	212774.9**	33077.6**	6.92**	6.39**	1.78	0.16**	7.8	0.36
Lines	3	27.75*	1044.9	0.44	14.13	213.77	0.57	0.19	3.64	12.37	455755.3	28916.4	11.46	9.99	1.73	0.21	11.42	0.53
Testers	4	8.27	1017.64	0.488	13.3	275.3	0.37	0.73	0.57	13.22	132348.5	3769.57	8.42	7.7	1.75	0.28	14.56	0.43
Lines x Testers	12	6.67**	902.27**	0.527**	7.51**	119.74**	0.24**	1.04**	1.86**	5	178838.6*	32580*	5.29	5.05**	1.81	0.11**	4.65	0.3
Error	28	1.88	251.4	0.056	1.75	35.21	0.1	0.27	0.82	4.16	63765.36	10931.2	2.57	1.16	944.56	0.03	3.66	0.83
Total	57	5.64	509.6	0.28	4.36	83.97	0.24	0.56	1.11	7.22	142775.5	25625.6	5.78	5.31	1122.35	0.119	5.67	0.71
σ2 GCA		1.79	86.65	0.045	1.329	23.25	0.041	0.057	0.143	0.959	25587.3	2485.8	0.8188	0.853	-104.75	0.0239	1.036	-0.038
σ2 SCA		2.39	325.4	0.235	2.881	42.26	0.070	0.021	0.520	0.419	57536.6	10824.3	1.359	1.942	-471.4	0.037	0.492	-0.264
σ2 GCA/σ2 SCA		0.749	0.266	0.1914	0.4619	0.552	0.5871	0.275	0.295	2.289	0.448	0.0079	0.6025	0.439	-0.2222	0.6128	0.0210	-0.1445

Table 2: General combining ability (GCA) effects of parents for yield and quality traits in cotton

Parents	DF	PH(cm)	No. of monopods	No. of Sympodia	No. of Bolls/Plant	Boll wt (g)	Lint Index(g)	Seed index(g)	GOT (%)	SCY (Kg/ha)	Lint yield (Kg/ha)	UHML (mm)	ML(mm)	UI (%)	Mic (ug/inch)	Bundle strength (g tex)	E (%)
Lines																	
TCH1716	-0.775	0.16*	13.525*	1.460**	6.918**	0.33**	0.108	0.863**	-1.545*	288.591**	67.102	1.165*	1.068**	0.5	-0.183**	1.115	0.315
GSHV 179	1.525**	-0.29**	2.185	0.320	-1.923	-0.12	0.068	-0.0498	0.755	-48.909	1.063	0.225	0.238	0.1	-0.053	0.385	-0.025
BGDS1033	-1.975***	-0.02	-8.945	-1.350**	-2.733	-0.22*	-0.203	-0.317	-0.075	-14.187	-3.685	0.035	0.037	-1	0.128*	-0.075	-0.045
F2453	1.225***	0.15	-6.765	-0.430	-2.263	0.01	0.028	-0.048	0.865	-225.496*	-64.479	-1.425*	-1.343***	-0.5	0.107	-1.425	-0.245
Testers																	
L765	0.275	-0.075	12.568*	2.020**	7.305**	0.325*	0.183	-0.475	1.005	140.623	76.017	0.12	0.15		0.038	0.09	0.035
GJHV516	0.275	0.325**	-3.545	-1.530**	-3.445	-0.225	0.092	0.15	-0.12	-199.007*	-76.138	0.007	-0.037		-0.125	0.965	0.235
GISV164	-1.1*	-0.188*	-16.933**	-0.243	-2.608	-0.113	-0.168	0.075	-0.12	6.698	-1.301	-1.68**	-1.613	-0.75	0.275**	-2.135	-0.365
L766	-0.725	0.188*	7.142	0.145	5.068*	0.1	0.420*	0.125	1.243	77.877	60.991	1.07	0.975	0.50	0.038	1.315	0.16
HYPS152	1.525**	-0.25**	0.767	-0.393	-6.32**	-0.088	-0.343	0.125	-2.008	-26.192	-59.57	0.483	0.525	0.25	-0.225**	-0.235	-0.065

Table 3: Specific combining ability (SCA) effects of hybrids for yield and quality traits in cotton

Cross Combinations	DF	PH(cm)	No. of monopods	No. of Sympodia	No. of Bolls/Plant	Boll wt (g)	Lint Index(g)	Seed index(g)	GOT (%)	SCY (Kg/ha)	Lint yield (Kg/ha)	UHML (mm)	ML(mm)	UI (%)	Mic (ug/inch)	Bundle strength (g tex)	E (%)
TCH1716 × L 765	1.525	19.663	-0.435*	1.09	-1.305	-0.105	-0.783*	-1.275	1.545	43.109	56.489	-0.24	-0.33	0.001	-0.118	-2.49	-0.715
TCH1716 × GJHV 516	-0.725	-15.875	-0.185	-2.66*	-2.405	-0.205	-0.258	-0.75	0.77	-75.201	-8.43	1.473	1.408	1.000	-0.255	-0.065	0.185
TCH1716 × GISV 164	0.900	-27.688*	0.178	-0.748	-4.493	-0.067	-0.283	0.675	-2.87	-87.451	-107.462	-0.19	-0.068	-0.250	-0.055	1.585	0.185
TCH1716 × L 766	0.525	24.038*	0.503**	1.865	12.083**	0.470	0.630	0.575	1.757	264.98	148.686	-0.99	-0.955	-0.500	0.183	-0.265	0.06
TCH1716 × HYPS 152	-2.225*	-0.138	-0.06	0.453	-3.88	-0.092	0.693	0.775	-1.293	-145.436	-89.283	-0.053	-0.055	-0.250	0.245	1.235	0.285
GSHV179 × L 765	-1.775	27.203*	-0.435*	3.33**	13.085**	0.345	0.958*	0.285	-0.955	490.524*	162.404*	0.800	0.700	0.400	0.052	1.190	0.525
GSHV179 × GJHV 516	0.475	1.965	0.215	0.48	3.685	-0.105	0.133	0.060	1.220	-65.476	2.719	-0.638	-0.513	-0.60	0.015	-0.035	0.025
GSHV179 × GISV 164	0.400	3.003	0.078	-0.458	-0.752	0.333	0.407	0.385	1.42	229.219	123.117	1.750	1.663*	1.150	-0.385*	0.215	-0.075
GSHV179 × L 766	0.225	-24.323*	0.003	-1.395	-7.428	-0.28	-0.33	0.535	-1.042	-575.1**	-245.025**	-0.6	-0.525	-0.100	0.152	-0.135	0.100
GSHV179 × HYPS 152	1.475	-7.848	0.14	-1.958	-8.59	-0.293	-1.168**	-1.265	-0.642	-79.166	-43.214	-1.312	-1.325	-0.850	0.165	-1.235	-0.575
BGDS 1033 × L 765	0.225	-9.517	0.095	-1.700	-3.755	0.195	-0.073	0.855	-0.825	-77.333	-49.608	-2.36	-2.3**	-1.400	0.027	-1.15	-0.255
BGDS 1033 × GJHV 516	0.475	2.095	-0.405*	1.350	1.495	-0.255	-0.698	-0.52	-1.8	43.057	-25.244	1.153	1.138	0.600	0.135	0.825	0.145
BGDS 1033 × GISV 164	1.600	8.382	-0.293	0.262	-0.843	-0.068	0.378	0.355	0.9	-120.983	-20.485	-1.56	-1.488	-0.650	0.185	-1.575	-0.155
BGDS 1033 × L 766	0.225	-1.842	0.533**	-0.625	-2.768	-0.180	0.240	-0.745	0.438	61.808	31.438	0.74	0.725	0.100	-0.127	0.675	0.020
BGDS 1033 × HYPS 152	-2.525*	0.883	0.07	0.713	5.870	0.308	0.153	0.055	1.288	93.452	63.899	2.028	1.925*	1.350	-0.165	1.225	0.245
F 2453 × L 765	0.025	-37.348**	0.775***	-2.720**	-80.250	-0.435	-0.102	0.135	0.235	-456.299*	-169.285*	1.8	1.93*	1.00	0.093	2.450	0.445
F 2453 × GJHV 516	-0.225	11.815	0.375	0.83	-2.775	0.565*	0.822*	1.21	-0.19	97.621	30.956	-1.988	-2.033*	-1.00	0.105	-0.725	-0.355
F 2453 × GISV 164	2.1*	16.303	0.037	0.943	6.088	-0.198	-0.502	-1.415*	0.46	-20.784	4.829	0	-0.108	-0.25	0.255	-0.225	0.045
F 2453 × L 766	-0.975	2.128	-1.038***	0.155	-1.888	-0.01	-0.54	-0.365	-1.153	248.312	64.902	0.85	0.755	0.50	-0.208	-0.275	-0.18
F 2453 × HYPS 152	3.275**	7.102	-0.15	0.792	6.60	0.077	0.323	0.435	0.647	131.151	68.598	-0.663	-0.545	-0.25	-0.245	-1.225	0.045
CD 95% SCA	2.031	23.467	0.35	1.962	8.783	0.481	0.767	1.343	3.02	373.723	154.737	2.376	1.6	45.486	0.282	2.835	1.35

Conclusion

From this study, it is evident that the genotypes TCH1716 and L 765 were found to be the potential combiners for yield and most of the fibre quality parameters as well. Further, the cross combination GSHV 179 x L 765 was found to be the best for commercial exploitation.

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