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Analysis of Heterosis and Combining Ability for Yield and Yield Contributing traits in Medium Maturity Hybrids of Maize (*Zea mays* L.)

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A B S T R A C T

The present investigation was under taken with a view to estimate the extent of heterosis, *per se* performance, combining ability. The hybrids were attempted by adopting line x tester mating design among 15 inbred lines and 3 testers in maize (*Zea mays* L.) during *Rabi* 2015. These were evaluated during *Kharif* 2016 and *Rabi* 2016-17 in three environments in randomized block design with three replications. Data were recorded for fifteen traits. Analysis of variance revealed that mean squares due to genotypes x environments and its components *viz.,* parents x environments, crosses x environments and parents v/s crosses x environments were significant for majority of the characters. This indicated the presence of considerable amount of variability in the present set of genotypes. An overall *per se* performance indicated that parental line L_{10} exhibited maximum mean for grain yield per plant (88.20g) along with maximum mean for harvest index (39.32%) and minimum mean value for days to 75 per cent brown husk (104.56 days). The hybrid L_2 x T_1 exhibited maximum mean value for grain yield per plant (163.13 g/plant) and exhibited maximum estimate of significant economic heterosis in E_1 (36.12%), E_2 (12.47%), E_3 (34.58%) and on pooled basis (28.29%) indicating dominance of genes for higher grain yield per plant. This hybrid also showed significant estimate of economic heterosis for grain protein content in E_1 (6.40 %), E_2 (3.95 %) and over the environment (4.41 %). Out of 45 hybrids five best hybrids which exhibited positive significant sca effects for grain yield per plant are *viz.*, L_2 x T_1 , L_7 x T_2, L_{10} x T_3, L_1 x T_3 and L_9 x T_1. Hybrid L_2 x T_1 also exhibited higher magnitude of economic heterosis with higher mean performance. These hybrids L_2 x T_1, L_7 x T_2, L_{10} x T3, L_1 x T_3, and L_9 x T_1 were crosses between poor x good gca effects of parent for grain yield per plant.

Introduction

In India, maize is the third important food crop after rice and wheat. According to latest data (2015-16), it is being cultivated on 8.69 m ha with 80%area during kharif season. The current maize production is 21.7 mt, with an average productivity of 2.5 t/ha. Despite maize being predominantly rainfed crop its productivity is more than rice which is mainly grown under assured irrigated/rainfed conditions. Maize contributes nearly 9% in the national food basket and more than 400 billion to the agricultural GDP at current

prices. In addition it generates employment to over 1000 million man days at the farm and downstream agricultural and industrial sectors. Maize is primarily used for feed (60%) followed by human food (24%), industrial (starch) products (14%) and bevarages and seed (1 % each). Thus, maize has attained an important position as industrial crop because 75% of its produce is used in starch and feed industries. In India, maize is predominantly cultivated as rainfed crop but due to focused research on single cross hybrids (SCH) since 2006, the productivity of maize has increased @ 134 kg/ha/annum. The adoption of SCH technology in India is around 60%, with this adoption of technology it has registered a growth rate of more than 7% in production and 6% in productivity in last five years. Study of combining ability is important for selecting parents for hybridization. Sprague and Tatum (1942), first time proposed the concepts of general combining ability (gca) and specific combining ability (sca). According to them, GCA variance is due to additive variance and SCA variance is due to non-additive variance, both act as an important diagnostic tool in selection of suitable parents and cross combination. Among the various design used for combining ability analysis, Line x Tester analysis (Kempthorne, 1957) has been extensively used to assess the combining ability of parents and crosses for different quantitative characters as well as to study the extent of heterosis for yield, yield contributing characters in maize.

Materials and Methods

The experimental was conducted in three locations *viz.,* Instructional Farm during *Kharif* 2016 and *Rabi* 2016-17, Rajasthan College of Agriculture, Udaipur (Rajasthan) and Agriculture Research Sub Station, Vallabhnagar, Udaipur and the pooled analysis result data are given below the materials consisted of 45 hybrids obtained by crossing of 15 lines *viz.,* EI-2303, EI -2308, EI-2315, EI-2317, EI-2325, EI-2414, EI-2431, EI-2440, EI-2446, EI-2508, EI-2516, EI-2517, EI-2546, EI-2547 and 3 testers EI-586-3-1, EI-BML-6, EI-670-2. The hybrids and parents were evaluated in randomized block design with three replications in four meter row with spacing of 60 x 25 cm. All the recommended agronomical practices and plant protection measures were followed as and when required to raise a good crop of maize. Five plants in parents and hybrids were randomly selected in each replication and observations were recorded for days to 50% tasseling, days to 50% silking, Anthesis-Siliking interval, 75 per cent brown husk, plant height (cm), ear height (cm), cob length (cm), number of grain rows per cob, cob girth (cm), 100 grain weight (gm), harvest index(%), grain yield per plant (gm), Grain Protein content (%),Grain starch content (%) and Grain oil content (%). The mean values were subjected to line x tester analysis as suggested by Kempthorne (1957).

Results and Discussion

The analysis of variance for experimental design (Table 2 to 3) revealed that the presence of significant amount of variability for parents in individual environment as well as pooled over the environments for all the characters except days to 50 per cent silking in E_3, days to 75 per cent brown husk in E_2 and E_3, plant height in E_3, cob length in E_2, cob girth in E_3, 100-grain weight in E_1. This suggested that the parental lines selected were quite variable for most of characters under study. The mean squares due crosses were significant in individual environment and over the environments for all the characters. This results suggested that the presence of considerable amount of variability among the hybrids.

Mean squares due parents' v/s crosses were significant for all the characters in all three environments as well as pooled over the environment except days to 50 per cent silking in E_3, anthesis silking interval in E_1, days to 75 per cent brown husk in E_1 & E_3, plant height were non-significant. This indicated the existence of applicable amount of a genetic variability in the experimental material of present.

Under pooled analysis of variance mean squares due to genotypes x environments, were significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, ear height were non-significant, mean squares due to parents x environments were significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, plant height, ear height, cob length, cob girth, 100-grain weight, harvest index, mean squares due to crosses x environments were significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, ear height, number of grain rows per ear were non-significant and mean squares due to parents v/s crosses x environments were significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, plant height, ear height, cob girth, 100-grain weight were non-significant.

Similar trends for variances and its components in maize were reported by Dubey *et al.*, (2001), Joshi *et al.*, (2002), Firoz *et al.*, (2007), Lal *et al.*, (2007), Dubey *et al.*, (2009), Sharief *et al.*, (2009), Sumalini and Shobha Rani (2010), Premlatha *et al.*(2011), Yousif and Sedeeq (2011), Abuali *et al.*, (2012), Lal and Kumar (2012), Anusheela *et al.*(2013), Abrha *et al.*, (2013), Singh *et al.*(2013), Motamedi *et al.*(2014), Rajesh *et al.*, (2014), Rastgari *et al.*, (2014) and Ruswandi (2015) for grain yield, quality traits and brown husk traits.

Combining ability referred as ability of a parent to transmit its performance to its off-springs. As combining ability often depend upon complex interaction systems among genes, certain combination nick well produce superior off-springs, whereas other involving equally promising parent produce disappointing progeny.

Sprague and Tatum (1942) produced the concept of general and specific combining ability as measure of gene action through their investigation in corn. They defined the term general combining ability (gca) as average performance of a line set of hybrids, which can be recognized as measure of additive gene action including additive x additive interactions.

The specific combining ability (sca) refers those instances when certain cross combinations do relatively better or worse than would be expected on the basis of average performance of parental lines involved. This is controlled by non-additive genetic variance including dominance and epistatic interactions.

With advancement of biometrical genetics, several method have been developed to assess the general and specific combining ability of different genetic material, *viz.*, top cross technique which was proposed by Jenkins and Brunson (1932) or Davis (1927), polly cross by Tysdal *et al.*, (1942), diallel cross by Griffing (1956) and Hayman (1954), line x tester mating design by Kempthorne (1957), partial diallel cross by Kempthorne and Curnow (1961), triallel cross by Rawlings and Cocherham (1962) and modified line x tester by Murty *et al.*, (1967).

Table.1 Pooled analysis of variance for different characters in maize

SN	Source	df	Days to 50% tasseling	Days to 50% silking	Antheis - silking interval	Days to 75 % brown husk	Plant height (cm)	Ear height (cm)	Cob Length (cm)	Number of Grain rows/ear
1.	Environment	2	238682.27**	262597.05**	572.84**	360045.40**	10826.19**	57.03	258.70**	106.90**
2.	Rep./Env	6	166.05**	155.75**	0.40**	873.41**	181.41	28.09	2.64*	14.98**
3.	Genotype	66	93.28**	88.78**	2.08**	66.22**	1051.11**++	937.70**	11.81**++	21.32**++
	Check	3	58.69**	51.44**	0.92**	1.44**	137.68**	961.30**	5.22**	2.58**
	P vs Chk	1	0.34**	1.98**	0.67*	2.22**	1869.53**	4541.81**	36.67**	191.28**
	Parent	17	56.72**	44.04**	3.72**	25.68**	494.90**	456.58**	6.50**	7.14**++
	Tester	2	23.59**	16.33**	4.15**	27.11**	229.85**	100.04**	3.08**	3.52**
	Line	14	65.17**	50.92**	3.92**	27.01**	564.71**	418.38**	7.45**	6.18**
	T v/s L	1	4.59**	3.21**	0.12	4.30**	47.78**	1704.48**	0.00**	27.83**
	P v/s C	1	117.15**	91.17**	1.63**	58.72**	27.32**	1328.93**	88.90**	748.48**+
	Cross	44	111.05**	110.46**	1.54**	87.94**	1322.26**++	1057.51**	12.65**++	11.62**
	Tester	2	663.12**	665.56**	1.22**	433.01**	6219.03**	10606.27**	18.42**	18.20**+
	Line	14	122.98**	109.55**	1.55**	88.39**	709.22**	590.10**	13.73**++	14.02**
	L x T	28	65.65**	71.27**	1.56**	63.07**	1279.01**++	609.15**	11.69**++	9.95**
4.	G x E	132	2.86	4.04	2.12**	7.03	293.46**	13.53	2.69**	1.39**
	Check x E	6	0.53	2.69	2.92**	4.55	100.90	3.32	2.34*	0.43
	Chk x P x E	2	1.55	3.34	0.49*	8.17	221.47	28.68	2.65	0.86
	P x E	34	0.87	2.49	2.54**	6.81	151.38	13.51	1.09	2.62**
	T x E	4	1.48	5.44	3.98**	6.56	23.90	22.81	0.95	0.57
	L x E	28	0.75	2.23	2.43**	6.90	176.24	12.17	1.17	3.09**
	T v/s L x E	2	1.30	0.23	1.15**	6.06	58.26	13.58	0.22	0.10
	P v/s C x E	2	5.07	5.58	3.98**	1.52	145.48	35.99	9.37**	3.31*
	Cross x E	88	3.73	4.74	1.90**	7.40	363.66**	12.64	3.20**	0.96
	T x E	4	7.33	9.64	4.07**	5.58	22.45	25.87	5.62**	2.18*
	L x E	28	3.86	3.71	1.18**	8.46	407.46**	9.04	3.30**	0.52
	L x T x E	56	3.41	4.90	2.10**	7.00	366.14**	13.49	2.97**	1.09
5.	Pooled Error	396	5.51	5.59	0.11	10.65	156.03	27.07	1.01	0.88
5.	Bartlet	2	69.85**	70.34**	118.09**	49.17**	3.46	9.20*	19.99**	10.78**

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.1 Continued…

SN	Source	df	Cob girth (cm)	100-grain weight (g):	Harvest index (%)	Grain Yield / Plant (g)	Grain protein content in (%)	Grain starch content in (%)	Grain Oil content in (%)
1.	Environment	2	4.94**	101.53**	206.40**	21883.04**	5.91**	49.18**	5.31**
2.	Rep./Env	6	3.33**	62.25**	21.80**	155.38*	0.14**	1.60**	0.06**
3.	Genotype	66	1.95**++	586.52**++	142.35**++	8718.03**++	3.85**++	68.97**++	1.22**++
	Check	3	0.02**	3.61**	5.44**	199.27**	0.64**+	35.58**++	0.55**++
	P vs Chk	1	10.28**	8260.37**	1329.45**	91059.46**+	18.56**+	3.27**	0.82**
	Parent	17	0.37**	31.04**	89.80**	869.90**++	4.36**++	115.91**++	1.53**++
	Tester	2	0.13**	9.79**	0.59**	1192.31**	1.51**	50.28**	2.26**++
	Line	14	0.41**+	33.62**	72.34**	775.98**++	5.07**++	116.04**++	1.47**++
	T v/s L	1	0.37**	37.36**	512.62**	1539.92**	0.15**	245.34**+	0.95**
	P v/s C	1	48.63**	31191.39**	6622.65**+	306628.71**+	81.65**+	129.51**+	0.57**
	Cross	44	1.66**++	139.26**++	26.61**	5485.67**++	2.17**++	53.16**++	1.18**++
	Tester	2	3.12**	626.07**	47.48**	10738.79**	0.22**	2.21**	0.74**
	Line	14	2.18**	187.51**++	24.67**	7104.46**++	3.53**++	45.37**++	1.69**++
	L x T	28	1.30**++	80.36**++	26.09**	4301.06**++	1.63**++	60.70**++	0.96**++
4.	G x E	132	0.14*	7.40*	19.06**	288.84**	0.12**	1.45**	0.04**
	Check x E	6	0.13	1.50	1.72	86.82	0.10**	1.04**	0.03**
	Chk x P x E	2	0.14	4.00	13.52	627.64**	0.45**	1.30**	0.01
	P x E	34	0.14	4.68	2.69	117.64**	0.08**	2.57**	0.04**
	T x E	4	0.01	0.44	3.39	53.19	0.01	10.41**	0.03**
	L x E	28	0.16*	4.89	2.44	113.08**	0.09**	0.86**	0.03**
	T v/s L x E	2	0.15	10.25	4.89	310.41**	0.04**	10.75**	0.25**
	P v/s C x E	2	0.15	3.48	67.53**	975.12**	2.24**	0.92*	0.59**
	Cross x E	88	0.14*	9.02**	25.87**	336.51**	0.09**	1.03**	0.03**
	T x E	4	0.23	9.70	43.28**	1699.76**	0.08**	0.61*	0.12**
	L x E	28	0.09	9.09*	25.09**	273.02**	0.09**	1.15**	0.02**
	L x T x E	56	0.15*	8.94**	25.02**	270.88**	0.09**	1.01**	0.02**
5.	Pooled Error	396	0.10	5.40	6.94	61.06	0.01	0.21	0.00
5.	Bartlet	2	7.89*	2.15	10.76**	3.70	1.88	25.00**	12.58**

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.2 GCA and SCA effects for days to 50 per cent tasseling and days to per cent silking

SN	Genotype	Days to 50 per cent tasseling				Days to 50 per cent silking			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	-1.62**	-1.80**	-2.44**	-1.96**	-1.72**	-1.73**	-2.21**	-1.89**
2	T_2	-0.47	-0.53	-0.36	-0.45	-0.36	-0.47	-0.85	-0.56*
3	T_3	2.09**	2.33**	2.80**	2.41**	2.08**	2.20**	3.06**	2.45**
4	L_1	-0.13	-0.78	1.47	0.19	-0.45	-0.67	1.06	-0.02
5	L_2	-0.24	0.00	-0.31	-0.19	-0.23	-0.11	-0.39	-0.24
6	L_3	1.53*	2.00**	2.69*	2.07**	0.99	2.00**	3.06**	2.02**
7	L_4	-2.58**	-3.33**	-2.09	-2.67**	-2.34**	-3.11**	-1.94	-2.46**
8	L_5	-2.58**	-2.44**	-4.87**	-3.30**	-2.56**	-2.33**	-4.61**	-3.17**
9	L_6	0.87	1.44*	1.02	1.11*	0.99	1.00	0.50	0.83
10	L_7	0.64	0.89	0.69	0.74	0.88	0.78	0.39	0.68
11	L_8	-0.13	-0.67	-0.53	-0.44	-0.12	-0.22	0.61	0.09
12	L_9	1.42*	1.44*	2.80*	1.89**	1.21*	1.89**	1.73	1.61**
13	L_{10}	-1.80**	-2.44**	-2.53*	-2.26**	-1.67**	-2.22**	-2.39*	-2.09**
14	L_{11}	0.42	1.22	1.36	1.00*	0.55	0.89	1.06	0.83
15	L_{12}	-3.69**	-4.00**	-4.64**	-4.11**	-3.23**	-3.89**	-4.72**	-3.95**
16	L_{13}	2.76**	3.22**	1.91	2.63**	2.55**	2.78**	1.50	2.28**
17	L_{14}	1.98**	2.44**	1.91	2.11**	2.10**	2.33**	2.50*	2.31**
18	L_{15}	1.53*	1.00	1.13	1.22**	1.33*	0.89	1.61	1.28**
19	L_1 x T_1	1.62	-1.09	-2.11	-0.53	2.16	-1.04	-3.68	-0.85
20	L_2 x T_1	0.40	0.80	2.00	1.07	-0.06	1.07	3.10	1.37
21	L_3 x T_1	2.62*	2.80*	3.33	2.92**	2.72*	2.29	2.65	2.55**
22	L_4 x T_1	1.07	2.47*	1.44	1.66	0.72	2.40	0.99	1.37
23	L_5 x T_1	1.40	0.91	-0.78	0.51	1.61	1.62	0.99	1.40
24	L_6 x T_1	-0.71	-0.64	-1.00	-0.79	-1.28	-0.04	-0.46	-0.60
25	L_7 x T_1	0.51	0.91	3.00	1.47	0.16	1.18	3.32	1.55
26	L_8 x T_1	0.62	-0.20	-0.44	-0.01	0.83	-0.49	0.10	0.15
27	L_9 x T_1	-3.27**	-2.64*	-2.44	-2.79**	-3.50**	-3.27**	-3.35	-3.37**
28	L_{10} x T_1	0.96	2.24	4.22	2.47**	1.39	2.18	3.76	2.44**
29	L_{11} x T_1	-0.27	-0.42	-0.67	-0.45	-0.84	0.40	-0.01	-0.15
30	L_{12} x T_1	1.18	2.13	1.33	1.55	1.27	1.84	1.10	1.40
31	L_{13} x T_1	-3.27**	-3.09*	-2.89	-3.08**	-3.50**	-2.49*	-2.46	-2.82**
32	L_{14} x T_1	-1.49	-1.31	-0.89	-1.23	-1.06	-2.04	-1.46	-1.52
33	L_{15} x T_1	-1.38	-2.87*	-4.11	-2.79**	-0.61	-3.60**	-4.57*	-2.93**
34	L_1 x T_2	-2.87*	-2.02	-2.20	-2.36*	-3.19**	-2.31	-1.37	-2.29*
35	L_2 x T_2	-3.42**	-4.47**	-5.09*	-4.33**	-3.41**	-4.20**	-6.26**	-4.62**
36	L_3 x T_2	-1.20	-1.13	-0.42	-0.92	-1.30	-0.98	-1.04	-1.11

37	L_4 x T_2	1.58	0.20	2.69	1.49	1.70	0.13	3.63	1.82
38	L_5 x T_2	1.24	1.64	1.47	1.45	0.59	1.69	1.63	1.30
39	L_6 x T_2	-0.87	-0.91	-0.42	-0.73	-0.64	-1.31	-1.15	-1.03
40	L_7 x T_2	-1.98	-2.36	-3.09	-2.47**	-1.86	-2.09	-4.04	-2.66**
41	L_8 x T_2	-3.20**	-3.47**	-3.87	-3.51**	-3.86**	-2.76*	-4.26	-3.62**
42	L_9 x T_2	4.58**	3.76**	4.80*	4.38**	5.14**	4.47**	4.63*	4.75**
43	L_{10} x T_2	-1.20	-0.02	-0.87	-0.70	-0.97	-0.09	-0.26	-0.44
44	L_{11} x T_2	1.91	2.31	2.91	2.38*	2.14	1.80	1.96	1.97*
45	L_{12} x T_2	0.69	0.20	0.58	0.49	1.59	0.24	1.74	1.19
46	L_{13} x T_2	3.24**	3.64**	1.69	2.86**	2.81*	2.24	2.85	2.63**
47	L_{14} x T_2	0.36	0.42	0.02	0.27	0.59	0.69	-0.81	0.15
48	L_{15} x T_2	1.13	2.20	1.80	1.71	0.70	2.47*	2.74	1.97*
49	L_1 x T_3	1.24	3.11*	4.31	2.89**	1.03	3.36**	5.05*	3.15**
50	L_2 x T_3	3.02*	3.67**	3.09	3.26**	3.47**	3.13*	3.16	3.26**
51	L_3 x T_3	-1.42	-1.67	-2.91	-2.00*	-1.41	-1.31	-1.61	-1.45
52	L_4 x T_3	-2.64*	-2.67*	-4.13	-3.15**	-2.41*	-2.53*	-4.61*	-3.19**
53	L_5 x T_3	-2.64*	-2.56*	-0.69	-1.96*	-2.19	-3.31**	-2.61	-2.71**
54	L_6 x T_3	1.58	1.56	1.42	1.52	1.92	1.36	1.61	1.63
55	L_7 x T_3	1.47	1.44	0.09	1.00	1.70	0.91	0.72	1.11
56	L_8 x T_3	2.58*	3.67**	4.31	3.52**	3.03*	3.24**	4.16	3.48**
57	L_9 x T_3	-1.31	-1.11	-2.36	-1.59	-1.64	-1.20	-1.28	-1.37
58	L_{10} x T_3	0.24	-2.22	-3.36	-1.78	-0.41	-2.09	-3.50	-2.00*
59	L_{11} x T_3	-1.64	-1.89	-2.24	-1.93*	-1.30	-2.20	-1.95	-1.82
60	L_{12} x T_3	-1.87	-2.33	-1.91	-2.04*	-2.86*	-2.09	-2.84	-2.60**
61	L_{13} x T_3	0.02	-0.56	1.20	0.22	0.70	0.24	-0.39	0.18
62	L_{14} x T_3	1.13	0.89	0.87	0.96	0.47	1.36	2.27	1.37
63	L_{15} x T_3	0.24	0.67	2.31	1.07	-0.08	1.13	1.83	0.96
	Standard error								
	Ti	0.29	0.31	0.55	0.23	0.30	0.31	0.56	0.23
	Lj	0.59	0.62	1.11	0.47	0.60	0.62	1.12	0.47
	Sij	1.18	1.24	2.22	0.93	1.19	1.24	2.23	0.94
	Ti-j	0.36	0.38	0.68	0.29	0.36	0.38	0.68	0.29
	Li-j	0.81	0.85	1.52	0.64	0.82	0.85	1.53	0.64
	Ti-Lj	0.63	0.66	1.18	0.50	0.63	0.66	1.18	0.50
	STi-Tj	1.44	1.52	2.71	1.14	1.46	1.52	2.73	1.15
	SiL-jL	1.61	1.70	3.03	1.28	1.63	1.70	3.06	1.29
	Sij-kl	1.65	1.74	3.11	1.31	1.67	1.74	3.13	1.32

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.3 GCA and SCA effects for Antheis - silking interval and Days to 75 per cent brown husk

SN	Genotype	Antheis-silking interval				Days to 75 per cent brown husk			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	-0.10**	0.07	0.24**	0.07*	-1.47**	-1.62**	-0.86	-1.32**
2	T_2	0.10**	0.07	-0.50**	-0.11**	-0.62	-0.62	-0.93	-0.72*
3	T_3	-0.01	-0.13**	0.26**	0.04	2.09**	2.24**	1.79*	2.04**
4	L_1	-0.32**	0.11	-0.41*	-0.20**	0.36	0.31	2.67	1.11
5	L_2	0.01	-0.11	-0.07	-0.06	0.02	0.42	0.34	0.26
6	L_3	-0.54**	0.00	0.37*	-0.06	0.80	-1.69	2.34	0.48
7	L_4	0.24**	0.22**	0.15	0.20**	-1.53	-1.69	-2.55	-1.92**
8	L_5	0.01	0.11	0.26	0.13	-2.87**	-2.13*	-3.33*	-2.78**
9	L_6	0.13	-0.44**	-0.52**	-0.28**	1.24	1.64	0.90	1.26
10	L_7	0.24**	-0.11	-0.30	-0.06	-0.20	0.42	-1.77	-0.52
11	L_8	0.01	0.44**	1.15**	0.54**	0.36	0.76	0.90	0.67
12	L_9	-0.21**	0.44**	-1.07**	-0.28**	0.69	-0.47	0.67	0.30
13	L_{10}	0.13	0.22**	0.15	0.17*	-1.87*	-2.24*	-1.21	-1.78**
14	L_{11}	0.13	-0.33**	-0.30	-0.17*	0.47	0.98	-0.44	0.34
15	L_{12}	0.46**	0.11	-0.07	0.17*	-4.42**	-2.91**	-3.88**	-3.74**
16	L_{13}	-0.21**	-0.44**	-0.41*	-0.35**	2.47**	3.53**	0.34	2.11**
17	L_{14}	0.13	-0.11	0.59**	0.20**	2.36**	1.42	2.34	2.04**
18	L_{15}	-0.21**	-0.11	0.48**	0.05	2.13*	1.64	2.67	2.15**
19	L_1 x T_1	0.54**	0.04	-1.57**	-0.33*	1.91	0.62	1.64	1.39
20	L_2 x T_1	-0.46**	0.27	1.10**	0.30*	1.24	1.18	0.97	1.13
21	L_3 x T_1	0.10	-0.51**	-0.68*	-0.37**	2.47	1.62	1.97	2.02
22	L_4 x T_1	-0.35*	-0.07	-0.46	-0.29*	-0.20	1.29	2.19	1.09
23	L_5 x T_1	0.21	0.71**	1.76**	0.89**	0.47	0.73	-0.03	0.39
24	L_6 x T_1	-0.57**	0.60**	0.54	0.19	-2.64	-1.71	-1.25	-1.87
25	L_7 x T_1	-0.35*	0.27	0.32	0.08	1.13	0.84	1.08	1.02
26	L_8 x T_1	0.21	-0.29	0.54	0.15	1.24	0.84	0.75	0.95
27	L_9 x T_1	-0.24	-0.62**	-0.90**	-0.59**	-4.42*	-1.93	-2.70	-3.02*
28	L_{10} x T_1	0.43**	-0.07	-0.46	-0.03	5.80**	2.51	1.53	3.28*
29	L_{11} x T_1	-0.57**	0.82**	0.65	0.30*	-1.87	-0.38	-0.92	-1.05
30	L_{12} x T_1	0.10	-0.29	-0.24	-0.14	0.36	1.84	0.19	0.80
31	L_{13} x T_1	-0.24	0.60**	0.43	0.26*	-4.20*	-3.27	-1.03	-2.83*
32	L_{14} x T_1	0.43**	-0.73**	-0.57	-0.29*	-0.42	-2.16	-0.03	-0.87
33	L_{15} x T_1	0.76**	-0.73**	-0.46	-0.14	-0.87	-2.04	-4.36	-2.42
34	L_1 x T_2	-0.33*	-0.29	0.83*	0.07	-2.93	-2.38	-3.96	-3.09*
35	L_2 x T_2	0.01	0.27	-1.17**	-0.30*	-3.60*	-3.49	-5.30	-4.13**
36	L_3 x T_2	-0.10	0.16	-0.61	-0.19	-0.04	0.29	-0.96	-0.24
37	L_4 x T_2	0.12	-0.07	0.94**	0.33*	1.96	1.29	2.26	1.83
38	L_5 x T_2	-0.66**	0.04	0.16	-0.15	3.29	2.40	1.37	2.35

39	L_6 x T_2	0.23	-0.40*	-0.73*	-0.30*	1.18	0.29	0.81	0.76
40	L_7 x T_2	0.12	0.27	-0.95**	-0.19	-3.38	-3.16	-3.19	-3.24*
41	L_8 x T_2	-0.66**	0.71**	-0.39	-0.11	-3.60*	-3.16	-4.52	-3.76**
42	L_9 x T_2	0.56**	0.71**	-0.17	0.37**	4.73**	0.07	4.70	3.17*
43	L_{10} x T_2	0.23	-0.07	0.61	0.26	-2.04	0.18	-0.07	-0.65
44	L_{11} x T_2	0.23	-0.51**	-0.95**	-0.41**	1.96	1.62	3.81	2.46
45	L_{12} x T_2	0.90**	0.04	1.16**	0.70**	-0.16	0.51	-1.74	-0.46
46	L_{13} x T_2	-0.44**	-1.40**	1.16**	-0.22	2.96	3.07	3.70	3.24*
47	L_{14} x T_2	0.23	0.27	-0.84*	-0.11	-1.27	1.18	2.04	0.65
48	L_{15} x T_2	-0.44**	0.27	0.94**	0.26	0.96	1.29	1.04	1.09
49	L_1 x T_3	-0.21	0.24	0.74*	0.26	1.02	1.76	2.33	1.70
50	L_2 x T_3	0.45**	-0.53**	0.07	-0.00	2.36	2.31	4.33	3.00*
51	L_3 x T_3	0.01	0.36*	1.30**	0.55**	-2.42	-1.91	-1.01	-1.78
52	L_4 x T_3	0.23	0.13	-0.48	-0.04	-1.76	-2.58	-4.45	-2.93*
53	L_5 x T_3	0.45**	-0.76**	-1.93**	-0.74**	-3.76*	-3.13	-1.34	-2.74*
54	L_6 x T_3	0.34*	-0.20	0.19	0.11	1.47	1.42	0.44	1.11
55	L_7 x T_3	0.23	-0.53**	0.63	0.11	2.24	2.31	2.10	2.22
56	L_8 x T_3	0.45**	-0.42**	-0.15	-0.04	2.36	2.31	3.77	2.81*
57	L_9 x T_3	-0.33*	-0.09	1.07**	0.22	-0.31	1.87	-2.01	-0.15
58	L_{10} x T_3	-0.66**	0.13	-0.15	-0.22	-3.76*	-2.69	-1.45	-2.63*
59	L_{11} x T_3	0.34*	-0.31	0.30	0.11	-0.09	-1.24	-2.90	-1.41
60	L_{12} x T_3	-0.99**	0.24	-0.93**	-0.56**	-0.20	-2.36	1.55	-0.34
61	L_{13} x T_3	0.67**	0.80**	-1.59**	-0.04	1.24	0.20	-2.67	-0.41
62	L_{14} x T_3	-0.66**	0.47**	1.41**	0.40**	1.69	0.98	-2.01	0.22
63	L_{15} x T_3	-0.33*	0.47**	-0.48	-0.11	-0.09	0.76	3.33	1.33
	Standard error								
	Ti	0.04	0.04	0.08	0.03	0.44	0.45	0.74	0.32
	Lj	0.07	0.08	0.17	0.07	0.89	0.89	1.48	0.65
	Sij	0.14	0.16	0.33	0.13	1.77	1.79	2.97	1.30
	Ti-j	0.04	0.05	0.10	0.04	0.54	0.55	0.91	0.40
	Li-j	0.10	0.11	0.23	0.09	1.21	1.23	2.03	0.89
	Ti-Lj	0.08	0.09	0.18	0.07	0.94	0.95	1.57	0.69
	STi-Tj	0.18	0.20	0.41	0.16	2.17	2.19	3.63	1.59
	SiL-jL	0.20	0.22	0.46	0.18	2.43	2.45	4.06	1.78
	Sij-kl	0.20	0.23	0.47	0.19	2.49	2.51	4.16	1.82

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.4 GCA and SCA effects for plant height (cm) and ear height (cm)

SN	Genotype	Plant height (cm)				Ear height (cm)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	-7.37**	-5.80**	-6.82**	-6.66**	-10.93**	-9.30**	-10.31**	-10.18**
2	T_2	0.28	-0.80	-0.21	-0.24	4.25**	3.81**	4.47**	4.18**
3	T_3	7.08**	6.60**	7.03**	6.90**	6.67**	5.50**	5.84**	6.00**
4	L_1	4.20	-1.64	-1.41	0.38	-7.61**	-8.90**	-8.89**	-8.47**
5	L_2	0.61	0.55	7.32	2.82	-4.50**	-5.68**	-5.44**	-5.21**
6	L_3	-8.51*	-14.35**	2.46	-6.80**	-7.50**	-7.13**	-7.44**	-7.36**
7	L_4	1.94	0.27	9.55*	3.92	-3.95*	-3.24	-3.22	-3.47**
8	L_5	-9.54*	-4.70	-10.06*	-8.10**	1.50	3.65	1.00	2.05*
9	L_6	-1.37	5.37	-0.71	1.10	2.27	2.76	3.89*	2.98**
10	L_7	2.96	5.38	-11.71*	-1.12	2.83	1.10	0.44	1.46
11	L_8	-5.06	0.76	0.70	-1.20	0.61	0.99	1.11	0.90
12	L_9	-1.68	5.92	11.00*	5.08*	4.05**	4.54*	5.33**	4.64**
13	L_{10}	-6.60	-11.94**	-11.05*	-9.86**	-6.95**	-5.79**	-3.44	-5.40**
14	L_{11}	7.63	-1.73	9.71*	5.20*	3.83*	3.21	4.44*	3.83**
15	L_{12}	-2.61	2.65	6.82	2.29	5.72**	2.99	1.89	3.53**
16	L_{13}	5.60	2.97	-21.09**	-4.17	2.05	2.87	2.00	2.31*
17	L_{14}	8.15	-1.94	7.49	4.56	6.16**	6.54**	5.67**	6.12**
18	L_{15}	4.29	12.44**	1.00	5.91*	1.50	2.10	2.67	2.09*
19	L_1 x T_1	9.80	8.29	-10.22	2.62	14.48**	12.53**	10.31**	12.44**
20	L_2 x T_1	5.62	1.58	8.32	5.18	4.37	4.30	4.87	4.51*
21	L_3 x T_1	9.35	15.91	16.18	13.81**	10.37**	10.41*	5.87	8.88**
22	L_4 x T_1	12.22	10.43	12.67	11.77*	6.15*	4.19	5.64	5.33*
23	L_5 x T_1	-1.92	-4.40	15.56	3.08	-2.30	-6.03	-0.91	-3.08
24	L_6 x T_1	-3.07	-8.18	-1.95	-4.40	-3.41	-4.14	-0.80	-2.78
25	L_7 x T_1	8.61	5.00	-2.79	3.61	5.04	3.19	1.31	3.18
26	L_8 x T_1	-10.78	9.84	-11.50	-4.15	-3.41	-1.70	-3.69	-2.93
27	L_9 x T_1	-22.16**	-3.67	-12.20	-12.68*	-11.85**	-9.92*	-11.58**	-11.12**
28	L_{10} x T_1	6.21	-0.50	-6.29	-0.19	0.81	2.41	2.87	2.03
29	L_{11} x T_1	-9.21	-17.40*	6.61	-6.67	-6.63*	-5.92	-6.02	-6.19**
30	L_{12} x T_1	-7.80	-20.45*	-5.52	-11.26*	-12.85**	-7.36	-7.47*	-9.23**
31	L_{13} x T_1	6.07	-3.88	3.39	1.86	-1.52	-1.59	-0.58	-1.23
32	L_{14} x T_1	6.85	7.22	-6.35	2.57	2.70	0.41	3.42	2.18
33	L_{15} x T_1	-9.81	0.21	-5.90	-5.17	-1.96	-0.81	-3.24	-2.00
34	L_1 x T_2	-3.93	-1.43	3.13	-0.74	-3.36	-4.59	-4.47	-4.14*
35	L_2 x T_2	13.41	17.16*	10.69	13.75**	6.86*	6.53	3.76	5.71**
36	L_3 x T_2	10.09	0.71	5.70	5.50	1.19	-0.36	2.42	1.08

37	L_4 x T_2	8.00	14.87	6.70	9.86*	3.30	3.75	2.87	3.31
38	L_5 x T_2	-9.00	-21.65**	7.31	-7.78	-12.81**	-8.14*	-11.36**	-10.77**
39	L_6 x T_2	-14.80	2.85	-31.73**	-14.56**	-0.25	1.41	3.76	1.64
40	L_7 x T_2	-10.37	-4.80	13.71	-0.49	-3.81	-4.59	-3.13	-3.84
41	L_8 x T_2	3.34	-6.38	3.23	0.06	1.41	1.53	1.53	1.49
42	L_9 x T_2	11.79	-2.66	3.42	4.19	3.97	1.64	4.64	3.42
43	L_{10} x T_2	0.27	1.03	-7.40	-2.03	0.97	-1.03	-0.91	-0.32
44	L_{11} x T_2	1.22	9.15	0.64	3.67	8.19**	8.30*	8.20*	8.23**
45	L_{12} x T_2	15.13	17.45*	5.53	12.70*	8.30**	10.86**	9.76**	9.64**
46	L_{13} x T_2	-2.26	-0.21	-20.19*	-7.55	1.64	1.64	1.31	1.53
47	L_{14} x T_2	-21.09*	-24.09**	-10.47	-18.55**	-12.14**	-13.36**	-13.02**	-12.84**
48	L_{15} x T_2	-1.77	-2.01	9.72	1.98	-3.47	-3.59	-5.36	-4.14*
49	L_1 x T_3	-5.87	-6.86	7.09	-1.88	-11.12**	-7.94	-5.84	-8.30**
50	L_2 x T_3	-19.03*	-18.75*	-19.01*	-18.93**	-11.23**	-10.83**	-8.62*	-10.23**
51	L_3 x T_3	-19.44*	-16.62*	-21.88*	-19.31**	-11.56**	-10.05*	-8.29*	-9.97**
52	L_4 x T_3	-20.23*	-25.30**	-19.37*	-21.63**	-9.45**	-7.94	-8.51*	-8.63**
53	L_5 x T_3	10.92	26.05**	-22.87*	4.70	15.10**	14.17**	12.27**	13.85**
54	L_6 x T_3	17.88*	5.32	33.69**	18.96**	3.66	2.73	-2.96	1.14
55	L_7 x T_3	1.76	-0.20	-10.92	-3.12	-1.23	1.39	1.82	0.66
56	L_8 x T_3	7.44	-3.46	8.28	4.09	1.99	0.17	2.16	1.44
57	L_9 x T_3	10.37	6.33	8.78	8.49	7.88*	8.28*	6.93	7.70**
58	L_{10} x T_3	-6.48	-0.53	13.69	2.23	-1.79	-1.39	-1.96	-1.71
59	L_{11} x T_3	7.99	8.25	-7.25	3.00	-1.56	-2.39	-2.18	-2.04
60	L_{12} x T_3	-7.33	3.01	-0.01	-1.45	4.55	-3.50	-2.29	-0.41
61	L_{13} x T_3	-3.80	4.09	16.80	5.69	-0.12	-0.05	-0.73	-0.30
62	L_{14} x T_3	14.24	16.87*	16.82	15.98**	9.44**	12.95**	9.60**	10.66**
63	L_{15} x T_3	11.58	1.80	-3.82	3.19	5.44	4.39	8.60*	6.14**
	Standard error								
	Ti	2.07	2.02	2.35	1.24	0.77	1.01	0.90	0.52
	Lj	4.14	4.04	4.69	2.48	1.54	2.01	1.79	1.03
	Sij	8.28	8.09	9.38	4.97	3.08	4.02	3.58	2.07
	Ti-j	2.53	2.48	2.87	1.52	0.94	1.23	1.10	0.63
	Li-j	5.67	5.54	6.42	3.40	2.11	2.75	2.45	1.42
	Ti-Lj	4.39	4.29	4.98	2.63	1.64	2.13	1.90	1.10
	STi-Tj	10.14	9.90	11.49	6.08	3.78	4.92	4.39	2.53
	SiL-jL	11.33	11.07	12.85	6.80	4.22	5.51	4.91	2.83
	Sij-kl	11.61	11.35	13.16	6.97	4.33	5.64	5.03	2.90

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.5 GCA and SCA effects for cob length (cm) and number of grain rows/ear

SN	Genotype	Cob Length (cm)				Number of Grain rows/ear			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	0.33*	0.50*	0.45**	0.43**	-0.28*	-0.57**	-0.42*	-0.42**
2	T_2	-0.11	-0.59**	0.12	-0.19	0.19	0.04	0.31	0.18
3	T_3	-0.21	0.09	-0.58**	-0.23*	0.09	0.52**	0.11	0.24**
4	L_1	-0.64	-0.91*	0.24	-0.44*	-0.80**	-1.35**	-1.28**	-1.14**
5	L_2	1.03**	1.07*	0.17	0.75**	-0.27	0.65	0.33	0.24
6	L_3	0.68*	-0.51	0.89**	0.36	-0.52	-0.78*	-0.53	-0.61**
7	L_4	0.12	-0.44	0.13	-0.07	-0.30	-0.18	-0.13	-0.20
8	L_5	-0.42	0.89*	0.01	0.16	0.21	0.14	0.22	0.19
9	L_6	0.67*	-0.49	0.01	0.06	-0.20	-0.12	-0.15	-0.15
10	L_7	0.36	-0.16	0.82**	0.34	0.28	0.25	0.10	0.21
11	L_8	-0.03	0.25	0.68*	0.30	0.28	-0.46	-0.07	-0.08
12	L_9	0.57	-0.13	-0.72*	-0.09	0.85**	0.23	0.34	0.47*
13	L_{10}	0.17	-0.11	1.14**	0.40*	1.16**	1.28**	0.89*	1.11**
14	L_{11}	-0.89**	-0.06	-1.21**	-0.72**	-0.19	-0.24	-0.20	-0.21
15	L_{12}	0.91**	2.77**	1.30**	1.66**	1.60**	1.58**	1.69**	1.62**
16	L_{13}	-0.96**	-1.43**	-0.93**	-1.11**	-0.50	-0.36	-0.31	-0.39*
17	L_{14}	-0.83*	-0.31	-1.01**	-0.72**	-0.24	0.06	0.19	0.00
18	L_{15}	-0.75*	-0.43	-1.52**	-0.90**	-1.34**	-0.70*	-1.11**	-1.05**
19	L_1 x T_1	0.11	0.90	-1.33*	-0.11	-0.26	-0.48	-0.18	-0.31
20	L_2 x T_1	-0.20	-1.01	-0.67	-0.63	-0.32	1.27	0.26	0.41
21	L_3 x T_1	-1.54*	-0.70	0.43	-0.60	0.66	0.47	1.35	0.83*
22	L_4 x T_1	1.01	1.86*	-1.25*	0.54	0.25	1.23	-0.20	0.43
23	L_5 x T_1	0.59	-0.06	2.69**	1.07**	0.51	0.64	0.69	0.61
24	L_6 x T_1	0.54	-0.33	0.67	0.30	1.16*	1.12	0.92	1.07**
25	L_7 x T_1	-0.61	-0.72	0.36	-0.32	-0.35	-0.21	-0.47	-0.35
26	L_8 x T_1	-0.42	-1.43	-0.63	-0.83*	-1.38*	-0.58	-1.33	-1.09**
27	L_9 x T_1	1.12	1.76*	-0.73	0.72	1.98**	0.69	1.28	1.32**
28	L_{10} x T_1	-1.38*	-1.83*	-1.60**	-1.60**	-0.63	-0.30	0.16	-0.26
29	L_{11} x T_1	-0.97	-0.42	-0.95	-0.78	0.05	-0.23	-0.38	-0.18
30	L_{12} x T_1	-0.69	0.25	0.96	0.17	-0.74	-1.23	-0.88	-0.95*
31	L_{13} x T_1	0.96	0.22	1.07	0.75	-0.20	-1.31	0.07	-0.48
32	L_{14} x T_1	0.97	1.69*	2.27**	1.64**	-0.04	-0.29	-0.40	-0.24
33	L_{15} x T_1	0.50	-0.19	-1.29*	-0.33	-0.72	-0.78	-0.89	-0.79*
34	L_1 x T_2	0.18	0.40	1.08	0.55	0.58	0.31	0.38	0.42
35	L_2 x T_2	0.05	-0.20	1.18*	0.34	0.87	-0.72	0.58	0.25
36	L_3 x T_2	0.06	0.32	-0.03	0.12	-0.09	-0.54	-0.54	-0.39

37	L_4 x T_2	-0.46	-0.46	1.49**	0.19	-0.01	-1.26	0.39	-0.29
38	L_5 x T_2	-1.09	-1.76*	-2.63**	-1.83**	-2.03**	-0.70	-2.13**	-1.62**
39	L_6 x T_2	0.16	-0.22	-1.16*	-0.41	-0.71	-0.96	-1.07	-0.91*
40	L_7 x T_2	1.31*	1.67*	1.31*	1.43**	2.07**	1.81**	2.26**	2.05**
41	L_8 x T_2	1.66*	2.47**	2.78**	2.30**	1.23*	0.76	2.19**	1.39**
42	L_9 x T_2	0.02	-0.56	-1.33*	-0.62	-0.50	-0.23	-0.17	-0.30
43	L_{10} x T_2	-0.06	-0.52	-1.09	-0.56	-1.67**	-0.83	-1.71*	-1.40**
44	L_{11} x T_2	0.36	0.46	0.45	0.42	0.15	-0.01	1.07	0.41
45	L_{12} x T_2	-0.56	0.40	-0.68	-0.28	-0.13	-0.03	-0.47	-0.21
46	L_{13} x T_2	-0.47	-0.00	-0.45	-0.30	0.23	1.10	-0.45	0.30
47	L_{14} x T_2	-1.29	-1.81*	-2.48**	-1.86**	-0.76	0.20	-0.59	-0.38
48	L_{15} x T_2	0.13	-0.19	1.55**	0.50	0.77	1.09	0.25	0.70
49	L_1 x T_3	-0.29	-1.29	0.25	-0.45	-0.32	0.17	-0.20	-0.12
50	L_2 x T_3	0.15	1.21	-0.51	0.28	-0.55	-0.56	-0.84	-0.65
51	L_3 x T_3	1.48*	0.38	-0.40	0.49	-0.57	0.07	-0.81	-0.44
52	L_4 x T_3	-0.54	-1.40	-0.23	-0.73	-0.24	0.03	-0.19	-0.13
53	L_5 x T_3	0.51	1.82*	-0.06	0.75	1.52**	0.07	1.44*	1.01**
54	L_6 x T_3	-0.70	0.55	0.49	0.11	-0.46	-0.15	0.15	-0.15
55	L_7 x T_3	-0.70	-0.96	-1.67**	-1.11**	-1.72**	-1.60*	-1.78*	-1.70**
56	L_8 x T_3	-1.24	-1.04	-2.15**	-1.48**	0.15	-0.18	-0.86	-0.30
57	L_9 x T_3	-1.14	-1.20	2.05**	-0.10	-1.48**	-0.46	-1.11	-1.02**
58	L_{10} x T_3	1.44*	2.35**	2.68**	2.16**	2.30**	1.13	1.54*	1.66**
59	L_{11} x T_3	0.61	-0.04	0.50	0.36	-0.20	0.23	-0.69	-0.22
60	L_{12} x T_3	1.25	-0.65	-0.28	0.11	0.87	1.27	1.35	1.16**
61	L_{13} x T_3	-0.50	-0.22	-0.63	-0.45	-0.04	0.21	0.38	0.18
62	L_{14} x T_3	0.32	0.12	0.20	0.21	0.80	0.09	0.99	0.63
63	L_{15} x T_3	-0.64	0.38	-0.26	-0.17	-0.05	-0.31	0.63	0.09
	Standard error								
	Ti	0.17	0.21	0.14	0.10	0.13	0.17	0.17	0.09
	Lj	0.33	0.41	0.28	0.20	0.27	0.35	0.35	0.19
	Sij	0.66	0.82	0.56	0.40	0.54	0.69	0.69	0.37
	Ti-j	0.20	0.25	0.17	0.12	0.16	0.21	0.21	0.11
	Li-j	0.45	0.56	0.38	0.27	0.37	0.47	0.47	0.25
	Ti-Lj	0.35	0.44	0.30	0.21	0.28	0.37	0.37	0.20
	STi-Tj	0.81	1.01	0.69	0.49	0.66	0.85	0.85	0.46
	SiL-jL	0.91	1.13	0.77	0.55	0.73	0.95	0.95	0.51
	Sij-kl	0.93	1.16	0.79	0.56	0.75	0.97	0.97	0.52

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.6 GCA and SCA effects for Cob girth (cm) and 100-grain weight (g)

SN	Genotype	Cob girth (cm)				100-grain weight (g):			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	-0.16**	-0.18**	-0.17**	-0.17**	-2.44**	-2.99**	-2.01**	-2.48**
2	T_2	-0.01	0.04	0.14*	0.06	0.90*	1.28**	1.06**	1.08**
3	T_3	0.17**	0.15**	0.03	0.12**	1.54**	1.71**	0.95*	1.40**
4	L_1	-0.18	-0.32**	-0.46**	-0.32**	-2.75**	-3.05**	1.83*	-1.32**
5	L_2	0.24*	0.38**	0.22	0.28**	2.00**	2.22*	2.04*	2.09**
6	L_3	-0.40**	-0.43**	-0.40**	-0.41**	-3.97**	-5.82**	-6.76**	-5.52**
7	L_4	-0.31**	-0.28**	-0.22	-0.27**	-3.04**	-3.81**	-5.38**	-4.08**
8	L_5	0.05	-0.03	0.14	0.06	0.74	1.25	0.65	0.88
9	L_6	0.20*	0.01	0.10	0.10	-0.15	-0.00	-0.60	-0.25
10	L_7	0.12	0.13	0.22	0.16*	-0.18	0.99	0.53	0.45
11	L_8	0.08	0.16	0.13	0.12*	1.07	1.27	0.67	1.00*
12	L_9	0.22*	0.33**	0.55**	0.37**	-2.27**	-1.98*	-0.34	-1.53**
13	L_{10}	0.15	0.17	-0.14	0.06	0.22	0.62	-0.12	0.24
14	L_{11}	-0.44**	-0.47**	-0.31*	-0.41**	3.21**	3.61**	3.94**	3.59**
15	L_{12}	0.57**	0.65**	0.42**	0.55**	4.53**	4.28**	4.38**	4.39**
16	L_{13}	0.04	-0.06	0.03	0.00	1.15	2.17*	0.91	1.41**
17	L_{14}	-0.16	-0.10	-0.27*	-0.18**	1.52*	0.05	0.94	0.84
18	L_{15}	-0.19	-0.14	-0.04	-0.12	-2.08**	-1.79*	-2.68**	-2.18**
19	$L_1 \times T_1$	0.08	0.22	-0.19	0.04	-8.77**	-10.79**	0.98	-6.19**
20	$L_2 \times T_1$	-0.40*	-0.12	-0.11	-0.21	-0.74	-0.36	-1.76	-0.95
21	$L_3 \times T_1$	0.50*	-0.08	0.04	0.15	0.89	-1.28	-1.92	-0.77
22	$L_4 \times T_1$	0.18	0.09	-0.04	0.08	1.57	1.85	1.85	1.76
23	$L_5 \times T_1$	0.40*	0.30	0.03	0.24	-0.13	-1.51	-2.48	-1.37
24	$L_6 \times T_1$	0.12	0.23	0.36	0.24	0.47	0.91	-0.06	0.44
25	$L_7 \times T_1$	0.07	-0.25	-0.24	-0.14	-1.25	-2.06	-3.17*	-2.16*
26	$L_8 \times T_1$	-0.31	-0.19	-0.23	-0.24	1.80	2.33	1.35	1.83*
27	$L_9 \times T_1$	0.57**	0.52*	0.42	0.50**	-0.06	0.38	1.42	0.58
28	$L_{10} \times T_1$	-0.10	-0.04	0.29	0.05	0.02	0.34	-0.22	0.05
29	$L_{11} \times T_1$	-0.15	-0.20	-0.21	-0.19	3.95**	4.64**	3.25*	3.95**
30	$L_{12} \times T_1$	-0.06	0.29	0.53*	0.25*	2.94	3.91*	2.23	3.02**
31	$L_{13} \times T_1$	-0.03	0.05	0.07	0.03	0.69	0.40	0.08	0.39
32	$L_{14} \times T_1$	-0.35	-0.34	-0.18	-0.29*	-3.02*	-0.83	-2.96	-2.27*
33	$L_{15} \times T_1$	-0.50*	-0.48*	-0.56*	-0.51**	1.64	2.08	1.39	1.70
34	$L_1 \times T_2$	-0.20	-0.06	0.19	-0.02	5.21**	5.29**	0.04	3.51**
35	$L_2 \times T_2$	0.69**	0.47*	-0.09	0.36**	1.91	3.01	2.81	2.57**
36	$L_3 \times T_2$	0.01	0.42*	0.21	0.22	-1.72	-0.07	0.48	-0.44

37	L_4 x T_2	-0.07	-0.03	-0.03	-0.04	1.06	1.63	2.82	1.84*
38	L_5 x T_2	-0.70**	-0.60**	-0.52*	-0.61**	1.41	1.10	1.32	1.28
39	L_6 x T_2	-0.21	-0.34	-0.47	-0.34**	-2.36	-2.71	-2.49	-2.52**
40	L_7 x T_2	0.44*	0.89**	0.65**	0.66**	3.79*	5.70**	5.78**	5.09**
41	L_8 x T_2	0.32	0.21	0.31	0.28*	0.03	-0.36	-0.14	-0.16
42	L_9 x T_2	-0.18	-0.51*	-0.29	-0.33*	0.80	0.97	-0.73	0.35
43	L_{10} x T_2	-0.59**	-0.71**	-0.35	-0.55**	-1.12	-1.78	-1.79	-1.57
44	L_{11} x T_2	-0.19	-0.16	-0.01	-0.12	-1.27	-2.35	-0.18	-1.27
45	L_{12} x T_2	-0.28	-0.50*	-0.26	-0.34**	-3.16*	-2.25	-2.18	-2.53**
46	L_{13} x T_2	0.12	0.12	-0.31	-0.02	0.07	-0.53	-0.08	-0.18
47	L_{14} x T_2	0.33	0.30	0.39	0.34**	0.04	-2.48	-0.98	-1.14
48	L_{15} x T_2	0.52**	0.47*	0.57*	0.52**	-4.67**	-5.17**	-4.67**	-4.84**
49	L_1 x T_3	0.12	-0.17	-0.00	-0.02	3.57*	5.50**	-1.02	2.68**
50	L_2 x T_3	-0.29	-0.36	0.20	-0.15	-1.17	-2.64	-1.05	-1.62
51	L_3 x T_3	-0.51*	-0.34	-0.25	-0.37**	0.83	1.35	1.44	1.21
52	L_4 x T_3	-0.11	-0.06	0.07	-0.03	-2.63	-3.49*	-4.67**	-3.60**
53	L_5 x T_3	0.30	0.31	0.49*	0.36**	-1.28	0.41	1.16	0.10
54	L_6 x T_3	0.09	0.11	0.11	0.10	1.88	1.79	2.55	2.07*
55	L_7 x T_3	-0.51*	-0.64**	-0.41	-0.52**	-2.53	-3.65*	-2.61	-2.93**
56	L_8 x T_3	-0.01	-0.01	-0.08	-0.03	-1.83	-1.97	-1.21	-1.67
57	L_9 x T_3	-0.39*	-0.02	-0.13	-0.18	-0.75	-1.35	-0.69	-0.93
58	L_{10} x T_3	0.69**	0.75**	0.05	0.50**	1.10	1.44	2.01	1.52
59	L_{11} x T_3	0.34	0.36	0.22	0.31*	-2.68	-2.28	-3.07	-2.68**
60	L_{12} x T_3	0.34	0.21	-0.27	0.09	0.23	-1.66	-0.05	-0.49
61	L_{13} x T_3	-0.09	-0.17	0.24	-0.01	-0.75	0.13	-0.00	-0.21
62	L_{14} x T_3	0.03	0.04	-0.21	-0.05	2.98*	3.31	3.93*	3.41**
63	L_{15} x T_3	-0.02	0.00	-0.01	-0.01	3.03*	3.10	3.28*	3.14**
	Standard error								
	Ti	0.05	0.05	0.06	0.03	0.38	0.43	0.40	0.23
	Lj	0.10	0.11	0.12	0.06	0.75	0.85	0.79	0.46
	Sij	0.19	0.21	0.25	0.13	1.50	1.71	1.58	0.92
	Ti-j	0.06	0.07	0.08	0.04	0.46	0.52	0.48	0.28
	Li-j	0.13	0.15	0.17	0.09	1.03	1.17	1.08	0.63
	Ti-Lj	0.10	0.11	0.13	0.07	0.80	0.91	0.84	0.49
	STi-Tj	0.24	0.26	0.30	0.16	1.84	2.09	1.94	1.13
	SiL-jL	0.27	0.29	0.34	0.17	2.06	2.34	2.16	1.26
	Sij-kl	0.27	0.30	0.35	0.18	2.11	2.39	2.22	1.30

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.7 GCA and SCA effects for Harvest index per cent and Grain Yield / Plant (g)

SN	Genotype	Harvest index (%)				Grain Yield / Plant (g)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	-0.12	-0.46	1.58**	0.33	12.10**	3.21*	0.79	5.37**
2	T_2	-0.42	-0.55	-1.09*	-0.68**	5.12**	5.54**	4.13**	4.93**
3	T_3	0.54	1.01**	-0.49	0.35	-17.21**	-8.75**	-4.92**	-10.30**
4	L_1	-4.09**	-1.71*	-0.73	-2.18**	8.77**	10.32**	10.32**	9.80**
5	L_2	-0.33	2.30**	2.08*	1.35*	5.82*	-5.73*	-1.45	-0.45
6	L_3	1.68	-0.69	-1.76	-0.26	-23.94**	-16.64**	-10.77**	-17.12**
7	L_4	0.34	-2.68**	0.29	-0.68	-16.62**	-5.09	-6.55*	-9.42**
8	L_5	2.16*	1.77*	-0.53	1.13*	51.45**	32.23**	30.42**	38.03**
9	L_6	1.99	0.76	-0.39	0.79	-12.78**	-14.61**	-17.26**	-14.88**
10	L_7	0.52	1.89*	0.29	0.90	-8.74**	-8.82**	-17.04**	-11.53**
11	L_8	1.98	-1.18	-0.45	0.12	-11.62**	-4.20	-10.53**	-8.79**
12	L_9	-1.05	1.16	3.05**	1.05*	-2.42	-2.61	-9.71**	-4.91**
13	L_{10}	1.28	-0.81	-1.97*	-0.50	7.41**	1.67	9.66**	6.25**
14	L_{11}	0.01	-2.10**	1.66	-0.14	-8.42**	-5.62*	-4.51	-6.18**
15	L_{12}	-0.12	1.53*	-0.50	0.31	33.39**	26.95**	25.41**	28.58**
16	L_{13}	-3.00**	-0.83	0.63	-1.07*	-10.24**	-2.15	4.16	-2.75
17	L_{14}	-1.84	2.04**	-1.69	-0.50	5.75*	12.02**	13.61**	10.46**
18	L_{15}	0.46	-1.47	0.03	-0.33	-17.81**	-17.73**	-15.74**	-17.09**
19	L_1 x T_1	3.76	-2.33	-0.12	0.44	-11.15*	-4.04	-9.09	-8.09**
20	L_2 x T_1	3.64	-1.50	-0.49	0.55	47.15**	30.70**	48.03**	41.96**
21	L_3 x T_1	0.32	3.83*	1.02	1.72	8.56	14.58**	17.66**	13.60**
22	L_4 x T_1	0.30	-0.53	3.28	1.02	-0.63	10.17	15.58**	8.37**
23	L_5 x T_1	0.39	2.82	1.23	1.48	-13.60**	3.79	-4.55	-4.79
24	L_6 x T_1	-3.20	1.01	0.52	-0.55	-3.21	-14.12*	-16.09**	-11.14**
25	L_7 x T_1	-3.16	-1.71	-0.39	-1.75	-37.96**	-36.18**	-40.01**	-38.05**
26	L_8 x T_1	0.63	0.61	-0.40	0.28	15.21**	-3.83	-3.40	2.66
27	L_9 x T_1	3.67	-0.39	-0.74	0.85	38.16**	28.59**	9.06	25.27**
28	L_{10} x T_1	1.46	1.71	3.42	2.20*	-34.68**	-26.16**	-29.18**	-30.01**
29	L_{11} x T_1	-1.21	-1.01	0.75	-0.49	2.38	0.99	0.88	1.42
30	L_{12} x T_1	0.61	-3.95*	-0.02	-1.12	-7.73	0.78	-1.93	-2.96
31	L_{13} x T_1	-2.69	-1.56	-3.16	-2.47*	-5.22	-2.57	12.06*	1.42
32	L_{14} x T_1	-4.31*	3.04	-5.03**	-2.10*	-3.87	0.39	-2.57	-2.02
33	L_{15} x T_1	-0.22	-0.06	0.13	-0.05	6.60	-3.09	3.55	2.35
34	L_1 x T_2	-1.16	-0.86	0.54	-0.49	-22.88**	-20.68**	-10.73	-18.09**
35	L_2 x T_2	-3.50	0.32	0.40	-0.93	5.41	5.46	-13.29*	-0.81
36	L_3 x T_2	0.34	-0.61	-1.95	-0.74	0.49	-4.40	1.35	-0.85

37	L_4 x T_2	-0.05	-0.90	-2.07	-1.01	8.51	11.06*	-0.85	6.24*
38	L_5 x T_2	0.39	-0.75	-6.45**	-2.27*	12.93**	-9.70	-9.70	-2.16
39	L_6 x T_2	4.56*	-2.19	0.16	0.84	6.97	11.21*	12.15*	10.11**
40	L_7 x T_2	2.30	2.28	0.69	1.76	39.39**	32.03**	40.93**	37.45**
41	L_8 x T_2	0.21	0.76	0.52	0.50	-2.63	25.66**	13.19*	12.07**
42	L_9 x T_2	-5.72**	-2.38	1.75	-2.12*	-35.13**	-23.04**	-15.65**	-24.61**
43	L_{10} x T_2	-1.02	-0.90	2.78	0.29	-4.03	-8.91	-5.28	-6.07
44	L_{11} x T_2	1.23	1.36	0.66	1.08	-24.42**	-17.50**	-10.32	-17.42**
45	L_{12} x T_2	5.74**	3.16*	-0.17	2.91**	21.88**	-9.14	-1.54	3.73
46	L_{13} x T_2	-2.60	1.34	3.88*	0.87	5.50	10.46	5.76	7.24*
47	L_{14} x T_2	-0.36	-1.38	-1.12	-0.95	4.87	9.07	8.91	7.62*
48	L_{15} x T_2	-0.37	0.74	0.36	0.24	-16.87**	-11.57*	-14.93*	-14.46**
49	L_1 x T_3	-2.60	3.18*	-0.42	0.05	34.02**	24.72**	19.82**	26.19**
50	L_2 x T_3	-0.14	1.18	0.09	0.38	-52.56**	-36.16**	-34.74**	-41.15**
51	L_3 x T_3	-0.66	-3.23*	0.93	-0.99	-9.05	-10.18	-19.01**	-12.75**
52	L_4 x T_3	-0.25	1.43	-1.21	-0.01	-7.87	-21.23**	-14.73*	-14.61**
53	L_5 x T_3	-0.78	-2.06	5.21**	0.79	0.66	5.91	14.25*	6.94*
54	L_6 x T_3	-1.36	1.18	-0.68	-0.29	-3.76	2.90	3.93	1.03
55	L_7 x T_3	0.85	-0.58	-0.30	-0.01	-1.43	4.15	-0.92	0.60
56	L_8 x T_3	-0.84	-1.38	-0.12	-0.78	-12.58*	-21.83**	-9.79	-14.73**
57	L_9 x T_3	2.05	2.77	-1.01	1.27	-3.03	-5.55	6.59	-0.66
58	L_{10} x T_3	-0.44	-0.80	-6.20**	-2.48*	38.72**	35.07**	34.46**	36.08**
59	L_{11} x T_3	-0.02	-0.36	-1.41	-0.59	22.03**	16.52**	9.45	16.00**
60	L_{12} x T_3	-6.35**	0.79	0.19	-1.79	-14.15**	8.36	3.47	-0.77
61	L_{13} x T_3	5.29*	0.22	-0.72	1.60	-0.27	-7.89	-17.83**	-8.66**
62	L_{14} x T_3	4.67*	-1.67	6.16**	3.05**	-1.00	-9.46	-6.34	-5.60
63	L_{15} x T_3	0.59	-0.68	-0.50	-0.20	10.27*	14.66**	11.39*	12.11**
	Standard error								
	Ti	0.51	0.38	0.45	0.26	1.22	1.37	1.44	0.78
	Lj	1.03	0.77	0.91	0.52	2.44	2.73	2.88	1.55
	Sij	2.05	1.54	1.82	1.05	4.88	5.47	5.76	3.11
	Ti-j	0.63	0.47	0.56	0.32	1.49	1.67	1.76	0.95
	Li-j	1.40	1.05	1.24	0.72	3.34	3.74	3.94	2.13
	Ti-Lj	1.09	0.82	0.96	0.56	2.59	2.90	3.05	1.65
	STi-Tj	2.51	1.88	2.22	1.28	5.98	6.70	7.05	3.80
	SiL-jL	2.81	2.11	2.49	1.43	6.68	7.49	7.88	4.25
	Sij-kl	2.88	2.16	2.55	1.47	6.85	7.67	8.08	4.36

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.8 GCA and SCA effects for Grain protein content in per cent, Grain starch content in per cent

SN	Genotype	Grain protein content in (%)				Grain starch content in (%)			
		E1	E2	E3	Pool	E1	E2	E3	Pool
1	T_1	0.03*	0.02	-0.03*	0.01	-0.05	-0.10	0.15*	-0.00
2	T_2	0.06**	0.00	0.05**	0.04**	0.15*	0.20*	0.03	0.13**
3	T_3	-0.09**	-0.02	-0.02	-0.04**	-0.11	-0.10	-0.18*	-0.13**
4	L_1	-0.17**	-0.23**	-0.26**	-0.22**	1.88**	1.72**	1.55**	1.72**
5	L_2	0.79**	0.79**	0.72**	0.76**	-1.71**	-1.07**	-0.68**	-1.15**
6	L_3	-0.37**	-0.36**	-0.50**	-0.41**	-1.30**	-1.19**	-1.15**	-1.21**
7	L_4	-0.33**	-0.33**	-0.41**	-0.36**	-0.36**	-0.45*	-0.34*	-0.38**
8	L_5	-0.03	-0.15**	0.26**	0.03	-1.37**	-1.32**	-1.38**	-1.36**
9	L_6	0.07*	0.09**	0.10**	0.08**	0.71**	0.86**	1.55**	1.04**
10	L_7	0.04	0.42**	0.36**	0.27**	-0.60**	-0.70**	-0.87**	-0.72**
11	L_8	0.25**	0.09**	0.40**	0.24**	0.94**	0.78**	-0.24	0.50**
12	L_9	0.11**	0.03	0.00	0.05**	-1.44**	-1.42**	-1.58**	-1.48**
13	L_{10}	0.45**	0.44**	0.43**	0.44**	-1.36**	-1.35**	-0.59**	-1.10**
14	L_{11}	-0.30**	-0.37**	-0.43**	-0.36**	1.68**	1.68**	1.11**	1.49**
15	L_{12}	0.30**	0.32**	0.26**	0.29**	3.13**	2.73**	2.25**	2.70**
16	L_{13}	-0.49**	-0.47**	-0.53**	-0.50**	-0.88**	-0.68**	-0.75**	-0.77**
17	L_{14}	-0.28**	-0.28**	-0.39**	-0.32**	0.48**	0.18	1.25**	0.64**
18	L_{15}	-0.03	0.00	-0.00	-0.01	0.20	0.20	-0.13	0.09
19	L_1 x T_1	-0.29**	-0.18**	-0.14*	-0.20**	-0.33	-0.09	-0.12	-0.18
20	L_2 x T_1	0.02	0.11*	0.14*	0.09**	2.02**	1.46**	0.87**	1.45**
21	L_3 x T_1	0.46**	0.53**	0.64**	0.54**	-3.16**	-3.19**	-3.44**	-3.26**
22	L_4 x T_1	0.08	0.03	0.09	0.07*	3.58**	3.75**	3.43**	3.59**
23	L_5 x T_1	0.52**	0.73**	0.35**	0.53**	-0.88**	-0.86*	-1.01**	-0.92**
24	L_6 x T_1	0.38**	0.43**	0.54**	0.45**	-0.84**	-0.91*	-1.80**	-1.18**
25	L_7 x T_1	-0.44**	-0.90**	-0.73**	-0.69**	1.38**	1.56**	1.53**	1.49**
26	L_8 x T_1	-0.08	-0.19**	-0.50**	-0.26**	-2.26**	-2.02**	-1.21**	-1.83**
27	L_9 x T_1	0.35**	0.42**	0.44**	0.40**	3.31**	3.37**	2.79**	3.16**
28	L_{10} x T_1	-0.34**	-0.39**	-0.40**	-0.38**	-2.69**	-2.62**	-2.06**	-2.46**
29	L_{11} x T_1	-0.53**	-0.46**	-0.45**	-0.48**	1.52**	1.24**	0.76**	1.18**
30	L_{12} x T_1	0.32**	0.30**	0.43**	0.35**	2.81**	2.94**	3.27**	3.01**
31	L_{13} x T_1	0.03	0.06	0.10	0.06	-0.85**	-1.12**	-1.09**	-1.02**
32	L_{14} x T_1	0.17**	0.16**	0.17**	0.17**	-3.52**	-3.48**	-1.86**	-2.95**
33	L_{15} x T_1	-0.64**	-0.65**	-0.68**	-0.65**	-0.09	-0.01	-0.05	-0.05
34	L_1 x T_2	-0.00	-0.06	-0.04	-0.03	-1.37**	-1.24**	-0.44	-1.02**
35	L_2 x T_2	0.12*	0.12*	-0.03	0.07*	0.09	-0.57	-0.75**	-0.41*

36	L_3 x T_2	-0.12*	-0.05	-0.03	-0.07*	-1.15**	-1.28**	-1.11**	-1.18**
37	L_4 x T_2	0.19**	0.23**	0.16**	0.19**	0.03	0.09	0.20	0.11
38	L_5 x T_2	-0.18**	-0.39**	-0.73**	-0.44**	4.52**	4.44**	4.49**	4.49**
39	L_6 x T_2	-0.35**	-0.29**	-0.28**	-0.31**	-1.74**	-1.92**	-0.68*	-1.45**
40	L_7 x T_2	0.87**	0.71**	0.67**	0.75**	0.95**	1.02**	0.38	0.78**
41	L_8 x T_2	-0.29**	-0.43**	0.27**	-0.15**	2.18**	2.31**	0.04	1.51**
42	L_9 x T_2	-0.31**	-0.29**	-0.37**	-0.32**	-3.04**	-3.08**	-2.70**	-2.94**
43	L_{10} x T_2	0.16**	0.22**	0.18**	0.19**	0.34	0.30	-0.39	0.09
44	L_{11} x T_2	0.22**	0.26**	0.34**	0.27**	-0.87**	-0.59	-0.11	-0.52**
45	L_{12} x T_2	-0.43**	-0.45**	-0.48**	-0.45**	-3.16**	-3.07**	-1.99**	-2.74**
46	L_{13} x T_2	-0.01	0.09	0.05	0.04	0.21	-0.01	0.27	0.16
47	L_{14} x T_2	-0.40**	-0.32**	-0.37**	-0.36**	2.46**	2.90**	2.22**	2.53**
48	L_{15} x T_2	0.53**	0.64**	0.68**	0.62**	0.55*	0.70	0.57*	0.61**
49	L_1 x T_3	0.29**	0.24**	0.18**	0.24**	1.71**	1.33**	0.56*	1.20**
50	L_2 x T_3	-0.14*	-0.23**	-0.11	-0.16**	-2.10**	-0.88*	-0.12	-1.03**
51	L_3 x T_3	-0.34**	-0.48**	-0.60**	-0.48**	4.32**	4.47**	4.55**	4.44**
52	L_4 x T_3	-0.27**	-0.26**	-0.24**	-0.26**	-3.61**	-3.84**	-3.63**	-3.69**
53	L_5 x T_3	-0.33**	-0.34**	0.38**	-0.10**	-3.64**	-3.58**	-3.48**	-3.57**
54	L_6 x T_3	-0.02	-0.14**	-0.26**	-0.14**	2.58**	2.83**	2.48**	2.63**
55	L_7 x T_3	-0.43**	0.19**	0.06	-0.06	-2.32**	-2.58**	-1.91**	-2.27**
56	L_8 x T_3	0.38**	0.62**	0.24**	0.41**	0.08	-0.29	1.17**	0.32
57	L_9 x T_3	-0.05	-0.13*	-0.07	-0.08*	-0.28	-0.28	-0.09	-0.22
58	L_{10} x T_3	0.18**	0.16**	0.23**	0.19**	2.35**	2.32**	2.45**	2.37**
59	L_{11} x T_3	0.31**	0.20**	0.11	0.21**	-0.66*	-0.65	-0.65*	-0.65**
60	L_{12} x T_3	0.11	0.15**	0.05	0.10**	0.34	0.13	-1.28**	-0.27
61	L_{13} x T_3	-0.02	-0.15**	-0.15*	-0.10**	0.65*	1.13**	0.82**	0.87**
62	L_{14} x T_3	0.23**	0.16**	0.19**	0.19**	1.06**	0.58	-0.36	0.43*
63	L_{15} x T_3	0.11	0.00	-0.00	0.04	-0.47	-0.69	-0.52	-0.56**
	Standard error								
	Ti	0.01	0.01	0.01	0.01	0.06	0.10	0.07	0.05
	Lj	0.03	0.03	0.03	0.02	0.13	0.19	0.14	0.09
	Sij	0.06	0.05	0.06	0.03	0.26	0.38	0.28	0.18
	Ti-j	0.02	0.02	0.02	0.01	0.08	0.12	0.09	0.06
	Li-j	0.04	0.04	0.04	0.02	0.18	0.26	0.19	0.12
	Ti-Lj	0.03	0.03	0.03	0.02	0.14	0.20	0.15	0.10
	STi-Tj	0.07	0.06	0.07	0.04	0.31	0.47	0.34	0.22
	SiL-jL	0.08	0.07	0.08	0.04	0.35	0.53	0.38	0.25
	Sij-kl	0.08	0.07	0.08	0.05	0.36	0.54	0.39	0.25

*,** Significantly deviating from zero for 5% and 1% level of significance

Table.9 GCA and SCA effects for Grain Oil content in per cent

SN	Genotype	Grain Oil content in (%)			
		E1	E2	E3	Pool
1	T_1	-0.11**	-0.12**	-0.02**	-0.08**
2	T_2	0.05**	0.06**	-0.03**	0.03**
3	T_3	0.06**	0.06**	0.05**	0.06**
4	L_1	0.16**	0.18**	0.09**	0.14**
5	L_2	0.14**	0.15**	0.12**	0.14**
6	L_3	0.20**	0.20**	0.21**	0.20**
7	L_4	-0.61**	-0.61**	-0.52**	-0.58**
8	L_5	0.16**	0.17**	0.13**	0.15**
9	L_6	0.12**	0.11**	0.24**	0.16**
10	L_7	-0.01	-0.04*	0.03*	-0.01
11	L_8	0.02	0.01	-0.11**	-0.03**
12	L_9	0.12**	0.11**	-0.01	0.07**
13	L_{10}	0.05**	0.04**	-0.07**	0.01
14	L_{11}	-0.40**	-0.42**	-0.39**	-0.40**
15	L_{12}	0.40**	0.41**	0.55**	0.46**
16	L_{13}	-0.11**	-0.10**	-0.13**	-0.11**
17	L_{14}	-0.10**	-0.08**	-0.04**	-0.07**
18	L_{15}	-0.14**	-0.12**	-0.09**	-0.12**
19	L_1 x T_1	-0.33**	-0.29**	-0.30**	-0.31**
20	L_2 x T_1	0.35**	0.34**	0.26**	0.32**
21	L_3 x T_1	0.18**	0.17**	0.10**	0.15**
22	L_4 x T_1	0.04	0.03	0.01	0.03
23	L_5 x T_1	0.20**	0.19**	0.03	0.14**
24	L_6 x T_1	0.26**	0.24**	0.30**	0.27**
25	L_7 x T_1	-0.21**	-0.21**	-0.29**	-0.23**
26	L_8 x T_1	-0.11**	-0.11**	-0.15**	-0.12**
27	L_9 x T_1	0.55**	0.54**	0.56**	0.55**
28	L_{10} x T_1	-0.33**	-0.32**	-0.33**	-0.32**
29	L_{11} x T_1	0.01	-0.04	-0.06**	-0.03*
30	L_{12} x T_1	0.01	0.02	0.18**	0.07**
31	L_{13} x T_1	-0.06	-0.04	0.14**	0.01
32	L_{14} x T_1	-0.28**	-0.26**	-0.19**	-0.24**
33	L_{15} x T_1	-0.29**	-0.27**	-0.26**	-0.27**
34	L_1 x T_2	0.06	0.04	-0.19**	-0.03
35	L_2 x T_2	0.24**	0.24**	0.34**	0.27**
36	L_3 x T_2	-0.34**	-0.35**	-0.27**	-0.32**

37	L_4 x T_2	0.13**	0.13**	0.08**	0.11**
38	L_5 x T_2	-0.50**	-0.51**	-0.42**	-0.48**
39	L_6 x T_2	-0.02	-0.02	-0.16**	-0.07**
40	L_7 x T_2	0.21**	0.19**	0.33**	0.24**
41	L_8 x T_2	-0.07*	-0.06*	-0.19**	-0.11**
42	L_9 x T_2	-0.11**	-0.11**	-0.23**	-0.15**
43	L_{10} x T_2	-0.27**	-0.29**	-0.06**	-0.21**
44	L_{11} x T_2	-0.07*	-0.02	-0.04	-0.04**
45	L_{12} x T_2	0.07*	0.08**	-0.00	0.05**
46	L_{13} x T_2	0.09**	0.09**	0.21**	0.13**
47	L_{14} x T_2	0.45**	0.45**	0.48**	0.46**
48	L_{15} x T_2	0.13**	0.15**	0.14**	0.14**
49	L_1 x T_3	0.27**	0.26**	0.49**	0.34**
50	L_2 x T_3	-0.59**	-0.58**	-0.59**	-0.59**
51	L_3 x T_3	0.17**	0.18**	0.17**	0.17**
52	L_4 x T_3	-0.17**	-0.16**	-0.09**	-0.14**
53	L_5 x T_3	0.29**	0.32**	0.39**	0.33**
54	L_6 x T_3	-0.24**	-0.22**	-0.14**	-0.20**
55	L_7 x T_3	-0.00	0.02	-0.04	-0.01
56	L_8 x T_3	0.18**	0.18**	0.34**	0.23**
57	L_9 x T_3	-0.43**	-0.43**	-0.33**	-0.40**
58	L_{10} x T_3	0.60**	0.60**	0.39**	0.53**
59	L_{11} x T_3	0.06	0.07*	0.11**	0.08**
60	L_{12} x T_3	-0.08*	-0.10**	-0.18**	-0.12**
61	L_{13} x T_3	-0.03	-0.05	-0.34**	-0.14**
62	L_{14} x T_3	-0.18**	-0.20**	-0.29**	-0.22**
63	L_{15} x T_3	0.15**	0.13**	0.11**	0.13**
	Standard error				
	Ti	0.01	0.01	0.01	0.00
	Lj	0.02	0.01	0.01	0.01
	Sij	0.03	0.03	0.02	0.02
	Ti-j	0.01	0.01	0.01	0.01
	Li-j	0.02	0.02	0.02	0.01
	Ti-Lj	0.02	0.02	0.01	0.01
	STi-Tj	0.04	0.04	0.03	0.02
	SiL-jL	0.04	0.04	0.03	0.02
	Sij-kl	0.05	0.04	0.03	0.02

*,** Significantly deviating from zero for 5% and 1% level of significance

Analysis of variance for combining ability revealed (Table 1) that mean squares due to lines, testers and lines x tester were significant for all the characters in all the environments. Significant mean squares due to lines and testers for different characters indicated significant contribution of lines and testers towards the general combining (gca) effects. Similarly significant mean squares due to lines x testers for different characters indicated significant contribution of hybrids for specific combining (sca) effects.

Results on pooled basis (Table 2) revealed that mean squares due to lines, testers and lines x testers were significant for all the characters. The interaction of lines with environments was significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, ear height, number of grain rows/ear, cob girth. Further, testers x environments interaction was significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent % brown husk, plant height, ear height, cob girth, 100-grain weight. The interaction of lines x testers x environments were significant for all the characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, ear height, number of grain rows/ear. This indicated that estimates of gca and sca effects were highly influenced by environments for large numbers of characters studied (Table 3).

Parents were classified as high or good, medium or average and low or poor combiners on the basis of their gca effects. Parents with desirable and gca effects were considered high or good combiners while parents showing non-significant estimates but in desirable direction were classified as average or medium combiners. Poor or low combiners had undesirable gca effects. The estimates of gca effects revealed that the good general combiner for yield were inbred lines L_1, L_5, L_{10}, L_{12}, and L_{14}, for oil content inbred lines L_1, L_2, L_3, L_5, L_6, L_9, and L_{12}, for protein content inbred lines L_2, L_6, L_7, L_8, L_9, L_{10}, and L_{12}, for starch content inbred lines L_1, L_6, L_8, L_{11}, L_{12}, and $L_{14,}$ for brown husk related traits inbred lines L_4, L_5, L_{10} and L_{12}, for plant type traits inbred lines L_3, L_5 and L_{10} (Table 3). Among the testers, T_1 was considered good general combiner for brown husk related traits, protein content. The tester T_2 was considered good general combiner for brown husk related traits, starch content. Tester T_3 was considered good general combiner for yield and yield contributing traits and oil content. The general combining effects observed is due to additive gene effects and additive x additive gene effects (Griffing, 1956 and Sprague, 1966).

A perusal of sca effect revealed that highest magnitude of positive significant sca effects for grain yield per plant was recorded in hybrid L_2 x T_1 in E_1 (47.15), in E_2 (30.70), in E_3 (48.03) and on pooled basis (41.96). Three hybrids *viz*., L_7 x T_2, L_1 x T_3 and L_{10} x T_3 exhibited positive significant sca effects in all the three environments as well as on pooled basis. Hybrid L_{10} x T_3 besides grain yield per plant also exhibited positive significant sca effects for cob length, numbers of grain rows per ear, cob girth, starch content, oil content. Hybrid L_7 x T_2 in addition to grain yield per plant also exhibited significant positive sca effects for cob length, numbers of grain rows per ear, cob girth, 100-grain weight (Table 4–9).

Out of 45 hybrids five best hybrids which exhibited positive significant sca effects for grain yield per plant are *viz*., L_2 x $T_{1,}$ L_7 x T_2, L_{10} x T_3, L_1 x T_3 and L_9 x T_1. Hybrid L_2 x T_1 also exhibited higher magnitude of economic heterosis with higher mean performance. These hybrids L_2 x T_1, L_7 x $T_{2,}$ L_{10} x T3, L_1 x T_3, and L_9 x T_1 were crosses between poor x

good gca effects of parent for grain yield per plant. Similar findings for identification of superior inbred lines, testers and hybrid based on gca and sca effects for grain yield and its component traits in maize were reported by Ismaeili *et al.,* (2005), Choukan (2006), Luders *et al.,* (2007), Lata *et al.,* (2008), Alam *et al.,* (2009), Jebaraj *et al.,* (2010), Kanagarasu *et al.,* (2010), Yousif and Sedeeq (2011), Guimaraes *et al.,* (2012), Patil *et al.,* (2012), Mural and Chikkalingaiah (2012), Abrha *et al.,* (2013), Izhar and Chakraborty (2013), Panwar *et al.,* (2013), Singh *et al.,* (2013), Ulaganathan and Ibrahim (2014), Jahan *et al.,* (2014), Rastgari *et al.,* (2014) and Kumar *et al.,* (2015). Luders *et al.,* (2007), Dar *et al.,* (2007), Kumari *et al.,* (2008), Lata *et al.,* (2008), Singh and Kumar (2009), Jebaraj *et al.,* (2010), Reddy *et al.,* (2011) and Motamedi *et al.,* (2014) were reported for brown husk related traits and plant type traits in maize. Kooner *et al.,* (2005), Singhal *et al.,* (2006), Vijayabharathi *et al.,* (2009), Kanagarasu *et al.,* (2010), Lal *et al.,* (2011), Rajitha *et al.,* (2014) and Khan *et al.,* (2016) were reported for grain yield and quality traits. which have shown high sca effects for grain yield involving parents of positive and significant gca effects can be exploited for the development of single cross hybrids since non additive gene action for most of the traits was observed. Further they can also be used for population improvement programme through reciprocal recurrent selection.

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