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## COMBINING ABILITY FOR GRAIN YIELD AND YIELD COMPONENT TRAITS IN MAIZE (*ZEA MAYS L.*)

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## ABSTRACT

Combining ability analysis for yield and its component traits was performed with five lines, nine testers, five checks and the resulting forty five crosses using Line  $\times$  Tester analysis. The analysis of variance indicated significant differences among parents, lines, testers, crosses, lines vs testers and parents vs. crosses for almost all the traits. Combining ability analysis suggested the preponderance of non-additive type of gene action for majority of the traits except days to 50% tasseling, days to 50% silking, internodal distance and cob height. In case of lines 18495(9.00), 18838 (7.48) and testers 18847 (38.61), 18342 (18.15), 18337 (17.45), 18600(10.85) showed good general combining ability. Among the hybrids 18838 $\times$  18850 (33.363), 18838 $\times$ 18627 (33.948) and 18495 $\times$ 18337 (7.362) found to be superior when specific combining ability effects were considered for grain yield per plant. These crosses may of prime importance in breeding programs either towards hybrid maize production or synthetic varieties.

## INTRODUCTION

Maize (*Zea mays* L.), belonging to the family *Poaceae* and tribe *Maydeae*, is one of the most important cereal crops and occupies a prominent position in global agriculture after wheat and rice. Good general combining parent result in higher frequency of heterotic hybrids than poor combining parent. From the genetic point of view, general combining ability measures additive gene effects and specific combining ability measures non additive gene effects, depending on genes with dominance (intra-allelic interactions) and epistasis (inter-allelic interactions).

Line  $\times$  tester (Kempthorne, 1957) analysis gives information on the combining ability status of parental lines. Exploitation of heterosis in maize (*Zea mays* L.) through the cultivation of single cross hybrids is having prime importance and it mainly depends on the development and identification of high *per se* performing, diverse and productive inbred lines. The two parent conventional single cross hybrids practically replaced double cross and three way cross hybrids in most of the developed countries (Mauria *et al.*, 1998). Single cross hybrids are considered most desirable as the breeding and seed production is much easier than the multi-parent hybrids.

An understanding of the gene action and combining ability is an important, well conceived and systematic breeding action for its improvement. Since yield is a complex character and is the result of interaction of various components, the genetics of such yield components, their heritability and combining ability need to be studied. In a hybrid breeding programme, plant breeder generally identify parental lines with good general combining ability, and crosses with high specific combining ability effect. Several workers like, Amiruzzaman *et al.* (2010), Kangarasu *et al.* (2010), Netravati *et al.* (2013), Ali *et al.* (2014) and Rajitha *et al.* (2014) has reported combining ability and gene action on several traits.

Combining ability studies provide information on the relative importance of GCA and SCA variance for interpreting the genetic basis of important traits. This helps us to assess the nature of gene action and in identifying superior parental lines for their *per se* performance. The best combinations with high general combining ability of individual lines are helpful to get more desirable recombinants which enables for further improvement of the crop. Therefore the present investigation was undertaken to access the nature of gene actions involved in the inheritance of grain yield and to identify best general combiner inbred lines and also the best hybrids with high SCA effects which can be exploited directly as single cross hybrid.

## MATERIALS AND METHODS

Five lines were crossed with nine testers evaluated in line  $\times$  tester design to obtain forty five crosses. These fourteen inbreds (five lines and nine testers), forty five crosses were evaluated in simple lattice design with two replications at the Zonal Agricultural and Horticultural research station, University of Agricultural and Horticultural Sciences, Shivamogga, during *kharif* 2014. Each treatment consisted of two rows each of thirteen plants. Normal package of practices were followed to

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raise a healthy crop. Observations were recorded for days to 50% tasseling, days to 50% silking, days to 50% brown husking, stem girth, internodal distance, plant height, cob height, cob length, cob girth, cob weight, number of kernels per row, number of rows per cob, grain yield per plant, 100 kernel weight and shelling percentage. The analysis of variance was carried out for individual as well as over the environments as per the standard procedure (Fisher, 1936). Analysis of general combining ability and specific combining ability was carried out following the method of Kempthorne (1957).

## RESULTS

Analysis of variance for combining ability for yield and yield contributing characters in maize is presented in the Table 1. Further the variation present in the hybrids is partitioned into portions attributable to lines, testers, lines x tester components. The *per cent* contribution towards the total variance was maximum due to the interaction of lines and testers for days to 50% brown husk maturity, stem girth, internodal distance, cob length, cob girth, cob weight, number of kernels per row,

number of rows per cob, grain yield per plant, 100 kernel weight and shelling percentage. While contribution of lines alone was maximum towards the total variance for days to 50 per cent tasseling, days to 50 per cent silking, plant height and cob height (Table 2).

However the ratio of additive variance to the dominance variance was less than one suggested the preponderance of non-additive gene action for majority of the traits except days to 50 per cent tasseling, days to 50 per cent silking, internodal distance and cob height (Table 3). While remaining characters governed by additive gene action.

### Estimates of general and specific combining ability

Among five lines, 18704, 18832 and 18838 were the best general combiners for all characters except number of rows per cob. Among nine testers 18328, 18337, 18342, 18627 and 18850 were the best general combiners for all characters (Table 4). Therefore these lines can be utilized in improvement of the respective traits in any breeding programme wherever hybridization is involved.

All forty five crosses recorded significant sca effect for grain

**Table 1: Analysis of variance for combining ability for fifteen characters**

Source of variation	df	Days to 50% tasseling	Days to 50% silking	Days to 50% brown husk maturity	Stem girth	Internodal distance	Plant height (cm)	Cob height (cm)
Replication	1	0.04444	0.10	0.90	2.05	0.031	3.084	22.09
Crosses	44	27.10**	26.65**	6.57**	7.46**	1.70**	698.63**	428.70**
Females (Lines)	4	126.84**	135.99**	3.72	14.61	1.95	3982.85**	2241.06**
Males (Testers)	8	64.59**	54.48**	10.70	10.36	4.87**	396.11	554.21**
Line × Tester	32	5.26**	6.03**	5.89**	5.84**	0.88	363.73**	170.77**
Error	44	0.090	0.38	0.47	0.093	0.58	7.46	4.42

  

Source of variation	df	Cob length (cm)	Cob girth (mm)	Cob weight (g)	Number of kernels per row	Number of rows per Cob	Grain yield per plant (g)	100 kernel weight (g)	Shelling percentage
Replication	1	0.27	0.042	0.24	0.021	0.32	2.91	0.28	0.65
Crosses	44	14.88**	42.82**	3208.74**	39.80**	5.42**	1451.29**	49.41**	86.32**
Females (Lines)	4	45.56*	42.77	2197.68	50.61	0.32	1083.57	42.76	100.47
Males (Testers)	8	11.55	90.87*	3753.09	47.39	5.19	3084.48*	82.97	165.08*
Line × Tester	32	11.88**	30.81**	3199.03**	36.56**	6.11**	1088.95**	41.85**	64.86**
Error	44	0.12	0.18	0.17	0.084	0.189	0.23083	1.54	0.65

**Table 2: Proportion of contribution of lines, testers and their interaction to total hybrid variance**

Sl. No.	Characters	Contribution of females (%)	Contribution of males (%)	Contribution of females × males (%)
1	Days to 50% tasseling	42.55	43.33	14.12
2	Days to 50% silking	46.39	37.17	16.45
3	Days to 50% brown husk maturity	5.15	29.62	65.23
4	Stem girth (mm)	17.81	25.27	56.92
5	Internodal distance (cm)	10.41	52.02	37.57
6	Plant height (cm)	51.83	10.31	37.86
7	Cob height (cm)	47.52	23.50	28.97
8	Cob length (cm)	27.83	14.11	58.06
9	Cob girth (mm)	9.08	38.58	52.34
10	Cob weight (g)	6.27	21.27	72.50
11	Number of kernels per row	11.56	21.65	66.79
12	Number of rows per cob	0.54	17.43	82.03
13	Grain yield per plant (g)	6.79	38.64	54.57
14	100 kernel weight (g)	7.87	30.53	61.60
15	Shelling percentage	10.58	34.78	54.65

**Table 3: Estimates of variance components as reference to the prevailing gene action for fifteen characters**

Sl. No.	Characters	$\sigma^2_{GCA}$	$\sigma^2_{SCA}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	$\sigma^2_A$	$\sigma^2_D$	$\sigma^2_A/\sigma^2_D$
1	Days to 50% tasseling	6.823**	2.57**	2.65	13.66	2.57	5.32
2	Days to 50% silking	6.77**	2.79**	2.43	13.54	2.79	4.86
3	Days to 50% brown husk maturity	0.49*	2.73**	0.18	0.97	2.73	0.36
4	Stem girth	0.88**	2.86**	0.31	1.77	2.86	0.62
5	Internodal distance	0.21**	0.20*	1.05	0.42	0.20	2.08
6	Plant height (cm)	155.92**	178.56**	0.87	311.84	178.56	1.75
7	Cob height (cm)	99.58	83.63	1.19	199.16	83.63	2.38
8	Cob length (cm)	2.03**	5.89**	0.34	4.06	5.89	0.69
9	Cob girth (mm)	4.59	14.15	0.32	9.18	14.15	0.65
10	Cob weight (g)	212.52	1599.45**	0.13	425.04	1599.45	0.27
11	Number of kernels per row	3.49*	18.24**	0.19	6.99	18.24	0.38
12	Number of rows per Cob	0.19	2.98**	0.06	0.37	2.98	0.13
13	Grain yield per plant (g)	148.84**	544.38**	0.27	297.69	544.38	0.55
14	100 kernel weight (g)	4.41**	20.34**	0.22	8.812	20.34	0.43
15	Shelling percentage	9.45**	32.16**	0.29	18.90	32.17	0.59

yield per plant, the cross 18838X18627 followed by 18838X18850 and 18832X18328 recorded highest significant scaeffect for grain yield per plant. Out of these crosses 18495x18328 for plant height and cob height, 18438x18494 for cob length, 18704x18337 for cob girth, 18838x18337 for number of kernels per row, 18838x18850 for number of rows per cob and grain yield per plant, 18838x18627 for 100 kernel weight and 18704x18328 for shelling percentage were found to be best specific combinations showing favourable sca effects for the characters mentioned (Table 5).

The crosses namely, 18838x18850,18838x18627 and 18495x18337 that's showed high SCA effects for grain yield per plant and these crosses involved parents having significant GCA effects. The gca effects of parents and sca effects of their hybrid combinations indicated that the crosses with high sca effects were resulted due to high x high and low x high gca combinations. Therefore, one can afford to include some low general combiners also along with good combiners in hybridization programmes.

## DISCUSSION

The knowledge of combining ability provides a useful tool for selection of desirable parents for the development of superior hybrids. Thus, the information regarding heterosis, combining ability and nature of gene action are the basic requirement for a thorough understanding of genetic nature of yield and its components.

The estimates of gca effects for yield and yield contributing characters revealed that out of five lines 18704, 18832 and 18838 were the best general combiners for all characters except number of rows per cob. Among nine testers 18328, 18337, 18342, 18627 and 18850 were best general combiners for grain yield per plant and also showed significant positive gca effects for most of the yield contributing characters whereas it also reveals that 18495,18698,18342,18494 and 18600 were best *per se* performers but they were not good combiners. So these parents could be used extensively in hybrid breeding programme aimed at increasing maize grain yields. The high significant positive gca effects for different characters could be helpful in identifying outstanding parents

with favourable alleles for yield and other desirable components.

It is evident that variances due to general combining ability(gca) were significant for most of the studied characters. All the Character showed significant variance due to specific combining ability (sca). However the ratio of additive variance to the dominance variance was less than one suggested the preponderance of non-additive gene action for majority of the traits. Similar results were reported by Kage *et al.* (2013) and Netravati *et al.* (2014) for non-additive gene action.

Among fourteen parents' three lines were best general combiners for all traits except number of rows per cob and five testers were best general combiner for all traits. Due to their good combining ability these lines can be utilized straight away as parents for production of good hybrids by crossing with other divergent lines and can also be employed in the development of synthetic varieties.

All forty five crosses recorded significant sca effect for grain yield per plant, plant height and cob height, cob length, cob girth, number of kernels per row number of rows per cob, 100 kernel weight and shelling percentage were found to be best specific combinations showing favourable sca effects for the characters mentioned. This finding is in the line with that of Amiruzzaman *et al.* (2010), Kangarasu *et al.* (2010), Netravati *et al.* (2013), Ali *et al.* (2014) Rajitha *et al.* (2014) and Khan and Dubey (2015). The specific combining ability, which represents the predominance of non additive gene action, is a major component that may be utilised in heterosis breeding. In the present study, most of the cross combinations with high and significant sca effects also showed very high heterotic effects.

The crosses namely, 18838x18850,18838x18627 and 18495x18337 that's showed high SCA effects for grain yield per plant and these crosses involved parents having significant GCA effects. The gca effects of parents and sca effects of their hybrid combinations indicated that the crosses with high sca effects were resulted due to high x high and low x high gca combinations. Therefore, one can afford to include some low general combiners also along with good combiners in hybridization programmes. These hybrids had combination

**Table 4: Estimates of general combining effects of parents**

Parents Males(Testers)	Days to 50% tassel ing	Days to 50% silking	Days to 50% brown husk maturity	Stem girth (mm)	Internodal distance (cm)	Plant height (cm)	Cob height (cm)	Cob length (cm)	Cob girth (mm)	Cob weight (g)	Number of kernels per row	Number of rows per cob	Grain yield per plant (g)	100 kernel weight (g)	Shelling percentage
<b>Females(Lines)</b>															
18495	3.878**	4.033**	0.389*	0.964**	0.232	25.056**	18.633**	1.127**	-2.219**	5.967**	0.716**	-0.197*	9.005**	-2.267**	-2.514**
18698	-2.289**	-2.411**	0.500**	-1.465**	-0.294	-11.130**	-6.232**	-2.671**	0.968*	-15.422**	-2.653**	0.007	-2.605**	-0.248	-2.147**
18704	-1.011**	-1.411**	-0.611**	-0.055	0.358*	-6.741**	-3.479**	-0.115	1.032**	6.874**	-0.317**	0.082	-7.411**	0.233	3.216**
18832	-2.122**	-1.856**	-0.056	0.199*	0.098	-9.166**	-9.942**	0.422**	-1.021**	-7.774**	0.402**	-0.048	-6.476**	0.233	0.797**
18838	1.544**	1.644**	-0.222	0.358**	-0.394*	1.981**	1.021*	1.237**	1.239**	10.356**	1.852**	0.156	7.487**	2.048**	0.649**
CD at 5% female	0.170	0.320	0.314	0.156	0.328	1.221	0.890	0.152	0.755	0.173	0.129	0.185	0.212	0.517	0.348

**Table 4: Cont...**

Parents Males(Testers)	Days to 50% tassel ing	Days to 50% silking	Days to 50% brown husk maturity	Stem girth (mm)	Internodal distance (cm)	Plant height (cm)	Cob height (cm)	Cob length (cm)	Cob girth (mm)	Cob weight (g)	Number of kernels per row	Number of rows per cob	Grain yield per plant (g)	100 kernel weight (g)	Shelling percentage
18328	0.789**	1.644**	0.767**	-0.228*	-0.581*	13.714**	9.406**	0.470**	3.471**	14.293**	2.406**	-0.144	-2.813**	0.759**	2.806**
18337	3.789**	2.644**	1.867**	0.744**	-0.534*	-0.452	9.539**	0.0037	3.659**	24.559**	2.806**	1.022**	17.454**	2.626**	1.798**
18342	2.489**	2.744**	0.667**	1.893**	-0.874**	-3.085**	0.806	0.170	-0.591	4.126**	2.139**	0.289*	18.154**	-0.341	-9.594**
18494	2.189**	2.144**	0.567**	0.984**	-0.327	-1.885*	0.539	2.040**	0.906	18.959**	-1.372**	-0.544**	-0.613**	1.859**	-2.238**
18600	-1.911**	-1.956**	-0.833**	-1.050**	0.653**	-5.651**	-0.885	-1.997**	0.745	-13.141**	-3.228**	-0.911**	10.854**	-2.174**	0.186
18627	-2.711**	-2.956**	-0.833**	-0.677**	0.693**	5.416**	11.893**	-0.297**	1.446**	11.459**	-2.628**	-0.778**	-4.614**	4.059**	1.630**
18697	0.589**	-0.156	-0.133	-1.195**	-0.407	-6.584**	-3.661**	-0.497**	-0.598	-6.274**	0.483**	-0.278**	-9.779**	1.093**	0.275
18847	-3.211**	-2.656**	-1.333**	-0.369**	1.126**	-2.954**	5.140**	-0.463**	-5.579**	-30.007**	-0.128	1.056**	38.613**	-4.907**	4.561**
18850	-2.011**	-1.456**	-0.733**	-0.102	0.253	1.481	-8.995**	0.537**	-3.459**	-23.974**	-0.478**	0.289*	9.971**	-2.974**	0.580**
CD at 1% male	0.228	0.429	0.421	0.209	0.440	1.638	1.194	0.203	1.013	0.232	0.174	0.248	0.284	0.693	0.468

**Table 5: Performance of top three promising hybrids w.r.t fifteen traits**

Characters	Desirable crosses	Per se performance	sca effects	gca status of parents
Days to 50% tasseling	18698x18847	57.5	-0.511*	Low x High
	18698x18850	58.00	-1.211**	Low x High
	18704x18850	58.00	-2.489**	High x High
Days to 50% silking	18698x18847	58.00	-0.789	Low x High
	18704x18850	58.50	-2.489**	High x High
	18698x18850	59.00	-0.989*	Low x High
Days to 50% brown husk maturity	18704x18328	104.50	-3.489**	High x High
	18495x18697	105.50	0.411	Low x Low
	18704x18600	105.50	-0.889	High x Low
Stem girth (mm)	18704x18494	37.33	1.303*	High x Low
	18838x18494	28.13	-0.178	High x Low
	18495x18328	27.48	1.645**	Low x High
Internodal distance (cm)	18495x18847	11.27	0.415	Low x High
	18698x18627	11.00	1.107*	Low x High
	18495x18600	10.77	0.388	Low x Low
Plant height (cm)	18495x18328	253.00	-2.622	Low x High
	18495x18847	252.67	13.711**	Low x High
	18832x18328	252.50	31.100**	High x High
Cob height (cm)	18495x18328	129.50	1.000	Low x High
	18495x18337	129.00	0.367	Low x High
	18495x18847	128.34	4.101**	Low x High
Cob length (cm)	18438x18494	25.53	2.127**	High x Low
	18495x18494	25.02	1.919**	Low x Low
	18838x18850	25.00	3.297**	High x High
Cob girth (mm)	18704x18337	57.00	3.554**	High x High
	18832x18328	56.50	5.296**	High x High
	18698x188337	56.34	2.960*	Low x High
Cob weight (g)	18838x18850	308.00	84.678**	High x High
	18832x18328	305.00	25.441**	High x High
	18838x18627	300.00	41.244**	High x High
Number of kernels per row	18838x18337	47.00	-60.856**	High x High
	18704x18342	46.00	43.059**	High x Low
	18704x18328	45.50	-11.107**	High x High
Number of rows per cob	18838x18850	19.00	5.564**	High x High
	18838x18697	18.00	2.944**	High x Low
	18832x18337	18.00	1.848**	High x High
Grain yield per plant (g)	18838x18850	233.00	33.363**	High x High
	18838x18627	222.00	36.948**	High x High
	18495x18337	216.00	7.362**	Low x High
100-kernel weight (g)	18838x18627	45.50	5.562**	High x High
	18832x18328	43.50	8.667**	High x High
	18838x18697	42.00	5.018**	High x Low
Shelling percentage	18704x18328	94.84	3.194**	High x High
	18495x18627	93.36	4.700**	Low x High
	18838x18600	93.31	6.851**	High x Low

of parents with low x low, low x high, high x low and high x high gca effects. These also had considerably high sca effects. Thus, these can be directly used as hybrids.

This holds true for the hybrids, which were obtained from high x high gca effect parent combinations. But these high yielding hybrids obtained from high x low gca effects and also low x high gca effects which indicates that even though the individual lines have less gca effects but when they are crossed, the gene contributing for grain yield from female and male combines well with each other without any negative effects. Thus low x low gca effect hybrids show higher yield when compared to high x high hybrids. These results were supported by Kangarasu *et al.* (2010), Kage (2012) and Netravati *et al.* (2013).

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