

UTILIZATION OF LINE X TESTER MODEL FOR EVALUATING COMBINING ABILITY OF SOME MAIZE INBRED LINES

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ABSTRACT

Combining ability for grain yield and its contributing characters was carried out in maize through line × tester analysis of 45 hybrids developed by crossing 15 females and 3 testers along with three checks. The 45 hybrids along with 18 parents and three standard checks were grown in randomized block design with three replications and were evaluated for seed yield and its ten yield contributing characters. The experiments were conducted at Agricultural Research Station farm, Madhira of PJTS Agricultural University, Hyderabad during kharif 2015. The analysis of variance indicated the presence of significant variability among the genotypes for most of the quantitative traits studied. Combining ability analysis showed the predominant role of non-additive gene action for inheritance of most of the characters studied. For ear length, MRC 1070 × BML 7, MRC 1081 × BML 7, MRC 1095 × BML 5, MRC 1132 × BML 13 and MRC 1157 × BML 13 recorded significant positive sca effects. For number of kernels per row, the lines viz., MRC 1081, MRC 1134, MRC 1148 and MRC 1157 and for test weight, the lines MRC 1058, MRC 1091, MRC 1104, MRC 1117, MRC 1125, MRC 1134 and the BML 13 had significant gca effects. For test weight, five crosses viz., MRC 1095 × BML 5 (L×L), MRC 1125 × BML 5 (H×L), MRC 1081 × BML 7 (L×H), MRC 1134 × BML 7 (H×H) and MRC 1117 × BML 13 (H×L) were identified as top specific combiners showing positive sca effects. Five crosses viz., MRC 1132 × BML 5 (L×L), MRC 1150 × BML 5 (H×L), MRC 1150 × BML 7 (H×L), MRC 1070 × BML 13 (H×H) and MRC 1081 × BML 13 (H×H) showed significant sca effects for grain yield per plant. Further, the promising single cross hybrids having a parental combination of high × high, high × low gca effects could be used for the improvement of parental lines for desired characters by selecting in advanced generations.

Key Words: Maize and Agricultural

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important crops in world agricultural economy and ranks third next to wheat and rice in production. It is a versatile crop with wider genetic variability and able to grow successfully throughout the world covering tropical, subtropical and temperate agro-climatic conditions. Given the great economic importance of maize, genetic breeding in this crop is very intense and mostly targeted at increasing grain yield. A frequent method used in maize breeding is to obtain inbred lines that are later crossed in order to develop different types of hybrids, which exhibit high heterosis when the inbred lines are complementary. Combining ability analysis is one of the powerful tools in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate productive genes (Sprague and Tatum, 1942). It also helps to understand the genetic architecture of various characters that enable the breeder to design effective breeding plan for future improvement of the existing materials (Kempthorne, 1957). Thus a study was undertaken to estimate the nature and magnitude combining ability in the newly developed lines to evaluate their potential to be exploited in yield heterosis.

MATERIALS AND METHODS

The present study was conducted at Agricultural Research Station farm, Madhira of PJTS Agricultural University, Hyderabad during kharif 2015 season. Fifteen selected inbred lines (MRC 1058, MRC 1070, MRC 1081, MRC 1091, MRC 1095, MRC 1104, MRC 1117, MRC 1119, MRC 1125, MRC 1132, MRC 1134, MRC 1144, MRC 1148, MRC 1150 and MRC 1157) were crossed to three testers (BML 5, BML 7 and BML 13) in line × tester mating design kharif 2014 to generate 45 F₁s for this study. All the eighteen parents (15 lines and 3 testers) together with 45 crosses and three standard checks (DHM 117, 30 V 92 and 900 M Gold) were evaluated during kharif 2015. Each genotype was grown in two rows of two meters length keeping row-to-row and plant to plant distance of 60 and 20 cm, respectively following randomized block design with three replications. The recommended packages of cultural practices, fertilizer levels and protection measures were followed to raise good crop. The data were recorded on days to 50% tasseling, days to 50% silking, days to maturity, plant height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, test weight (g) and seed yield per plant (g). Mean values

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of the ten quantitative characters recorded on the hybrids and parents were subjected to statistical analysis and variances were estimated following the method of Panse and Sukhatme (1961). The mean data of quantitative characters recorded on all the genotypes are subjected to the analysis of variance (ANOVA). Treatments might be only line x tester hybrids or line x tester hybrids and parents. The combining ability analysis was done according to the procedure developed by Arunachalam and Bandopadhyaya (1979).

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed significant variation among parents and hybrids in respect of 10 characters, thereby indicating the presence of sufficient variability and justifying the appropriateness of genetic material which has been involved in the study. Highly significant mean square variances for almost all the characters were also observed in case of lines and testers, which indicated the significance of additive variance and significance of mean sum of squares for line × tester indicate the significance of dominance variance.

Table 1: Analysis of variance (line x tester) for grain yield and its component characters in maize (*Zea mays L.*)

	df	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear length (cm)	Ear girth (cm)	No of kernel rows	Number of kernels per row	Test weight (g)	Yield per plant (g)
Replicates	2	2.163	13.400**	12.474*	985.171**	5.693	0.025	0.880	19.010*	3.071	104.120
Crosses	44	12.302**	10.070**	9.762**	1054.858**	8.577**	1.560**	2.834**	32.492**	10.670**	519.818**
Line effect	14	13.077	12.648*	15.426*	1541.168*	8.409	2.188	4.863**	71.513**	16.802**	546.252
Tester effect	2	46.496*	52.356**	6.452	4432.642**	61.571**	1.436	4.583	6.674	37.443**	1227.621
Line x Tester effect	28	9.472**	5.760**	7.166**	570.432**	4.876*	1.255**	1.695**	14.825**	5.692	456.043**
Error	88	1.527	1.703	2.747	195.332	2.568	0.535	0.564	4.909	1.372	101.857
Total	134	5.074	4.625	5.195	489.353	4.588	0.864	1.314	14.177	4.450	239.132

The analysis of variance for combining ability revealed that the variances due to sca were highly significant than variances due to gca for most of the characters viz., days to 50% flowering, days to maturity, ear girth, number of kernel rows per year, number of kernels per row and seed yield per plant. This indicated the predominance of non additive gene action and preponderance of dominant gene effects for these traits. For characters viz., days to 50% silking, plant height, ear length and test weight, lower values for degree of dominance indicated the preponderance of additive gene effects. The ratio of gca to sca variance was less than the unity for all the traits. The higher sca variance revealed the predominance of non additive genetic variance. Also from the estimates of additive and dominance variance, it was observed that dominance variance was predominant for all the characters which suggested the predominance of non-additive gene action in the inheritance of those characters. Similar results indicating preponderance of non additive gene action were also reported earlier by Sumalini and Shoba Rani (2011), Kumar et al., (2012), Ajay Singh et al., (2013) and Aminu et al., (2014a).

Among the parents with significant gca effects, the ones with higher magnitude of gca effects were considered as superior to those with lower magnitude. MRC 1070, MRC 1081, MRC 1132, MRC 1134, MRC 1148 and MRC 1150 among lines and BML 7 and BML 13 among testers had significant gca effects in desirable direction for maturity characters like days to 50% tasselling and days to 50% silking. Jagadish Kumar et al., (2010), Bhavana et al., (2011), Abrha et al., (2013), Hemalatha et al., (2013) and Lahane et al., (2014) also reported non additive gene effects and good combiners for maturity characters. For days to maturity, the lines viz., MRC 1081, MRC 1095, MRC 1104 and MRC 1117 were found to be good general combiners in the material under study. The lines MRC 1058, MRC 1081, MRC 1095, MRC 1119, MRC 1132 and MRC 1148 and among testers, BML 5 were good general combiners for plant height, the results of which are in accordance with the earlier findings of Jagadish Kumar et al., (2010), Ram Reddy et al., (2011) and Ajay Singh et al., (2013) reported non additive gene action and predominant role of gca effects for this trait.

For ear characters like ear length and ear girth, lines MRC 1119, MRC 1134, MRC 1144 and MRC 1148 among lines and BML 13 among testers have positive significant gca effects suggesting their ability to transmit additive genes in desirable direction for the traits under study (Table 2). The parents viz., MRC 1058, MRC 1070, MRC 1091, MRC 1119, MRC 1148 and BML 7 had significant gca effects for number of kernel rows indicating them to be good sources of favorable genes for increased number of kernel rows per year. For number of kernels per row, the lines viz., MRC 1081, MRC 1134, MRC 1148 and MRC 1157 and for test weight, the lines MRC 1058, MRC 1091, MRC 1104, MRC 1117, MRC 1125, MRC 1134 and the BML 13 had significant gca effects in desirable positive direction indicating them to be good general combiners for those traits. Bhavana et al., (2011), Singh et al., (2013) and Kumar et al., (2013) reported additive gene effects for ear characters. Rama Reddy et al., (2011),

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Sumalini and Shoba Rani (2011), Kumar et al., (2012) and Govind et al., (2013) reported non additive and additive gene effects and significant gca effects for kernel rows per cob, ear diameter and test weight. The lines MRC 1070, MRC 1081, MRC 1134 and MRC 1150 and the BML 7 were found to be good general combiners for grain yield per plant as indicated by positive significant gca effects in desirable direction for that trait. Ram Reddy et al (2011), Sumalini and Shoba Rani (2011), Singh et al., (2010), Abrah et al., (2013) reported additive and non additive gene effects and good combiners for grain yield per plant.

Table 2: Estimates of general combining ability for grain yield and its component characters in maize (*Zea mays* L.)

Lines	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear length (cm)	Ear girth (cm)	No of kernel rows	Number of kernels per row	Test weight (g)	Seed yield/plant (g)
MRC 1058	0.430	0.178	-0.237 **	19.841**	0.366	-1.225**	0.537 **	1.986	1.398**	7.563
MRC 1070	1.652**	1.400**	0.207	-6.136**	1.245*	0.318 *	0.954 **	0.514	1.974	14.355**
MRC 1081	1.096*	0.956*	-1.459 **	25.993	0.760	-0.022**	-0.546**	2.81 *	0.126	7.940**
MRC 1091	-1.1015	-1.267	0.652	-4.277**	0.149	0.426*	0.676 **	0.709	1.947**	-8.128**
MRC 1095	-0.459	0.511	1.126 **	8.285**	0.443	-0.568**	-0.824**	-0.153**	-0.662**	-3.048
MRC 1104	-1.238	-1.044 **	1.570**	3.854	0.361	-0.055**	-0.379**	-1.486**	1.526 **	-5.234**
MRC 1117	0.207	-0.156**	2.904**	11.963	0.036	0.088	0.093	-0.375**	1.011 *	4.148
MRC 1119	-2.237	-2.378**	1.763 *	15.803**	0.291**	0.800 **	0.439 *	-1.180**	0.056	4.242
MRC 1125	-1.570	-1.267**	1.096	11.005	-0.304**	0.256	0.232	1.847	2.073**	-6.057
MRC 1132	0.874*	0.622	0.763	15.526	-0.487**	0.049	-0.319**	0.847	-0.800**	-6.449
MRC 1134	0.874*	1.178*	0.652	5.296	2.291**	0.388**	-0.821**	2.733**	2.572**	12.118
MRC 1144	0.096	-0.044**	0.207	-3.285**	1.195*	0.173**	-0.282**	-1.458**	0.491	-1.646**
MRC 1148	0.874*	0.511	1.652*	19.007**	1.067**	0.280**	1.005**	4.569**	-0.743**	-4.721
MRC 1150	1.541**	1.844**	-0.570**	5.309	1.000	0.289*	-1.476**	6.865**	0.342	11.421**
MRC 1157	-1.126	-1.044**	-0.874**	-2.313**	-1.114**	0.484**	0.703	3.625**	-0.475**	-2.288**
Testers										
BML 5	-1.148	-1.244**	-0.437**	11.442**	-0.541**	-0.107**	0.256	-0.432**	-0.695**	-4.615**
BML 7	0.785**	0.578**	0.207	5.162	-0.801**	-0.107**	0.101**	0.123	-0.338**	-1.055**
BML 13	0.363**	0.667**	0.230	6.280	1.342**	0.206	-0.357**	0.308	1.033**	5.670**
Degree of dominance	1.117	0.784	1.499	0.786	0.592	1.569	1.092	1.150	0.873	1.426

*Significant at $P=0.05$ level, **Significant at $P=0.01$ level

Among hybrids with significant sca effects, the ones with high magnitudes were considered as superior to others. The hybrids from different combinations of parents with high/low gca effects are referred as H×H (High × High), H×L (High × Low) and L×L (Low × Low) combinations. For days to 50% tasselling and days to 50% silking, the hybrids, MRC 1117 x BML 7 and MRC 1150 x BML 13 were found to have high sca effects involving parents with L x H and H x H combinations. One out of 45 hybrids ie., MRC 1104 x BML 7 showed negative significant sca effect for days to maturity involving parents with H x L gca effects for that character indicating that such parental combination will give rise to hybrids with lesser number of days for maturity. Such parental combination revealed the significance of non-additive genetic variance in the inheritance of earliness to maturity (Table 3). Kumar et al., (2010), Sumalini and Shoba Rani (2011) and Abrah et al., (2013) also reported similar results. With respect to plant height, out of 45 crosses, 5 crosses viz., MRC 1081 x BML 5, MRC 1091 x BML 13, MRC 1104 x BML 7, MRC 1132 x BML 5 and MRC 1157 x BML 7 recorded significant negative sca effects, whereas only one cross viz., MRC 1134 x BML 7 showed positive significant sca effect for this trait. Kumar et al., (2010), Bhavana et al., (2011) and Abrah et al., (2013) also reported good specific combiners for this trait.

For ear length, 5 out of 45 crosses viz., MRC 1070 x BML 7, MRC 1081 x BML 7, MRC 1095 x BML 5, MRC 1132 x BML 13 and MRC 1157 x BML 13 recorded significant positive sca effects in desirable direction involving parents with HxL, LxL, LxL, LxH and LxH combining ability for this trait. Predominant involvement of non-additive gene action for good specific combining ability status was observed in the inheritance of this trait (Table 3). The hybrid MRC 1070 × BML 7 (H×L) with over dominance and epistasis gene action variance was the top of the few good specific combiners for ear length. The hybrid MRC 1058 × BML 13 (L×L) recorded the highest significant positive sca effects followed by MRC 1070 × BML 13 (H×L), MRC 1134 x BML 7 (H×L) and MRC 1157 x BML 7 (H×L) for ear girth. For number of kernel rows per ear, crosses MRC 1150 × BML 5 (L×L), MRC 1119 × BML 7 (L×H) and MRC 1081 × BML 13 (L×L) were the top three specific combiners with sca effects in

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positive direction. For the trait, number of kernels per row, three crosses viz., MRC 1132 x BML 5, MRC 1117 x BML 7 and MRC 1150 x BML 7 showed positive significant sca effects involving the parents with HxL, LxL and HxL combining ability estimates, respectively. It was found that very less proportion of over dominance and epistasis gene action variance indicated the importance of non-additive gene action in the inheritance of this character.

Table 3: Estimates of specific combining ability for grain yield and its component characters in maize (*Zea mays* L.)

SCA effects	Days to 50% tasselling			Days to 50% silking			Days to maturity			Plant height (cm)		
	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13
Parent	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13
MRC 1058	-1.630*	0.104	1.526*	-0.756	0.089	0.667	-0.452	1.904	-1.452	13.637	-2.301	-11.335
MRC 1070	-0.185	-1.785*	1.970**	0.022	-1.133	1.111	0.104	0.126	-0.23	-11.651	2.745	8.907
MRC 1081	1.370	-0.230*	-1.141	1.133	-1.022	-0.111	-1.563	-0.207	1.77	-19.697 *	12.932	6.765
MRC 1091	1.815*	-0.785*	-1.030	1.022	-0.800	-0.222	0.659	1.015	-1.674	7.597	10.052	-17.649*
MRC 1095	1.593*	-1.341*	-0.252	0.911	-1.244	0.333	-0.896	0.126	0.77	6.081	7.393	-13.474
MRC 1104	1.037	0.104	-1.141	0.800	-1.022	-0.778	2.215 *	-4.763 **	2.548	1.275	-0.995	-0.28
MRC 1117	-2.407**	4.326**	-1.919 *	-1.756*	2.756**	-1.000	-0.119	-0.096	0.215	6.127	-5.904	-0.222
MRC 1119	-1.296	0.437	0.859	-0.867	0.644	0.222	-0.785	-0.096	0.881	-6.068	-1.005	7.073
MRC 1125	0.370	-0.230	-0.141	0.022	0.200	-0.222	0.215	0.57	-0.785	11.744	-13.563	1.819
MRC 1132	0.926	0.659	-1.585 *	0.800	0.978	-1.778*	-0.785	-0.43	1.215	-20.213 *	-5.834	26.048**
MRC 1134	0.259	-1.007	0.748	1.244	0.089	-1.333	0.326	0.348	-0.674	-15.143	23.836 **	-8.692
MRC 1144	0.370	-0.896	0.526	0.133	-1.356	1.222	-0.896	0.459	0.437	11.081	-1.357	-9.724
MRC 1148	-1.407	0.993	0.415	-2.089**	1.089	1.000	0.326	0.681	-1.007	3.47	2.699	-6.169
MRC 1150	-2.074**	-1.007	3.081**	-1.422**	-0.911	2.333**	1.215	0.904	-2.119	4.07	-10.118	6.048
MRC 1157	1.259	0.659	-1.909*	0.800	0.644	-1.444*	0.437	-0.541	0.104	7.692	-18.579 *	10.887
GCA/SCA	0.047	0.021	0.004	0.089	0.019	0.024	0.015	0.001	0.002	0.07	0.016	0.021

SCA effects	Ear length (cm)			Ear girth (cm)			No. of kernel rows			No. of kernels per row		
	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13
Parent	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13
MRC 1058	5.213	3.743	-8.956	0.334	-1.023	0.688*	0.549	0.288	-0.837	-0.457	-1.929	2.386
MRC 1070	-6.139	14.338 **	-8.199	-0.626	-0.009	0.635*	0.466	-1.212 **	0.746	-2.568 *	0.793	1.775
MRC 1081	-5.554	10.352 *	-4.798	0.254	-0.003	-0.252	-1.201 **	0.121	1.08*	-2.364	2.054	0.309
MRC 1091	1.731	5.541	-7.272	-0.427	0.416	0.01	-0.756	0.066	0.691	-1.763	1.099	0.664
MRC 1095	10.666 *	-0.661	-10.004*	-0.449	1.211	-0.762	-0.423	-0.434	0.857	-0.402	1.793	-1.392
MRC 1104	-9.580 *	1.286	8.294	0.288	-0.553	0.265	-0.201	-0.212	0.413	0.932	-1.04	0.108
MRC 1117	2.629	-1.695	-0.934	-0.689	0.397	0.292	-0.59	-0.101	0.691	-0.929	2.515 *	-1.586
MRC 1119	-1.547	3.153	-1.606	0.242	0.098	-0.341	-0.353	1.052 *	-0.699	-0.874	-0.346	1.219
MRC 1125	2.554	-2.869	0.315	0.353	-0.707	0.354	0.271	0.177	-0.448	0.098	-0.207	0.108
MRC 1132	3.127	-12.417 **	9.29*	0.6	-1.08	0.480*	0.435	-0.447	0.012	4.098 **	-2.707 *	-1.392
MRC 1134	-6.57	4.783	1.787	-0.296	0.614*	-0.318	0.157	0.396	-0.553	2.355	-1.71	-0.645
MRC 1144	-0.288	-2.808	3.096	0.196	-0.062	-0.134	-0.299	0.19	0.109	0.237	-2.485	2.247
MRC 1148	-1.343	-0.64	1.984	0.446*	0.155	-0.601	0.248	0.07	-0.318	-1.318	1.127	0.192
MRC 1150	3.639	-10.158 *	6.519	0.533*	-0.064	-0.47	1.229 **	-0.239	-0.99*	1.134	3.025 *	-4.159
MRC 1157	1.462	-11.948 *	10.486*	-0.761	0.608*	0.153	0.467	0.286	-0.753	1.821	-1.985	0.164
GCA/SCA	0.167	0.027	0.018	0.004	0.002	0.015	0.012	0.003	0.018	0.004	0	0.002

SCA effects	Test weight (g)			Yield per plant (g)		
	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13
Parent	BML 5	BML 7	BML 13	BML 5	BML 7	BML 13
MRC 1058	-0.029	0.913	-0.884	-11.859 *	5.004	6.856
MRC 1070	-0.742	0.021	0.72	-5.965	-9.248	15.213*
MRC 1081	-2.647 **	1.452 *	1.195	-19.346 **	5.49	13.856*
MRC 1091	-0.517	0.026	0.492	-10.818	1.735	9.083
MRC 1095	1.387 *	-1.303	-0.084	-0.712	-2.702	3.413
MRC 1104	0.943	-1.331 *	0.388	-2.409	-5.8	8.209
MRC 1117	-2.018 **	0.044	1.974**	-1.74	-5.887	7.628
MRC 1119	-0.31	0.199	0.112	-2.558	9.002	-6.443
MRC 1125	2.518 ***	-1.266	-1.253	4.394	9.84	-14.234*
MRC 1132	-0.02	-0.304	0.325	15.280 **	-13.524 *	-1.756
MRC 1134	0.247	2.007 **	-2.254**	8.028	3.638	-11.667*
MRC 1144	0.495	-1.106	0.61	5.036	-9.774	4.738
MRC 1148	-0.162	0.438	-0.276	-0.602	6.235	-5.633
MRC 1150	0.497	0.913	-1.411*	16.586 **	12.606 *	-29.192**
MRC 1157	0.357	-0.703	0.346	6.685	-6.615	-0.07
GCA/SCA	0.022	0.008	0.065	0.016	0.001	0.016

*Significant at P=0.05 level, **Significant at P=0.01 level

For test weight, five crosses viz., MRC 1095 x BML 5 (LxL), MRC 1125 x BML 5 (HxL), MRC 1081 x BML 7 (LxH), MRC 1134 x BML 7 (HxH) and MRC 1117 x BML 13 (HxL) were identified as top specific combiners showing positive sca effects. Kumar et al. (1998) and Mohammad (1993) reported good specific combiners for this trait. Out of 45 crosses studied for sca effects for grain yield per plant, five crosses viz., MRC 1132 x BML 5 (LxL), MRC 1150 x BML 5 (HxL), MRC 1150 x BML 7 (HxL), MRC 1070 x BML 13 (HXH) and MRC 1081 x BML 13 (HxH) showing significant sca effects were in positive desirable direction. The predominance of over dominance,

epistasis and non-additive gene action were observed in the inheritance of this trait (Table 3). Kumar et al., (2012) and Govind et al., (2013) stressed the importance of sca variance for grain yield per plot and reported good specific combiners for this trait. In most of the cases significantly higher sca effects were associated with high heterosis for different characters.

The present study provided combining ability information on few inbred lines. The promising lines have to be maintained and used in hybridization program. On the other hand, the promising single crosses need to be tested across locations and seasons to fix the desirable characters through advanced selection generations.

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