Asian Journal of
Plant Sciences

Genetic Analysis of Yield Traits in Local and Cimmyt Inbred Line Crosses Using Line×Tester Analysis in Maize (*Zea mays* L.)

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Abstract: The present study was undertaken to characterize the genetic architecture of various local and CIMMYT inbred line crosses using Line×Tester design. The material was generated at Winter Maize Nursery, Amberpet, Hyderabad 2004-2005. The parental lines (15), testers (3) and test crosses (45) were evaluated at two diverse locations of Kashmir valley namely Larnoo and Wadura during 2005. The analysis of variance revealed significant mean squares due to progenies, crosses and parents v/s crosses for all traits. G×E interaction was significant for all traits except ear diameter and 100-seed weight. The analysis for combining ability revealed significant variances due to GCA and SCA for all traits with preponderance of latter. Correspondingly the estimates of genetic components of variance also revealed predominance of non-additive component. The present study identified various parents and crosses in terms of *per se* performance and GCA and SCA estimates. The implications on maize breeding in light of results of present study have been discussed.

Key words: Maize, line×tester, GCA, SCA, additive component, non-additive component

INTRODUCTION

Maize is an important cereal crop of the world. Its cultivation extends over a wide range of geographical and environmental conditions ranging from 58°N to 40°S. It is the staple food of over 200 million people in developing countries in Asia, Latin America and Africa. In India, maize is grown over an area of 7.42 million ha with production of 14.72 million tones and productivity of 1983 kg ha^{-1} (Anonymous, 2005).

Maize possesses superb genetic diversity and enormous biological diversity which justifies the attention it continues to enjoy from geneticists and plant breeders. In fact, maize has been subjected to extensive genetic studies than any other crop (Hallauer and Miranda, 1988). Maize breeders have used several biometrical techniques to study the genetic architecture of quantitative traits including grain yield. The general conclusion from such studies have bean that great bulk of genetic variance is additive, followed by dominance whereas epistasis is of little importance (Beck *et al.*, 1990; Zaffar, 1999; Kumar *et al.* 2005). The estimates of genetic components of variance help predict expected genetic gain from selection, thereby allowing comparison among breeding methods for optimizing management of available genetic variability. Amongst a large array of biometrical procedures for relative estimation of genetic components, line×tester is an efficient procedures as it allows for inclusion of a large number of lines and provides reliable estimates of genetic components, estimates of combining ability and gene action governing a complex trait. The present investigation was undertaken to characterize local and exotic germplasm lines of white maize in terms of their combining ability and the gene effects for various quantitative traits.

MATERIALS AND METHODS

The material for present investigation was developed at winter maize nursery, Amberpet, Hyderabad during 2004-2005. Fifteen white maize inbred lines including

Table 1: Parental lines used in the present study

Line	Source
WI-9	Inbred line developed at Maize Research Station, Pahalgam SKUAST-K
W-6	-do-
W-7	-do-
GLET-7	Selection from Global Line Evaluation Trail material
GLET-27	-do-
CML-77	CIMMYT
CML-79	-do-
CML-111	-do-
CML-138	-do-
CML-173	-do-
CML-213	-do-
CML-214	-do-
CML-240	-do-
CML-244	-do-
CML-463	-do-
Testers	
W$_3$	Elite inbred line developed at Maize Research Station, Pahalgam SKUAST-K
W$_5$	-do-
W$_3$×W$_5$	High yielding hybrid with yield potential of 67 q ha^{-1} released as 'Shalimar Hybrid Maize-I"

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three local (WI-9, W-6 and W-7) and twelve exotic
(GLET-7, GLET-27, CML-77, CML-79, CML-111, CML-138,
CML-173, CML-213, CML-214, CML-240, CML-244 and
CML-463) were crossed to three testers W_3, W_5 and
$W_3 \times W_5$ in a line×tester fashion. The tester genotypes
were developed at maize Research Station, Pahalgam. The
inbred testers W_3 and W_5 were elite inbred lines with
good combining ability whereas, $W_3 \times W_5$ was a promising
high yielding hybrid released by SKUAST-K. The source
of germplasm lines used is given in Table 1. The parents
(both lines and testers) and test crosses, (63 entries in all)
were evaluated at two diverse locations in Kashmir valley
viz., high altitude Rice Research Station, Larnoo and
Regional Research Station, Wadura which represents
distinct climatic regions. The design used was RBD with
three replications at each location. Each genotypes was
represented by two rows of 2 m length with inter and
intra-row spacing of 65 and 20 cm, respectively. Data was
recorded on six quantitative traits including grain yield
plot-1, 100-seed weight, kernel rows ear^{-1}, ear length, ear
diameter and plant height, from 10 randomly selected
competitive plants from each replications. The data was
analysed as per line×tester procedure of Singh and
Chowdary (1999) using WINDOSTAT software.

RESULTS

The pooled analysis of variance (Table 2) revealed
significant mean squares due to progenies, lines, testers,
crosses and parents v/s crosses for all traits except kernel

rows ear^{-1} for which mean squares due to lines was non-
significant, indicating substantial variability in parental
lines for these traits. Environmental component was
significant for all traits but progenies×environment
interaction was non-significant for ear diameter and 100-
seed weight. Comparatively mean squares due to testers
was greater than lines for all traits except 100-seed weight.
The analysis of variance for combining ability (Table 3)
revealed significant variances due to GCA and SCA with
greater magnitude of latter. Correspondingly the
dominance variance was greater than additive component
for all traits. The degree of dominance was in the range of
over dominance for all traits.

The estimates of general combining ability (Table 4)
revealed that the parents, CML-244, CML-79 and
CML-214 were good general combiners for grain yield.
CML-214 was a good general combiner for all traits. For
100-seed weight GLET-27 was the best general combiner
followed by CML-210 and CMl-79. For kernel row ear^{-1}
CML-214, W-7 and CML-244 were good general combiner.
For ear length CML-214, W-6 and CMl-111 were good
general combiners for plant height, CML-463, CML-214
and GLET-27 were best general combiners in order of
merit. Among testers, W_3 was a good general combiner
for plant height and grain yield while as W_5 was a good
general combiner for ear length, kernel rows ear^{-1} and
100-seed weight and $W_3 \times W_5$ was a good combiner for ear
diameter and grain yield.

The best crosses identified on the basis of per se
performance and SCA effects are presented in Table 5. For

Table 2: Analysis of variance pooled over environments for six quantitative traits in maize

Source	df	Plant height (cm)	Ear length (cm)	Ear diameter (cm)	Kernel rows ear^{-1}	100-seed weight (g)	Grain yield plot^{-1} (g)
Environment	1	64194.38**	251.66**	10.61**	2.19**	538.80**	62.61**
Replicates	2	112.41	3.77**	0.25*	0.03	11.93*	0.28**
Progenies	62	1328.81**	12.23**	0.80**	3.77**	39.62**	1.70**
Lines	14	582.54**	2.36**	0.25*	0.79	12.59*	0.19**
Testers	2	4044.38**	51.99	2.07**	1.40**	9.78	2.36**
Crosses	44	418.16*	17.53**	0.55**	2.44**	25.79**	1.25**
Parents v/s crosses	1	44963.85**	402.79**	17.94**	110.14**	1064.74**	43.10**
Progenies×environment	62	650.24**	4.34**	0.09	1.14**	10.82	0.40**
Pooled error	248	211.19	0.98	0.12	0.44	5.98	0.07

*,**, Significant at 5 and 1% level of significance, respectively

Table 3: Pooled Analysis of variance for combining ability in a line×tester analysis in maize

Source of variation	Plant height (cm)	Ear length (cm)	Ear diameter (cm)	Kernel rows ear^{-1}	100-seed weight (g)	Grain yield plot^{-1} (g)
σ^2 line	12.067**	1.131**	0.043**	0.216**	0.793**	0.091**
σ^2 tester	0.776	0.262	0.006*	0.050*	0.192**	0.028**
σ^2 GCA	4.364**	0.406**	0.012**	0.077**	0.293	0.039**
σ^2 SCA	40.116**	2.180**	0.055**	0.155**	2.763**	0.108**
σ^2 GCA×E	11.360**	0.009	0.001	0.062*	0.312**	0.002
σ^2 SCA×E	67.444**	1.103**	0.010	0.198**	0.103**	0.016
σ^2 e	2.071	0.190	0.002	0.026	0.019	0.009
σ^2 A	14.456	1.627	0.048	0.309	1.171	0.155
σ^2 D	168.464	8.723	0.220	0.620	11.054	0.434
Degree of dominance	3.031	2.315	2.144	1.415	3.072	1.672
Predictability ratio	0.183	0.271	0.303	0.498	0.174	0.419
2 σ^2 GCA/(2 σ^2 + SCA)						

*,**, Significant at 5 and 1% level of significance, respectively

Table 4: Pooled estimates of general combining ability effects of lines and testers in a line×tester analysis in maize

Parent	Plant height (cm)	Ear length (cm)	Ear diameter (cm)	Kernel rows ear^{-1}	100-seed weight (g)	Grain yield plot^{-1} (g)
Lines						
WI-9	-6.652**	-1.273*	0.081	-0.179	0.044	-0.604**
W-6	-10.707**	1.659*	-0.006	0.319	0.044	-0.228
W-7	-3.874*	0.404	-0.025	0.902**	0.378	-0.093
GLET-7	3.626*	-1.543*	0.157	0.270	0.682*	-0.135
GLET-27	3.848*	0.599	-0.010	-0.082	2.031**	0.239
CML-77	-3.763*	0.776	-0.112	0.081	0.161	0.157
CML-79	-3.096	0.277	0.172	0.200	0.743*	0.316*
CML-111	-2.374	1.232*	0.158	-0.290	-0.269	0.209
CML-138	3.737*	0.511	0.244*	0.060	-0.257	0.072
CML-173	2.848	-0.842	-0.163	0.421	-1.148**	-0.032
CML-213	2.737	0.475	0.073	0.140	1.078**	0.079
CML-214	4.715	1.991**	0.512**	1.021**	0.525*	0.292*
CML-240	2.015	0.406	-0.251*	-0.445	0.644*	-0.348*
CML-244	2.570	0.165	0.031	0.623*	-0.217	0.557**
CML-463	5.348*	-1.516*	-0.381	-0.600*	-3.154	-0.478**
Testers						
W$_3$	0.915*	-0.608**	-0.082**	-0.269**	-0.569*	0.146*
W$_5$	-1.307*	0.362	0.020	0.152*	0.529*	-0.048
W$_3$×W$_5$	0.393	0.246	0.080**	0.041	0.041	0.194**

*,**, Significant at 5 and 1% level of significance, respectively

Table 5: Best crosses identified on the basis of *per se* performance and SCA effects in maize

Crosses	*Per se* performance	SCA effects
Plant height (cm)	CML-244×W$_5$ (227.50)	CML-213×W$_5$ (12.050**)
	CML-263×W$_3$ (221.66)	CML-77×W$_5$ (12.19**)
	CML-244×(W$_3$×W$_5$) (219.33)	CML-79×W$_5$ (10.53**)
Ear length (cm)	CML-240×W$_3$ (18.50)	CML-213×W$_3$×W$_5$) (3.39**)
	CML-240×W$_5$ (18.45)	CML-77×W$_5$ (2.94**)
	W-7×(W$_3$×W$_5$) (17.9)	W-7×(W$_3$×W$_5$) (2.23**)
Ear diameter (cm)	CMl-240×(W$_3$×W$_5$) (4.95)	W-7×(W$_3$×W$_5$) (0.46**)
	CML-214×W$_3$ (4.87)	CML-240×W$_5$ (0.44**)
	CML-79×W$_3$ (4.82)	CML-213×(W$_3$×W$_5$) (0.35**)
Kernel diameter (cm)	CML-240×(W$_3$×W$_5$) (16.08)	CML-173×W$_3$ (0.58**)
	CML-173×W$_3$ (16.00)	CML-214×W$_3$ (0.56**)
	CML-244×W$_5$ (15.97)	CML-240×W$_3$ (0.51**)
100-seed weight (g)	CML-214×W$_5$ (31.40)	CML-138×W$_3$ (2.95**)
	CML-240-×W$_5$ (31.18)	CML-79×(W$_3$×W$_5$) (2.29**)
	GLET-27×W$_3$ (31.00)	CML-214×(W$_3$×W$_5$) (2.20**)
Grain yield plot^{-1} (g)	CML-173×W$_3$ (1715)	CML-213×(W$_3$×W$_5$) (0.68**)
	GLET-27×W$_3$ (1710)	CML-79×(W$_3$×W$_5$) (0.57**)
	CML-463×W$_3$ (1700)	CML-244×W$_3$ (0.54**)

grain yield, CML-173×W$_3$ had highest mean performance followed by GLET-27×W$_3$ while as on the basis of SCA effects CML-213×(W$_3$×W$_5$), CML-79×(W$_3$×W$_5$) and CML-244×W$_3$ were the best crosses in order of merit. The parents CML-244, CML-240 and CML-214 were most frequently one of the parents in the best crosses besides possessing good GCA effects.

DISCUSSION

The success of plant breeding operation relies heavily on genetic variation. In fact plant breeding uses selection from the available genetic variability for crop improvement (Asins, 2002). The present study revealed substantial variability in parents as well as crosses which is encouraging for isolation of desirable genotypes using appropriate selection schemes. There was preponderance of SCA variances indicating greater role of non-additive components of variance in the inheritance of the traits studied. Similar, results in maize have been reported for yield and yield components traits by Dodiya and Joshi (2002) and Kumar *et al.* (2005). Thus hybrid breeding can be an efficient breeding strategy for improvement of grain yield and related traits in maize. In fact heterosis breeding has been the corner stone of maize improvement at national and international level. However, the stability of yield superiority needs to be tested over space and time. Recurrent selection can also be an efficient procedure for exploitation of both additive components of variance (Doerksen *et al.*, 2003). Such a procedure increases the frequency of desirable alleles while maintaining the genetic variation without reaching a dead end. Thus both selfed progeny recurrent selection and reciprocal recurrent selection used individually or simultaneously in combination should permit benefits of both additive and non-additive gene effects in test cross

and *per se* evaluation to be realised (Dhillon, 1991). The progress from simultaneous use of both procedures will be the total of expected gain from these procedures individually (Hallauer and Miranda, 1988). Popi and Kannenberg (2001) opined that under such schemes there is an increase in non-additive component relative to additive component. However, they were able to show that combining ability estimates are not changed substantially.

The average degree of dominance was in the range of over-dominance which further indicates the suitability of hybrid breeding. In fact, maize contains more over dominant loci as compared to other cereals even though all share common descent. The higher estimates for dominance variance also compensates for any upward bias due to linkage disequilibrium. Such overshadowing effect of non-additive variance has also bean reported by Das *et al.* (1997) and Suneetha *et al.* (2000). Furthermore, the present study revealed differential interaction of GCA and SCA variances. Whereas, both GCA and SCA variances interacted significantly for plant height, kernel rows ear-1 and 100-seed weight, only SCA interacted significantly with the environment and neither GCA nor SCA interacted with environment for ear diameter and grain yield indicating variance influence of environment on additive and non-additive components. Comparatively environmental interaction of non-additive component was greater than additive component for all traits, except 100-seed weight for which GCA×E was greater than SCA×E interaction. Similar results have been reported in maixe by Joshi *et al.* (1998), Zelleka (2000) and Betran *et al.* (2003). Such results further establish that need to carry out variance component studies across environments to get unbiased estimates.

A number of parental lines and testers were observed to posses good general combining ability effects for various traits especially CML-214, CMl-244 and CML-240, which not only had good GCA but also entered into specific cross combinations exhibiting superior mean performance and SCA effects for grain yield and related traits. These lines can be used in planned hybridzation programme to broaden the genetic base of local germplasm. Furthermore, the crosses recording superior performance can also serve as a source of improved lines with desirable alleles for a trait.

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