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Full Research Article

Combining Ability and Gene Action Studies for Grain Yield and Quality Parameters in Yellow Seeded Maize (*Zea mays* L.) Using Line×Tester Crosses

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Abstract

The present investigation was carried out at All India Co-ordinated Maize Improvement Project, MPUAT, Udaipur. 15 inbred lines were crossed with three testers viz; (EI-561-1, EI-586-2 and EI-708-2) in line×tester mating design to develop 45 hybrids. These 45 hybrids, 18 parents and along with the three checks were evaluated in randomized block design with three replications during *kharif* 2014. The combining ability analysis revealed that the mean squares among parents were highly significant for yield and all quality characters indicating presence of genetic variability among the parents. The variance due to SCA was higher than GCA by the σ^2 GCA/σ^2 SCA ratio being less than one for the all characters, suggesting significant role of non -additive gene actions like dominance, epistasis and other interaction effects in the expression of these characters. Parents L_1, L_{15}, L_5, L_4 and L_7 were the good general combiners and genetically worthy parents, as they contributed favourable genes for grain yield and quality traits. Whereas the crosses, $L_4 \times T_3$ followerd by $L_7 \times T_3$, $L_{15} \times T_2$ and $L_{10} \times T_2$ for grain yield plant^{-1}, $L_8 \times T_2$, $L_9 \times T_3$ for oil content and $L_8 \times T_3$, $L_{15} \times T_2$, $L_5 \times T_2$, $L_5 \times T_1$ for protein content were identified as most promising crosses. based on SCA effects, better *per se* and both or one of the parents with high GCA for grain yield and quality traits also, could be exploited profitably for yield quality traits in maize.

1. Introduction

Maize is the dominant staple crop. Nutritionally, however, the protein of maize is deficient in two essential amino acids, lysine and tryptophan (Bhatia and Rabson, 1987). The protein in corn is mainly as prolamin (Zein). Maize (*Zea mays*) is a relevant food and animal feed across the world and occupies a key place in the world economy and trade as an industrial grain crop (White and Johnso, 2003). Maize is globally cultivated in area of 184 mha with a productivity of 5519 kg ha^{-1} and production of 1016 mt (FAOSTAT). Globally, India ranks 4th in area and 7th in production of maize. In India, maize is the third important cereal crop after rice and wheat. It is cultivated on an area of 9.22 mha with a production of 24.34 mt and productivity of 2583 kg ha^{-1} (Annual report, 2014, Directorate of Maize Research, IARI, Pusa Campus, New Delhi).). Maize endosperm protein is comprised of different fractions mainly albumins, globulins, zeins or prolamines and glutelins. Kernel of maize contains pericarp (6%), endosperm (82%) and germ and 61–78% of starch, 6–12% of proteins, 3.1–5.7% of oil, 1.0–3.0% of sugar and 1.1–3.9% of ash on dry weight basis (Miller, 1958) and (Watson, 2003). Most of the oil is present in germ of the seed. Apart from linoleic acid, maize oil is also rich in other useful products like sitosterol, vita¬min E (antioxidant) and other functional nutrients.

There is a strong possibility to develop hybrids having higher yielding ability and nutritionally superior and industrially important with respect to high starch, protein and oil content. Line×tester method has been used in various studies (Vijayabharathi et al., 2009) (Wali et al., 2010) and (Hefny 2010) to determine general combining ability (GCA) and specific combining ability (SCA) of the lines under study. Petrovice (1998) suggested that combination of lines with significant positive or negative GCA can lead to positive and significant SCA in their test crosses. However, (Hossain and Aziz, 1998) showed that parents with high GCA for a trait did not give necessarily a high SCA for the same trait. Line×tester analysis is also helpful in estimating genetic variance components and types of gene effects (Venkatesh et al., 2001) using line×tester method found significant differences between lines, testers and line×tester combinations indicating the contribution of both additive and non-additive (dominance) gene actions in controlling grain yield.

In view of these considerations, information about genetics parameters of the populations involved is essential for the development of breeding programmes. Knowledge about the mechanisms of traits or gene transfer, combining ability and mothernal effects may directly help breeders to identify and produce superior lines, crosses or populations. The objectives of this study were to estimate GCA, SCA and the gene effects for grain yield starch, oil and protein content in maize using hybrids produced by the line×tester mating system.

2. Materials and Methods

The present investigation was carried out at All India Co-ordinated Maize Improvement Project, MPUAT, Udaipur. 15 inbred lines were crossed with three testers viz; (EI-561-1, EI-586-2 and EI-708-2) in line×tester mating design to develop 45 hybrids. These 45 hybrids, 18 parents and along with the three checks (Table 1) were evaluated in randomized block design with three replications during *kharif* 2014. The experimental material consisted of a total of 66 entries (45 F1 hybrids, 18 parents and 3 checks) were planted in randomized block design with three replications with a single row plot of four meter length, maintaining crop geometry of 60×25 cm^2. The border rows were also planted to neutralize the border effect. All the recommended agronomy inputs and practices were applied to the crop during the season, to raise the successful crop. The observations were recorded on randomly selected five competitive plants of each entry in each replication for seed yield, starch, oil and protein content. The starch content was estimated by using anthrone reagent method (Morris, 1948).), while oil was estimated by using Soxhlet method developed by AOAC (1965) and protein content was estimated by using Kjeldhal's (1883) method and the value of nitrogen content was multiplied by a factor of 6.25 and averaged and their mean values were subjected to various statistical and biometrical analyses. The observations taken for hybrids and parents were subjected to L×T analysis and the general combining ability effects of different crosses were worked out. The combining ability variance analysis was based on the method developed by Kempthorne (1957).

3. Results and Discussion

The combining ability analysis revealed that the mean squares among parents were highly significant for yield and all quality characters indicating presence of genetic variability among the parents (Table 2). The hybrids differed significantly for all the characters indicating genetic variability among the hybrids. The variance due to parent versus hybrids was significant for

Table 1: Combining ability analysis and estimates of genetic variances for L×T analysis for yield and its component traits

SoV	d.f.	GY$^{@}$ (g)	Starch (%)	Oil (%)	Protein (%)
Replication	2	3.55	0.10	0.02**	0.01
Parent	17	594.64**	1.97**	0.57**	0.49**
Crosses	44	2364.09**	14.65**	1.20**	5.86**
Parent v/s Crosses	1	21794.03**	53.13**	0.01	44.68**
Line	14	2097.63**	6.84**	2.03**	5.48**
Tester	2	2108.32**	12.08**	0.37**	4.81**
Line×Tester	28	2515.60**	18.74**	0.85**	6.12**
Error	130	27.06	0.41	0.01	0.04
σ^2 GCA		-15.282	-0.344	0.013	-0.036
σ^2 SCA		829.51	6.110	0.282	2.030
σ^2 GCA/ σ^2 SCA		-0.018	-0.056	0.046	-0.018
σ^2 A/ (σ^2 A+ σ^2 D)		-0.038	-0.127	0.084	-0.037

*Significant at p=0.05; ** at p=0.01; $^{@}$Grain yield plant^{-1}

Table 2: Estimate of GCA effects of 18 parents for yield and quality traits

Genotype	GY$^{@}$ (g)	Starch (%)	Oil (%)	Protein (%)
L_1	28.41**	0.35	-0.13**	0.69**
L_2	10.86**	-0.19	-0.56**	-0.53**
L_3	-0.14	-0.33	-0.37**	-0.95**
L_4	6.19**	0.65**	1.51**	-0.90**
L_5	4.41*	1.67**	-0.02	1.38**
L_6	-24.03**	-1.37**	-0.11**	-1.10**
L_7	14.75**	0.31	0.03	0.24**
L_8	-13.03**	-1.41**	0.24**	0.74**
L_9	-17.47**	0.39	0.32**	-0.62**
L_{10}	11.53**	-0.01	-0.07**	1.23**
L_{11}	-18.92**	-0.75**	-0.29**	-0.14*
L_{12}	-1.03	0.32	0.07**	0.18**
L_{13}	-2.92	0.16	-0.09**	-0.09
L_{14}	-15.25**	-0.98**	-0.32**	-0.49**
L_{15}	16.64**	1.19**	-0.21**	0.36**
SE (^{g}i)	1.79	0.22	0.02	0.06
T_1	7.90**	0.46**	-0.04**	-0.16**
T_2	-3.94**	0.10	0.10**	-0.21**
T_3	-3.96**	-0.56**	-0.06**	0.38**
SE (^{g}j)	0.90	0.11	0.01	0.03

all the characters except oil content indicating the presence of substantial differences between the crosses. The lines and testers were showed significant differences for all the characters studied. Similar findings were reported by (Abrha et al., 2013); (Panwar et al., 2013). This indicated prevalence of additive variance for all the characters. The mean squares due to line×tester interaction component also emerged significant for all the characters indicating that combining ability contributed remarkably in the expression of these characters and it also provided a direct test indicating that dominance or non additive variance was important for the characters under study. This is in accordance with earlier reports by (Luders et al., 2007); (Panwar et al., 2013). The significance of GCA variance (σ^2 GCA) and SCA variance (σ^2 SCA) obtained from line×tester design could not be tested, hence these statistics appeared to be of exploratory nature only. However, such estimates were used to determine the additive (σ^2 A) and non-additive (σ^2 D) components of population variance and predictability ratio σ^2 A/ (σ^2 A+σ^2 D). The variance due to SCA was higher than GCA by the σ^2 GCA/σ^2 SCA ratio being less than one for the all characters, suggesting significant role of non -additive gene actions like dominance, epistasis and other interaction effects in the expression of these characters. Similar result reported by (Dar et al., 2007). Variance by nature must not be negative as they are squared quantities. But they do occur some time, particularly when estimates of genetic variance are calculated from expectation of ANOVA as done for determination of σ^2 GCA from ANOVA for combining ability in the present analysis. The possible reasons that could be assigned for occurrence of negative estimates of variances are: (a) small sample size and presence of aberrant values, (b) presence of genotype×environment (G×E) interaction which might have inflated the error variance, and (c) lack of random mating while developing half sibs. However, occurrence of negative estimates should not be considered as invalid results and as such, they should be promptly reported. A repeated experimentation and then averaging will give the correct picture (Roy and Senapati, 2012).

A predictability ratio greater than 0.5 indicates additive gene action, less than 0.5 indicates non-additive gene action and equal to 0.5 indicates predominance of both additive and non-additive gene action for a character. In the present study the predictability ratios were low the value of 0.50 for grain yield, starch, oil and protein content indicating the predominance of non-additive gene action for these characters. The GCA effect of parents is presented in Table 3. The estimates of GCA showed that among the lines, L_1, L_{15}, L_7, L_{10}, L_2, L_4 and L_5 exhibited positive and significant GCA effects for grain yield. Similar results were reported by (Rokadia and Kaushik,

Table 3: Estimate of specific combining ability effects of 45 hybrids for yield and quality traits in maize

Characters Crosses	Grain yield plant^{-1}	Starch content (%)	Oil content (%)	Protein content (%)
$L_1\times T_1$	2.43	1.68**	-0.25**	-1.12**
$L_2\times T_1$	28.65**	3.50**	0.12**	0.49**
$L_3\times T_1$	3.65	-1.19**	0.31**	-0.51**
$L_4\times T_1$	-11.01**	-0.09	-0.03	0.14
$L_5\times T_1$	1.43	-0.84	0.44**	1.66**
$L_6\times T_1$	-19.79**	-0.79	-0.45**	-0.30*
$L_7\times T_1$	0.76	1.52**	0.46**	1.22**
$L_8\times T_1$	-28.79**	-2.60**	-0.27**	-1.41**
$L_9\times T_1$	-23.68**	-1.68**	-0.93**	-0.35**
$L_{10}\times T_1$	8.65*	0.26	0.32**	0.50**
$L_{11}\times T_1$	6.76	0.11	-0.02	0.77**
$L_{12}\times T_1$	37.87**	2.84**	0.36**	-1.44**
$L_{13}\times T_1$	22.76**	-0.87	-0.14**	1.70**
$L_{14}\times T_1$	-10.24**	-0.52	0.32**	0.17
$L_{15}\times T_1$	-19.46**	-1.34**	-0.24**	-1.52**
$L_1\times T_2$	5.94	1.49**	-0.16**	0.87**
$L_2\times T_2$	-40.84**	-3.04**	-0.43**	-1.16**
$L_3\times T_2$	14.16**	3.00**	-0.07	1.05**
$L_4\times T_2$	-34.50**	-3.07**	-0.01	-0.08
$L_5\times T_2$	30.61**	0.24	0.24**	1.69**
$L_6\times T_2$	9.72**	0.76	0.31**	0.07
$L_7\times T_2$	-40.06**	-3.21**	-0.03	-0.84**
$L_8\times T_2$	30.05**	3.46**	1.29**	-0.15
$L_9\times T_2$	-3.84	-1.67**	-0.21**	-0.94**
$L_{10}\times T_2$	32.50**	3.00**	-0.24**	-1.66**
$L_{11}\times T_2$	-12.06**	-2.45**	-0.12**	-1.52**
$L_{12}\times T_2$	-13.95**	-0.34	-0.32**	0.66**
$L_{13}\times T_2$	-12.73**	0.14	-0.08*	-0.47**
$L_{14}\times T_2$	0.27	0.92*	-0.34**	-0.02
$L_{15}\times T_2$	34.72**	0.79	0.18**	2.49**
$L_1\times T_3$	-8.37*	-3.17**	0.41**	0.25
$L_2\times T_3$	12.19**	-0.46	0.31**	0.66**
$L_3\times T_3$	-17.81**	-1.81**	-0.24**	-0.54**
$L_4\times T_3$	45.52**	3.17**	0.04	-0.06
$L_5\times T_3$	-32.04**	0.60	-0.67**	-3.34**
$L_6\times T_3$	10.07**	0.03	0.14**	0.23
$L_7\times T_3$	39.30**	1.69**	-0.43**	-0.38**
$L_8\times T_3$	-1.26	-0.86	-1.02**	1.55**
$L_9\times T_3$	27.52**	3.35**	1.14**	1.28**

Continue...

Characters Crosses	Grain yield plant^{-1}	Starch content (%)	Oil content (%)	Protein content (%)
$L_{10}\times T_3$	-41.15**	-3.26**	-0.08*	1.16**
$L_{11}\times T_3$	5.30	2.33**	0.14**	0.74**
$L_{12}\times T_3$	-23.93**	-2.50**	-0.05	0.78**
$L_{13}\times T_3$	-10.04**	0.73	0.22**	-1.22**
$L_{14}\times T_3$	9.96**	-0.40	0.02	-0.15
$L_{15}\times T_3$	-15.26**	0.56	0.06	-0.97**
SE (Sij)	3.58	0.44	0.04	0.13

2007) and (Kumar et al., 2015). The lines L_5, L_{15} and L_4 had positive and significant GCA effects for starch content. The parents L_4, L_8, L_9 and L_{12} were exhibited positive and significant GCA effects for oil content.imilarly, the L_1, L_5, L_{10}, L_{15}, L_8, L_7 and L_{12} had positive and significant GCA effects for protein content and hence these lines were good combiners for above respective traits. The line L_1 was found to be the best general combiner for grain yield. None of the parents evinced good GCA effects for all the characters. Among the testers, T_1 showed significantly high or very high GCA effect for grain yield and starch content. T_2 and T_3 were exhibited significant and positive GCA effects for oil content and protein content repectively. The estimates of SCA effects for yield and quality traits are presented in Table 4. Out of 45 crosses only 16 croses viz., $L_4\times T_3$, $L_7\times T_3$, $L_{12}\times T_1$, $L_{15}\times T_2$, $L_{10}\times T_2$, $L_5\times T_2$, $L_8\times T_2$, $L_2\times T_1$, $L_9\times T_3$, $L_{13}\times T_1$, $L_3\times T_2$, $L_2\times T_3$, $L_6\times T_3$, $L_{14}\times T_3$, $L_6\times T_2$ and $L_{10}\times T_1$ exhibited significantly positive SCA value for yield plant^{-1}. These results are in conformity with findings of (Reddy et al*.,* 2011), (Sravanti et al*.,* 2015); (Kumar et al*.,* 2015).

These cross combinations need further evaluation in segregations to identify desirable transgressive segregants in the advanced genlerations. The magnitude of SCA effects is of vital importance in selecting cross combinations with higher probability of generating transgressive segregates. Significant yield performance in specific crosses was due to the combinations on the basis of their *per se* performance and SCA effects. (Ahmad et al., 2014).

The five top ranking cross combinations selected on the basis of *per se* performance involved high, medium and low general combiners. 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 insignificant estimates but in desirable direction were classified as average or medium combiners. Poor or low combiners had undesirable GCA effects. Crosses with desirable SCA effects for yield, starch, oil and protein along with mean performance and GCA effects of parents involved in the crosses are listed in Table 5.

Table 4: Top five crosses with high SCA effects, *per se* performance and GCA effects of parents for grain yield and quality parameters in maize

Characters	Crosses	SCA effects	Mean Performance of crosses	GCA effects		GCA status of parent
				Female parent	Male parent	
Grain yield plant^{-1} (g)	$L_4\times T_3$	45.52**	120.67	6.19**	-3.96**	H×L
	$L_7\times T_3$	39.30**	123.00	14.75**	-3.96**	H×L
	$L_{12}\times T_1$	37.87**	117.67	-1.03	7.90**	M×H
	$L_{15}\times T_2$	34.72**	120.33	16.64**	-3.94**	H×L
	$L_{10}\times T_2$	32.50**	113.00	11.53**	-3.94**	H×L
Starch content (%)	$L_2\times T_1$	3.50**	66.58	-0.19	0.46**	M×H
	$L_8\times T_2$	3.46**	64.94	-1.41**	0.10	L×M
	$L_9\times T_3$	3.35**	65.99	0.39	-0.56**	M×L
	$L_7\times T_3$	317**	64.25	0.31	-0.56**	M×L
	$L_{10}\times T_2$	3.00**	65.90	-0.01	0.10	M×M
Oil content (%)	$L_8\times T_2$	1.29**	5.76	0.24**	0.10**	H×H
	$L_9\times T_3$	1.14**	5.52	0.32**	-0.06**	H×L
	$L_7\times T_1$	0.46**	4.57	0.03	-0.04**	M×L
	$L_5\times T_1$	0.44**	4.49	-0.02	-0.04**	M×L
	$L_1\times T_3$	0.41**	4.33	-0.13**	-0.06**	L×L
Protein content (%)	$L_{15}\times T_2$	2.49**	11.65	0.36**	-0.21**	H×L
	$L_{13}\times T_1$	1.70**	8.07	-0.09	-0.16**	M×L
	$L_5\times T_2$	1.69**	11.86	1.38**	-0.21**	H×L
	$L_5\times T_1$	1.66**	11.89	1.38**	-0.16**	H×L
	$L_8\times T_3$	1.55**	11.68	0.74**	0.38**	H×H

*Significant at *p*=0.05; ** at *p*=0.01; H: High GCA value; M: Medium; GCA value; L: Low GCA value

The top ranking five cross combinations selected on the basis of *per se* performance in general exhibited highly significant and positive SCA effects for all the traits. But the ranking of cross combinations was not consistent for *per se* performance and SCA effects. No cross combination exhibited significantly positive SCA effect and high *per se* performance coupled with parents having high GCA effects consistently for all the characters. The hybrid $L_8\times T_2$ for oil content and $L_8\times T_3$ for protein content, had high SCA performance and high mean values. Similar finding were reported by (Mahesh et al*.,* 2013) and (Khan and Dubey, 2015).

These desirable cross combinations involved high×high type of general combiners. (Ali et al., 2012) and (Aly, 2013) reported about interaction between positive and) positive alleles in crosses involving high×high combiners which can be fixed

Table 5: List of inbred lines used as parents and checks

Sl. No.	Symbol/Code	Pedigree	Origin
Details of parents			
1.	L_1 (EI-770)	WN-Hyd-R2013-TLYQ-32⊕ y	DMR, Hyderabad
2.	L_2 (EI-771)	WN-Hyd-R2014-P65Q-2013⊕y	DMR, Hyderabad
3.	L_3 (EI-772)	WN-Hyd-R2014-P69-7⊕y	DMR, Hyderabad
4.	L_4 (EI-773)	WN-Hyd-R2014-CML161/165⊕ y	DMR, Hyderabad
5.	L_5 (EI-774)	WN-Hyd-R2014-S42-1⊕ y	DMR, Hyderabad
6.	L_6 (EI-775)	WN-Hyd-R2014-S42-21⊕ y	DMR, Hyderabad
7.	L_7 (EI-776)	WN-Hyd-R2014-P64C1-17B⊕ y	DMR, Hyderabad
8.	L_8 (EI-777)	WN-Hyd-R2014-High Oil QPM-C13⊕ y	DMR, Hyderabad
9.	L_9 (EI-778)	WN-Hyd-R2014-EC-612103-1⊕ y	DMR, Hyderabad
10.	L_{10} (EI-779)	WN-Hyd-R2014-EC-618201⊕ y	DMR, Hyderabad
11.	L_{11} (EI-780)	WN-Hyd-R2014-EC-655779⊕ y	DMR, Hyderabad
12.	L_{12} (EI-781)	WN-Hyd-R2014-12202-06H138⊕ y	DMR, Hyderabad
13.	L_{13} (EI-782)	WN-Hyd-R2014-CM-128⊕ y	DMR, Hyderabad
14.	L_{14} (EI-783)	WN-Hyd-R2014-CM-131⊕ y	DMR, Hyderabad
15.	L_{15} (EI-784)	WN-Hyd-R2014-CM-202⊕y	DMR, Hyderabad
16.	T_1 (EI-561-1)	KH-510-9-2-2-1-1	MPUAT, Udaipur
17.	T_2 (EI-586-2)	UHP-3(y)-5-3-1-2	MPUAT , Udaipur
18.	T_3 (EI-708-2)	DMR-WN8	MPUAT , Udaipur
Details of checks			
1.	C_1	Prakash	PAU, Ludhiana
2.	C_2	Pratap Hybrid Maize-3(PHM-3)	MPUAT , Udaipur
3.	C_3	HM-9	CCSHAU, Karnal

in subsequent generations if no repulsion phase linkages are involved. However, crosses between medium×low indicated importance of non-additive genetic variation.

The desirable performance of combination like high×low may be ascribed to the interaction between dominant allele from good combiners and recessive alleles from poor combiners. Moreover, a high×low cross can result in strong transgressive segregants for the desired characters due to segregation of genes with strong potentials and their specific buffers (Langham 1961). Such combinations were observed in the hybrids: $L_4 \times T_3$, $L_7 \times T_3$, $L_{15} \times T_2$ and $L_{10} \times T_2$ for grain yield plant^{-1}, $L_9 \times T_3$ for oil content and $L_{15} \times T_2$, $L_5 \times T_2$, $L_5 \times T_1$ for protein content. These cross combination exhibited significantly positive SCA effect, high *per se* performance. (Lilian et al., 2011) (Chakraborthy et al., 2012); (Jahan et al., 2014) reported the possibility of interaction between positive alleles from a good combiner and negative alleles from a poor combiner in high×low cross combination and suggested for the exploitation of F_1 generation, as their high yielding ability would be unfixable in succeeding generation. Involvement of both poor combiners also produced superior specific combining hybrid as evidenced from the combinations, $L_1 \times T_3$ for oil content. Involvement of both combiners with low GCA has been attributed to over dominance and epistasis interaction, which has been suggested by (Malik et al*.*, 2004).

4. Conclusion

L_1, L_{15}, L_5, L_4 and L_7 were the good general combiners and genetically worthy parents, as they contributed favourable genes for grain yield and quality traits. Whereas the crosses, $L_4 \times T_3$ followed by $L_7 \times T_3$, $L_{15} \times T_2$ and $L_{10} \times T_2$ for grain yield plant^{-1}, $L_8 \times T_2$, $L_9 \times T_3$ for oil content and $L_8 \times T_3$, $L_{15} \times T_2$, $L_5 \times T_2$, $L_5 \times T_1$ for protein content were identified as most promising crosses.

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