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Evaluation of yield and yield attributing traits along with quality parameters in normal maize (*Zea mays* L.)

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Abstract
Twelve inbred lines were crossed with each of five testers in a line × tester design to evaluate combining ability and heterosis to identify promising hybrids of maize for various quality parameters like protein, tryptophan, lysine, starch contents and grain yield. The analysis of variance revealed highly significant differences for all the traits reflecting adequate diversity in the genetic material chosen for the study. Significant differences among the genotypes for quality attributes such as protein, tryptophan, lysine and starch contents were observed. The cross combination, BQPM-2 × BAUIM-2 (21.54) showed highest magnitude of economic heterosis over the best check HQPM-1 for protein content whereas for tryptophan, lysine contents and starch contents BQPM-2 × BAUIM-2 showed highest magnitude of economic heterosis as 5.56. 5.47 and 5.89 respectively over the best check HQPM-1. Hemavathy and Balaji (2008) [8] suggested that the exploitation of heterosis is the best method to increase the qualitative traits like lysine, tryptophan along with increase in the grain yield in maize. These promising crosses with good yield along with good quality parameters can be tested extensively over environments in the future and can be utilized as good performers profitably by the maize breeders.

Keywords: Maize, *Zea mays* L., Lines × tester, grain maturity stage and composition

Introduction
Maize (*Zea mays*) is the third most important cereal in India after rice and wheat. During 2010, the Maize utilization pattern in India has been as human food human food (24%), animal feed (11%), poultry feed (52%), starch (11%), brewery (1%) and Seed (1%) (DMR, 2010) [4]. Maize is a rare crop, which can be used at any stage of its growth and has very big market potential. Hence the present investigation was planned to evaluate various maize genotypes (including twelve lines, five testers, sixty crosses and two checks for baby corn and three checks for grain purpose) for chemical composition at baby corn and hard dough stage.

Materials and Methods
The experiment was carried out with twelve lines, five testers, sixty crosses and three checks following line x tester mating design for grain maturity purpose in RBD with three replicates at B.A.U Research farm during Kharif 2010.
The matured genotypes after the harvest were cleaned by removing stones, grits, and other foreign particles and dried thoroughly in the sun. The cleaned grains were powdered and sieved through 40 mesh sieve and stored in airtight containers until further analysis is done. The nitrogen present in each sample of grains was determined through determining total nitrogen content by using the standard Micro-kjeldahl method as given in A.O.A.C. (1970) [1]. Crude protein content was calculated by multiplying 6.25 to the estimated total nitrogen content of maize grains. Tryptophan content in kernel protein was estimated by papain hydrolysis method by Hernandez and Bates (1969) [7]. The lysine content in kernel protein was estimated by Colorimeter method designed by Tsai *et al.* (1972) [13] and modified by Villegas *et al.* (1971) [14]. The starch content in kernel was estimated by Anthrone reagent method given by Clegg (1956) [2].

Results and Discussion
The analysis of variance revealed highly significant differences for all the traits reflecting adequate diversity in the genetic material chosen for the study. Significant differences among

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The genotypes for quality attributes such as protein, tryptophan, lysine and starch contents were observed. Significant variation found in the present study could be attributed due to the genetic cause. Genetic variability for protein content has been reported by Dodiya and Joshi (2003) [6] while for tryptophan content, lysine content and starch content by Hossain *et al.* (2007) [9], Xuelu and Larkins (2001) [15] and Devi and Prodhan (2004) [5] respectively.

The proximate composition of maize genotypes at complete maturity stage is depicted in table 1. The protein content of the genotypes ranged from 8.22 % (V 341) to 9.57% (BQPM-2). Similar variations for protein content of different types of maize was ranging from 5.8 -13.7 % by Cortez and Wild Altamirano (1972) [3]. The mean value for protein content among the crosses ranged from 8.19 per cent (CML 161×HKI 193-1) to 11.61 per cent (BQPM-2×BAUIM-2). The tryptophan content varied from 0.38 % (BAUIM-3) to 0.66 % (BQPM-4) while BAUIM-4, BQPM-2 and BQPM-4 were significantly superior to the check HQPM-1. The mean tryptophan content among the crosses ranged from 0.39 per cent (CM 152×BAUIM-2) to 0.76 per cent (BQPM-4 × K-1105). Relatively more amount of lysine content was observed in BQPM-2 (2.62 %) followed by CML 161 (2.56 %) and BQPM-4 (2.50%). Among the crosses lysine content ranged from 1.57 per cent (CM 152×BAUIM-2) to 3.02 per cent (BQPM-2×BAUIM-2). Significantly higher starch content was observed in BQPM-4 (67.87%) followed by BQPM-2 (67.57%). Similar values were reported by Ranhotra (1985) [11]. The crosses showed a range of 47.23 per cent (BQPM-4×HKI-163) to 71.27 per cent (BQPM-2×BAUIM-2) for starch content. These differences may be due to the genetic makeup of the variety, grain size and nutrient availability to the crop.

The maximum positive and highly significant gca effect was revealed by BAUIM-4 (0.80) followed by V 341 (0.71) and CM 111 (0.68) for protein content. For tryptophan content, the maximum positive and highly significant gca effect was revealed by BQPM-2 (0.16) followed by BQPM-4 (0.14) and CML 161 (0.12). For lysine content, the maximum positive and highly significant gca effect was revealed by BQPM-2 (0.61) followed by BQPM-4 (0.55) and CML 161 (0.53). However for starch content the maximum positive and highly significant gca effect was revealed by BAUIM-4 (1.54) followed by CM 111 (1.36) and BQPM-2 (0.51). Similar findings were reported by Osorno and Carena (2008) [10]. ZongHua *et al.* (2007) [16] noted that inbred line, with high starch content and high gca was one of important resource in high starch breeding.

However in case of crosses, BAUIM-3 × HKI-163 (0.56), BAUIM-1 × HKI 193-1 (0.56) and V 351 × CM 150 (0.56) revealed maximum positive and highly significant sca effect for protein content. For tryptophan content, the cross BQPM-2 × BAUIM-2 (0.12) showed the maximum positive value for sca effect followed by BQPM-4 × K-1105 (0.08). For lysine content, BQPM-2 × BAUIM-2 (0.46) revealed the maximum positive value for sca effect followed by BQPM-4 × K-1105 (0.33) and CM 111 × K-1105 (0.21). For starch content, the maximum positive and highly significant sca effect was revealed by the cross BQPM-2 × BAUIM-2 (2.82) followed by BQPM-4 × K-1105 (1.99) and BAUIM-4 × HKI-163 (1.07).

For heterosis, BQPM-2 × BAUIM-2 (21.54) showed highest magnitude of economic heterosis over the best check HQPM-

1 for protein content followed by BQPM-4 × K1105 (20.45) and BAUIM-4 × HKI-163 (19.69). For tryptophan and lysine contents, BQPM-2 × BAUIM-2 showed highest magnitude of economic heterosis over the best check HQPM-1. For starch content, BQPM-2 × BAUIM-2 (5.89) showed highest magnitude of economic heterosis over the best check HQPM-1 followed by BAUIM-4 × HKI-163 (5.14) and CM 111 × K1105 (4.87). Selvaraj *et al.* (2006) [12] suggested that exploitation of heterosis is the best method to increase the qualitative parameters like total starch content along with increase in grain yield in maize Hemavathy and Balaji (2008) [8] also suggested that the exploitation of heterosis is the best method to increase the qualitative traits like lysine, tryptophan along with increase in the grain yield in maize. These promising crosses with good yield along with good quality parameters can be tested extensively over environments in the future and can be utilized as good performers profitably by the maize breeders.

Table 1: Mean performance of Parents and checks for Quality parameters in Normal Maize Hybrids

Parents	Protein (%)	Tryptophan (%)	Lysine (%)	Starch (%)
Bauim-3	9.24	0.38	1.57	64.58
Cm111	9.15	0.39	1.56	64.57
Cm151	8.28	0.40	1.61	63.23
Cm152	8.52	0.41	1.65	63.53
Bau1m-1	9.31	0.40	1.61	65.53
Bau1m-4	9.34	0.48	1.89	65.53
V341	8.22	0.39	1.57	63.73
1025	8.57	0.39	1.50	64.48
Bqpm-2	9.57	0.63	2.62	67.57
Bqpm-4	9.46	0.66	2.50	67.87
Cml161	8.34	0.63	2.56	65.22
V351	8.85	0.39	1.56	64.30
Cm-150 (t1)	8.49	0.39	1.57	63.71
Bau1m-2(t2)	9.25	0.41	1.65	65.63
K1105 (t3)	9.25	0.39	1.57	64.38
193-1 (t4)	9.30	0.60	2.30	67.47
Hk-163 (t5)	9.23	0.62	2.46	67.31
Mean	8.96	0.47	1.86	65.21
Checks				
Hqpm-1	9.57	0.68	2.71	67.31
Vivek hybrid-9	9.42	0.45	1.78	66.67
Suwan	9.45	0.46	1.83	66.53
Mean	9.48	0.53	2.11	66.84
Sem ±	0.05	0.00	0.02	0.03
Cd at 5%	0.20	0.01	0.06	0.11
Cd at 1%	0.15	0.01	0.05	0.08

Maximum and minimum values in Bold figure.

Table 2: Mean performance of crosses for Quality parameters in Normal Maize Hybrids

Crosses	Protein (%)	Tryptophan (%)	Lysine (%)	Starch (%)
CM152× BAU1M-2	9.26	0.39	1.57	66.35
BQPM-2× BAU1M-2	11.61	0.71	3.02	71.27
BQPM-4× K1105	11.50	0.76	2.82	70.42
BQPM-4× HKI163	11.40	0.61	2.41	47.23
CML161× 193-1	8.19	0.57	2.28	67.48
SE m±	0.05	0.00	0.02	0.03
CD at 5%	0.20	0.01	0.06	0.11
CD at 1%	0.15	0.01	0.05	0.08

Maximum and minimum values in Bold figure.

Table 3: GCA effects of parents for quality parameters for Normal Maize Hybrids

Parents	Protein (%)	Tryptophan (%)	Lysine (%)	Starch (%)	
Bauim-3	-0.67 **	-0.05 **	-0.21 **	-0.72 **	**
Cm111	0.68 **	-0.03 **	-0.13 **	1.36 **	**
Cm151	0.15 **	-0.04 **	-0.17 **	-0.30 **	**
Cm152	-1.03 **	-0.04 **	-0.15 **	-0.59 **	**
Bau1m-1	0.55 **	-0.04 **	-0.16 **	0.16 **	**
Bau1m-4	0.80 **	0.02 **	0.07 **	1.54 **	**
V341	0.71 **	-0.01 **	-0.02 **	-0.43 **	**
1025	-0.91 **	-0.04 **	-0.14 **	-1.11 **	**
Bqpm-2	0.63 **	0.16 **	0.61 **	0.51 **	**
Bqpm-4	0.62 **	0.14 **	0.55 **	0.20 **	**
Cml161	-1.12 **	0.12 **	0.53 **	0.21 **	**
V351	-0.42 **	-0.04 **	-0.18 **	0.21 **	**
Cm-150 (t1)	-0.15 **	-0.02 **	-0.08 **	-0.74 **	**
Bau1m-2(t2)	0.25 **	0.01 **	0.04 **	0.08 **	**
K1105 (t3)	0.07 **	-0.01 **	-0.05 **	0.38 **	**
193-1 (t4)	-0.26 **	0.01 **	0.02 **	0.07	
Hki-163 (t5)	0.08 **	0.00	0.01 *	0.29 **	**
Se(gi-gj)±(line)	0.04	0.00	0.01	0.01	
Cd at 5%	0.08	0.01	0.02	0.02	
Cd at 1%	0.10	0.01	0.03	0.02	
Se(gi-gj)±(tester)	0.02	0.00	0.01	0.01	
Cd at 5%	0.05	0.00	0.02	0.02	
Cd at 1%	0.06	0.01	0.02	0.03	

*,**=Significant at P = 0.05 and P = 0.01 respectively. Maximum and minimum values in Bold figure.

Table 4: SCA effects of crosses for Quality parameters of Normal Maize Hybrids

Crosses	Protein (%)	Tryptophan (%)	Lysine (%)	Starch (%)
Bau1m-3× hki-163	0.56**	0.03**	0.13**	1.00**
Cm111× k1105	0.25**	0.05**	0.21**	0.99**
Bau1m-1× 193-1	0.56**	-0.01**	-0.04**	-0.51
Bau1m-4× hki163	0.17**	0.03**	0.13**	1.07**
Bqpm-2× bau1m-2	0.35**	0.12**	0.46**	2.82**
Bqpm-4× k1105	0.43**	0.08**	0.33**	1.99**
V351× cm150	0.56**	0.01**	0.03**	-0.06**
SE-Sij-Skl ±	0.08	0.01	0.03	0.04
CD at 5%	0.17	0.01	0.05	0.09
CD at 1%	0.22	0.02	0.07	0.11
SE-Sij-Sik ±	0.14	0.01	0.04	0.07
CD at 5%	0.27	0.02	0.09	0.14
CD at 1%	0.36	0.03	0.11	0.18

*,** = Significant at P = 0.05 and P = 0.01 respectively, Maximum and minimum values in Bold figure.

Table 5: Heterosis (%) over better check

	Protein %	Tryptophan%	Lysine%	Starch%
Cm111×k1105	19.27 **	-29.63 **	-29.22 **	4.87 **
Bau1m-4×k1105	17.94 **	-32.41 **	-32.01 **	3.34 **
Bau1m-4×hki163	19.69 **	-26.39 **	-26.08 **	5.14 **
Bqpm-2×bau1m-2	21.54 **	5.56 **	5.47	5.89 **
Bqpm-4×k1105	20.45 **	-1.39 **	-1.40 **	4.63 **

*, ** = Significant at P = 0.05 and P = 0.01 respectively., Maximum and minimum figures in Bold figure.

Acknowledgement

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