

GENE EFFECTS FOR GRAIN YIELD BY GENERATION MEAN ANALYSIS IN MAIZE

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ABSTRACT

The present study was conducted at Agricultural research station, Karimnagar during rabi 2011-12. The gene effects for grain yield was studied through generation mean analysis by using ten inbreds, their 45  $F_1$  crosses by following diallel mating design, their corresponding  $F_2$ ,  $BC_1$  and  $BC_2$  progenies. The scaling tests of ABC were significant indicating role of epistatic effects. In general, the magnitude of dominance effect was higher than additive effect indicating that yield is largely governed by dominance effect. The epistasis was of duplicate type in most of the crosses for grain yield. Significant role of dominance variance along with duplicate epistasis in the inheritance of grain yield favours the use of research material (maize inbred lines) for the development of single cross hybrids. Few crosses exhibited additive and additive x additive type of epistatic interactions. A breeding procedure which exploit both additive and dominance components, such as family selection with intermating, will be suitable for improvement of yield.

**Key words:** Inbred lines, generation mean analysis, gene effects, additive, dominance, epistasis, duplicate

INTRODUCTION

Maize (*Zea mays L*) is one of the important cereal food crops of the world. The global maize production has crossed 1017 million tonnes which was highest among all food crops, with an average productivity of >5.5 t/ha. Globally it is being grown on approximately 183 million hectares (FAOSTAT, 2014). In India, it is cultivated in 9.4 Mn hectare with annual production of 23 MnMT and average productivity of 2.5 MT/hectare (India maize summit, 2014). The demand for maize will continue to increase in coming days due to burgeoning population. However, the challenge to meet the future demand is very high under the scenario of shrinking natural resources like land and climate change. In this context, enhancement of yield is the most viable option. The estimation of gene action and the inheritance of the grain yield is an interesting procedure for the breeders in order to formulate the most efficient breeding method to bring about the maximum improvement of the attribute. Haq *et al.* (2013), Ravikant *et al.* (2006); Sofi *et al.* (2006) observed the important role of non allelic interactions in the inheritance of quantitative characters. Generation mean analysis (GMA) has been used most extensively to estimate the gene effects and components of genetic variance. In the present investigation, GMA was taken-up to study gene action of grain yield in forty five crosses of maize.

MATERIALS AND METHODS

Ten elite inbred lines *viz.*, BML-6, BML-7, BML-10, BML-13, CM-119, BPPTI-34, CM-131, BPPTI-38, BPPTI-35 and BPPTI-44, were crossed in a half-diallel fashion during winter (*rabi*) season of 2010, to generate 45  $F_1$  crosses and each were selfed to generate  $F_2$ s as well as backcrossed to both the parents  $P_1$  and  $P_2$  to generate backcross generations  $BC_1P_1$  and  $BC_1P_2$  respectively during rainy season (*kharif*) of 2011. The experimental material comprising parents,  $F_1$ s,  $F_2$ s,  $BC_1P_1$ s and  $BC_1P_2$ s were evaluated in a complete randomized block design with two replications at Maize Research Centre, Agricultural Research Institute, Karimnagar, during *rabi* 2011. The parents and  $F_1$ s were sown in single row,  $F_2$ s in four rows while  $BC_1P_1$  and  $BC_2P_2$ s in two rows plot of four meters length. The spacing adopted was 75 cm between rows and 20 cm within the row. The production conditions were adopted as per recommended package of practices. The data on grain yield were collected on ten competitive plants from  $P_1$ ,  $P_2$  and  $F_1$ , 40 plants from  $BC_1P_1$  and  $BC_1P_2$  and 60 plants from  $F_2$  generations derived from each cross combinations. The genetic parameters namely  $m$ ,  $d$ ,  $h$ ,  $i$ ,  $j$  and  $l$ , which stands for mean, additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effect, respectively; were estimated by following the scaling tests A,

B, C and D (Mather and Jinks, 1971) and to detect the presence of  $i$ ,  $j$ , and  $l$  interactions using six parameter model (Hayman, 1958). The scales A, B, C and D were computed by simple linear combinations of means of different generations' viz.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1P_1$  and  $BC_1P_2$  which are as follows;  $A = P_1 + F_1 - 2BC_1P_1$ ,  $B = P_2 + F_1 - 2BC_1P_2$ ,  $C = P_1 + P_2 + 2F_1 - 4F_2$ ,  $D = 2F_2 - BC_1P_1 - BC_1P_2$ . The generation mean analysis was carried out on forty five crosses using Windostat 8.0 Advanced Plant Breeding package (Indostat Services, Hyderabad) as per Hettiarachchi *et al.*, (2009).

## RESULTS AND DISCUSSION

In any planned breeding programme to improve the yields, it is essential to know different gene effects controlling yield and its components. Therefore, generation mean analysis was carried out with the present material. The data generated at Karimnagar on six generations viz.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  for yield for 45 crosses were analyzed for generation mean analysis by following Hayman (1958). Scaling tests of ABC values were significant in most of the crosses for yield (Table 1).

Table 1: Scaling tests for grain yield in different generations of maize hybrids

S. No.	Crosses	A	S.E	B	S.E	C	S.E
1	BML - 6 x BML - 7	90.79**	17.34	15.00	15.44	98.19**	31.95
2	BML - 6 x BML - 10	-13.33	11.15	-7.53	10.44	171.94**	29.27
3	BML - 6 x BML - 13	23.60	18.14	-63.00**	11.69	80.33**	28.81
4	BML - 6 x CM - 119	47.00**	15.59	-23.59*	11.36	56.86*	23.85
5	BML - 6 x BPPTI-34	71.39**	17.11	71.30**	13.31	178.69**	28.32
6	BML - 6 x CM - 131	42.60*	16.04	-35.60**	12.54	269.66**	28.94
7	BML - 6 x BPPTI-38	-26.40	19.45	-90.80**	20.50	251.59**	48.22
8	BML - 6 x BPPTI-35	-2.00	14.59	-94.50**	11.64	-41.57	31.67
9	BML - 6 x BPPTI-44	39.30**	10.16	25.702*	10.79	216.26**	25.38
10	BML - 7 x BML - 10	14.60	16.48	134.20**	18.45	34.80	31.30
11	BML - 7 x BML - 13	27.40	18.65	-6.20	21.52	-91.46*	35.63
12	BML - 7 x CM - 119	46.60**	12.51	23.40	16.16	22.00	21.87
13	BML - 7 x BPPTI-34	41.40*	15.74	81.10**	16.72	331.03**	35.95
14	BML - 7 x CM - 131	-1.80	13.12	21.80	20.68	-20.67	24.15
15	BML - 7 x BPPTI-38	-87.79**	14.29	-55.79**	20.44	-78.33*	30.04
16	BML - 7 x BPPTI-35	7.00	12.76	-0.90	14.66	29.84	25.24
17	BML - 7 x BPPTI-44	43.20*	19.05	-118.4**	18.22	127.06**	36.20
18	BML - 10 x BML - 13	54.80**	18.49	39.20*	19.57	52.40	33.81
19	BML - 10 x CM - 119	213.59**	19.48	114.59**	13.21	17.87	23.44
20	BML - 10 x BPPTI-34	37.59**	12.88	-39.89**	14.03	163.43**	26.22
21	BML - 10 x CM - 131	14.20	12.18	-45.80**	11.87	-12.67	34.09
22	BML - 10 x BPPTI-38	13.00	13.83	76.80**	17.82	-20.73	28.67
23	BML - 10 x BPPTI-35	74.19**	11.55	23.10**	8.11	94.90*	36.05
24	BML - 10 x BPPTI-44	51.30**	16.57	33.49*	16.54	43.67	34.23
25	BML - 13 x CM - 119	25.20	16.97	18.00	15.58	119.33**	30.81
26	BML - 13 x BPPTI-34	-25.20	16.76	-1.10	11.71	-22.57	24.53
27	BML - 13 x CM - 131	-72.60**	15.12	14.20	17.77	131.73**	30.22
28	BML - 13 x BPPTI-38	-75.39**	16.72	-25.99*	12.51	-114.7**	23.51
29	BML - 13 x BPPTI-35	-51.00**	16.74	-14.10	17.23	45.17	33.10
30	BML - 13 x BPPTI-44	-42.79*	18.38	111.79**	18.46	122.66**	31.65
31	CM - 119 x BPPTI-34	30.50*	13.03	33.40**	12.16	112.43**	26.88
32	CM - 119 x CM - 131	-15.60	15.01	-54.80**	18.23	36.80	24.97
33	CM - 119 x BPPTI-38	-48.99**	10.21	-41.60**	9.26	-45.00*	21.95
34	CM - 119 x BPPTI-35	32.80*	15.52	-14.70	12.84	93.96**	20.93
35	CM - 119 x BPPTI-44	54.40**	14.92	49.19**	18.08	-19.07	31.18
36	BPPTI- 34 x CM - 131	11.90	9.91	-80.19**	10.44	-46.56*	18.29
37	BPPTI- 34 x BPPTI-38	3.70	11.24	9.60	14.13	189.10**	23.90
38	BPPTI- 34 x BPPTI-35	105.90**	14.64	16.30	17.08	35.67	27.55
39	BPPTI- 34 x BPPTI-44	33.10**	12.36	3.80	15.71	-35.23	21.30
40	CM - 131 x BPPTI-38	-24.00	17.47	-20.60	17.69	-104.6**	30.87
41	CM - 131 x BPPTI-35	-4.60	13.31	-47.70**	10.67	18.63	24.11
42	CM - 131 x BPPTI-44	-169.8**	13.95	-22.00	19.26	-119.3**	36.31
43	BPPTI- 38 x BPPTI-35	68.00**	13.49	98.90**	16.41	-129.5**	22.52
44	BPPTI-38 x BPPTI-44	-53.19**	9.94	-38.80**	13.06	-71.93**	25.06
45	BPPTI-35 x BPPTI-44	-76.5**	14.70	82.00**	15.99	-11.63	32.39

Table 2: Estimates of generation mean parameters, mean (m), additive (d), dominance (h), additive × additive (i), additive × dominance (j) dominance × dominance (l) for grain yield in different generations of maize hybrids

	M	S.E	D	S.E	H	S.E	I	S.E	J	S.E	L	S.E	Epistasis
BML-6 x BML - 7	101.69**	5.92	28.40**	8.76	70.90*	31.35	-113.39*	29.45	7.60	8.81	37.90	47.43	C
BML-6 x BML-10	130.40**	5.93	-1.20	4.60	-86.57**	26.85	213.66**	25.44	-192.80**	4.69	-2.90	34.57	C
BML-6 x BML-13	116.93**	6.16	10.40	9.01	-63.83*	31.42	159.13**	30.52	-119.74**	9.79	43.30	46.15	D
BML-6 x CM-119	93.86**	3.52	15.00*	6.75	13.23	21.75	10.07	19.50	-33.47	6.91	35.30	36.04	C
BML-6 x BPPTI-34	120.40**	6.24	2.80	9.73	48.95	32.35	-106.70*	31.66	-36.00	9.78	0.05	48.14	C
BML-6 x CM-131	163.86**	5.75	-2.40	8.01	-224.77**	29.38	255.66**	28.04	-262.66**	8.13	39.10	43.17	D
BML-6xBPPTI-38	161.20**	7.79	5.20	5.22	-298.20**	37.65	486.00**	32.84	-368.80**	5.75	32.20	52.55	D
BML-6 x BPPTI-35	101.73**	6.60	16.40*	6.90	37.62	31.04	151.43**	29.79	-54.94	7.07	46.25	42.01	C
BML-6xBPPTI-44	129.86**	5.09	-9.301*	4.18	-103.86**	23.28	86.26**	22.02	-151.26**	5.91	6.80	30.40	D
BML-7xBML-10	80.39**	3.65	-48.6**	7.55	169.80**	25.16	-262.81**	21.01	114.005**	7.57	-59.80	43.51	D
BML-7x BML - 13	71.73**	3.23	-6.60	7.62	145.07**	25.97	-133.87**	19.97	112.67**	8.48	16.80	46.87	C
BML-7 xCM - 119	90.80**	2.47	0.80	7.49	86.99**	20.43	-118.00**	17.95	47.99**	7.59	11.60	37.09	C
BML-7x BPPTI-34	147.73**	5.76	-7.60	6.04	-164.08**	29.44	86.03*	26.01	-208.53**	6.06	-19.81	43.31	C
BML-7 x CM-131	95.33**	4.45	-43.8**	10.77	67.66*	29.11	-60.66	27.94	40.66	10.82	-11.79	49.38	D
BML-7 PPTI-38	94.26**	3.63	-33.50**	8.15	17.43	25.50	208.86**	21.85	-65.26**	8.47	-16.00	44.34	D
BML-7 x BPPTI-35	96.93**	2.69	-16.40**	5.32	4.52	18.94	17.63	15.11	-23.73	5.48	3.95	33.01	C
BML-7 x BPPTI-44	124.26**	4.57	74.20**	6.58	-140.46**	27.41	277.46**	22.52	-202.27**	7.75	80.80	44.75	D
BML-10xBML-13	78.80**	4.13	-26.79**	8.10	38.60	27.44	-135.60**	23.14	41.60	8.91	7.80	46.82	C
BML-10 x CM-119	77.06**	3.97	27.50**	10.03	346.33**	27.00	-638.53**	25.59	310.33**	10.11	49.50	46.47	C
BML-10xBPPTI-34	113.33**	3.84	39.80**	5.85	-83.88**	22.05	168.03**	19.32	-165.74**	5.87	38.75	35.14	D
BML-10xCM-131	93.33**	6.88	-13.20**	4.58	22.46	30.69	50.54	28.99	-18.94	4.71	30.00	38.70	C

BML-10xBPPTI-38	84.66**	3.84	-60.60**	7.17	167.63**	24.25	-200.34**	21.01	110.53**	7.52	-31.90	40.55	D
BML-10xBPPTI-35	96.00**	8.43	-6.00	5.36	18.65	35.96	-99.69*	35.39	2.40	5.52	25.55	41.94	C
BML-10xBPPTI-44	100.26**	5.08	-8.90	5.80	119.03**	27.14	-125.93**	23.39	41.13	7.10	8.90	41.36	C
BML-13xCM-119	115.33**	5.60	16.20	8.32	-83.53**	29.83	32.93	27.89	-76.13**	9.18	3.60	45.34	D
BML-13xBPPTI-34	96.13**	3.02	23.59**	6.37	67.51**	20.55	30.03	17.56	-3.73	7.38	-12.05	35.37	D
BML-13xCM-131	131.33**	4.66	-51.99**	7.61	-214.13**	26.85	248.53**	24.08	-190.13**	8.54	-43.39	42.91	C
BML-13xBPPTI-38	92.666**	2.24	-18.80**	6.36	64.23**	18.98	88.06*	15.55	13.34	7.71	-24.70	34.65	D
BML-13xBPPTI-35	113.867**	5.72	-15.40	8.07	-102.62**	30.44	175.36**	28.00	-110.27**	8.97	-18.45	46.22	C
BML-13xBPPTI-44	125.06**	4.86	-60.50***	8.75	-34.87	28.99	-15.33	26.17	-53.66*	10.34	-77.29	47.18	C
CM-119xBPPTI-34	98.93**	5.23	21.60**	6.56	-13.98	26.10	-15.37	24.70	-48.54	6.68	-1.45	37.57	C
CM-119x CM-131	117.20**	2.98	-1.60	8.83	-86.79**	23.96	177.59**	21.30	-107.20**	8.97	19.60	43.26	D
CM-119xBPPTI-38	77.20**	4.76	-10.40	5.41	-35.30	22.57	136.19**	21.90	-45.59*	5.99	-3.70	30.84	C
CM-119xBPPTI-35	114.67**	3.84	14.20	8.64	-65.81**	24.19	57.76	23.12	-75.86**	8.82	23.75	40.40	D
CM-119xBPPTI-44	83.34**	5.20	6.80	7.81	154.06**	28.49	-226.27**	26.02	122.66**	8.89	2.60	44.13	C
BPPTI-34xCM-131	93.13**	3.42	1.80	5.72	38.32*	18.83	90.020**	17.82	-21.73	5.83	46.05	29.30	C
BPPTI-34xBPPTI-38	121.60**	4.59	-32.69**	7.05	-147.65**	24.39	162.49**	23.16	-175.80**	7.41	-2.95	36.96	C
BPPTI- 34 x BPPTI-35	97.06**	3.63	12.20	7.55	136.63**	23.99	-208.74**	20.94	86.53**	7.67	44.80	40.88	C
BPPTI- 34 x BPPTI-44	74.66**	2.52	-4.20	6.89	140.38**	19.47	-109.04**	17.07	72.13**	8.02	14.65	34.83	C
CM - 131 x BPPTI-38	92.40**	4.71	12.80	8.75	88.09**	28.46	-15.40	25.70	59.99*	9.10	-1.70	46.67	D
CM - 131 x BPPTI-35	111.33**	4.90	33.20**	6.83	-72.28**	24.89	123.23**	23.87	-70.93**	7.03	21.55	36.43	D
CM - 131 x BPPTI-44	71.86**	5.55	-48.50**	5.41	-56.27	28.56	264.26**	24.68	-72.46**	6.86	-73.90	42.26	C
BPPTI- 38 x BPPTI-35	65.33**	1.83	-18.30*	7.26	306.21**	19.44	-463.37**	16.26	296.46**	7.71	-15.45	36.75	D
BPPTI-38 x BPPTI-44	86.66**	4.33	3.70	3.94	31.03	21.08	112.06**	19.04	-20.07	6.11	-7.20	29.61	D
BPPTI-35 x BPPTI-44	95.86**	5.10	-65.50**	5.44	50.78	26.32	-22.63	23.11	17.13	6.92	-79.25	39.02	D

This indicated inadequacy of additive dominance model and confirmed the role of epistatic components. Study of various main gene effects for yield revealed that both additive 'd' and the dominance 'h' component were found to be important in their effect. The magnitude of dominance was higher than additive effect and varied between the crosses. Thus, it was evident that dominance effect primarily governed yield (Table 2). The parameter 'm' was significant for all the crosses for yield. Nine cross combinations viz., BML-6 × BML-7, BML - 6 × CM - 119, BML-6 × BPPTI-35, BML-7 × BPPTI-44, BML - 10 × CM - 119, BML-10 × BPPTI-34, BML-13 × BPPTI-34, CM-119 × BPPTI-34 and CM-131 × BPPTI-35 possessed significant positive additive effects. Among these, BML-6 × BPPTI-35, BML- 7 × BPPTI-44, BML- 10 × BPPTI-34 and CM-131 × BPPTI-35 had significant additive × additive epistatic component. Similar results were reported by Amer (2004) and Ma *et al.* (2007). Thus, these crosses could be exploited to spot true breeding and high yielding segregants from the F<sub>2</sub> base materials.

Significant positive 'h' gene effects were registered in 16 crosses at Karimnagar. Guo *et al.*(1986), Muhammad Saleem *et al.* (2002), Barati *et al.* (2003), Haq *et al.* (2010) also reported significant non additive effects for grain yield per plant. The crosses; BML-7 × BML-10, BML-7 × CM-119, BML-10 × CM-119, BML-10 × BPPTI-38, BML-10 × BPPTI-44, BML-13 × BPPTI-34, BML-13 × BPPTI-38, CM-119 × BPPTI-44, BPPTI-34 × CM-131, BPPTI-34 × BPPTI-44, CM-131 × BPPTI-38 and BPPTI-38 × BPPTI-35 possessed significant 'h' effects. Since 'h' effects arising from non additive gene action cannot be fixed in nature as such these hybrids could be utilized in heterosis breeding. Though, in crosses; BML-13 × BPPTI-38 and BPPTI-34 × CM-131, 'h' component was significant, the additive × additive epistatic interaction was also significant. Therefore, in these crosses, careful selection could be rewarding to get homozygous

high yielding lines from segregating generations. Though, in crosses, BML- 6 × BML-7, BML-10 × CM-119 and BML-13 × BPPTI-34, 'h' component was significant, the 'd' component was also significant. Apart from using the hybrids in heterosis breeding, they can be utilized for spotting true breeding and high yielding segregants from the F<sub>2</sub> base materials.

Study of interaction components revealed that additive × additive (i) type of epistatic gene effect were more predominant at Karimnagar location. Similar, results were reported in sweet corn hybrids by Jyothi kumara *et al.*, (2009) and Haq *et al.* (2013). Twenty crosses exhibited positive significant additive × additive type of gene effects for yield. Thus, these crosses could be exploited to spot true breeding and high yielding segregants from future generations. Similarly, 10 crosses for 'j' component also exhibited significant positive gene effects for high grain yield. None of the crosses exhibited significance for 'l' component. On contrary, Jyothi kumara *et al.* (2009) reported significant 'l' component for cross; DMB 323 × SCI 310 of sweet corn hybrid. The sign of 'l' and 'h' components were in opposite direction for most of the crosses studied indicating duplicate type of gene action (Table 2). Duplicate type of epistasis was also observed by Jyothi kumari *et al.* (2009) and Haq *et al.* (2013) in the studies conducted on maize hybrids.

In the present investigation, generation mean analysis revealed that the crosses with additive 'd' gene action could be improved by progeny selection in early generations where as the hybrids with significant 'h' components may be utilized for heterosis. The genotypes with significant d and h components may be improved through family selection with intermating. The crosses; BML- 6 × BML-7, BML- 10 × CM-119 and BML-13 × BPPTI-34 can be used for isolating inbred lines in the early generations and can be exploited commercially as single cross hybrids.

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