QUANTITATIVE INHERITANCE OF YIELD AND ITS COMPONENT TRAITS IN MAIZE (*Zea mays* L.)

K. MURALI KRISHNA*, G.K. CHIKKAPPA, K. SINGH DANGI and N. KULKARNI

College of Agriculture, Professor Jayashankar Telangana State Agricultural University (PJTSAU), Rajendranagar,
Hyderabad, Telangana State, India
*Corresponding author's email: kmurali73@yahoo.com
Email addresses of co-authors: chikkappagk@gmail.com, dangiks24@gmail.com, nm_kulkarni@hotmail.com

SUMMARY

The genetics of yield and its contributing traits 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 test of A, B, C were significant indicating role of epistatic effects. In general, the magnitude of dominance effect was higher than additive effect indicating that yield and its components are largely governed by dominance effect. A breeding procedure which exploit both additive and dominance components, such as family selection with intermating, will be suitable for improvement of yield and its traits. The epistasis was complementary and duplicate type in the crosses for grain yield and its contributing traits.

Key words: Generation mean analysis, gene effects, dominance, epistasis, complementary, duplicate

Key findings: Adequate genetic variability was observed in the breeding material evaluated which may be exploited further in breeding programmes. The crosses, BML-13 x CM-119 and BML-13 x CM-131 exhibited significant additive, dominance and additive x additive effects for grain yield. These crosses can be utilized for isolating desirable lines in the early generations and also can be exploited for heterosis breeding.

INTRODUCTION

Maize is one of the important cereal food crops of the world; it has the highest production (827 M t) with an average productivity of greater than 5 t/ha. It is being grown on approximately 161 M ha across the globe. Under the scenario of shrinking natural resources, climate change and burgeoning population, the demand for maize will continue to increase in coming days. However, the challenge to meet the future demand under shrinking resources like land, the need to increase in per unit production i.e. productivity is very high. In this context, enhancement of yield is of urgent need. Since yield is a complex trait and is governed by several yields contributing traits like ear length, ear girth, number of kernels per row, number of kernel rows, test weight and PFSR disease score etc. The study of genetics of yield and its components is necessary to understand the inheritance pattern of the characters.

The nature and magnitude of genetic variation present in the population is elucidated by genetic analysis of quantitative traits. Estimating the type of gene effects in plant

population is essential to decide the type of breeding procedure to be followed (Arora *et al.,* 2010). Applying the generation mean analysis as the most common tool helps in the estimation of gene effects and components of genetic variance (Hayman and Mather, 1955).

Thus, knowing the genetic diversity and relationships among breeding materials is essential to the plant breeders for improving the crop. Therefore, the present investigation was taken up to study gene action of quantitative traits in nine high yielding crosses of maize under PFSR stress conditions.

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 diallel fashion in *rabi* 2010 and generated hybrids were back crossed with both the parents during *kharif* 2011. Experimental materials were sown at Maize Research Centre, A.R.I, Rajendranagar on 20-09-2011 in a complete randomized block design with two replications. The parents and F_1^s were sown in single row, F_2^S in four rows while BC_1 and BC_2s in each of two rows plot of four meters length. The spacing adopted was 75 cm between rows and 20 cm within the row. All the recommended package of practices was adapted. Data was collected on ten competitive plants from P_1, P_2 and F_1, 40 plants from B_1 and B_2 and 60 plants from F_2 generations for each cross for grain yield and its contributing traits.

The genetic parameters namely *m, d, h, i, j* and *l* were estimated by following the scaling tests A, B, C and D of Mather and Jinks (1971) and six parameter models of Hayman (1958). The analysis was carried out on nine best heterotic and high yielding crosses using Windostat 8.0 Advanced Plant Breeding package (Indostat Services, Hyderabad) as per Hettiarachchi *et al*. (2009).

RESULTS AND DISCUSSION

Scaling tests of ABC values were significant in most of the crosses for yield and its characters.

This indicated inadequacy of additive dominance model and confirmed the role of epistatic components. Study of various main gene effects for yield and its components revealed that both additive '*d*' and the dominance '*h*' component were important. The magnitude of dominance was higher than additive effect and varied between the crosses (Table 1). Thus, it is evident that dominance effect primarily governed the yield and yield contributing characters.

The parameter 'm' was significant indicating variability among all the crosses. For flowering and maturity, positive sign indicates long duration and negative sign earliness. Five crosses recorded significance in negative direction for days to tasseling and silking and four crosses for maturity for additive gene effects and additive x additive allelic interaction. These crosses can be used for developing early duration inbreds. The additive and additive x additive gene effects for days to tasseling, days to silking and days to maturity is indicative of a good potential in the improvement of these traits. Prevalence of epistasis is indicative of greater genetic diversity in the parental lines. Similar results were reported by Hassan *et al.,* 2012. Eight crosses recorded significant dominant variance in negative direction for days to tasseling and silking and four crosses exhibited negative significance for '*h*' component for maturity. In case where dominance was of major importance, the trait could be successfully utilized in the formation of hybrids and promoting earliness in the material. Similar results were reported by Hassan *et al.,* 2012, Iqbal *et al.,* 2011, Sofi *et al.,* 2006 and Saleem *et al.,* 2002 for tasseling, Darrah and Hallauer, 1972 for silking and by Abadi, 2011, Tollenaar *et al.,* 2004 for maturity. Atanaw *et al.,* 2006 reported contrasting effects for these characters in maize and they were of the opinion that these traits were mainly controlled by additive type of gene action. These crosses can be utilized for hybrid development as non-additive gene action is of higher magnitude. The cross, BML-13 x CM-131 recorded negative significance for *d, h, i, j, l* components. This cross can be utilized for isolating pure lines from segregating generations and also can be utilized for heterosis breeding.

Table 1. Gene effects for grain yield and yield components in nine crosses of maize.

		Days to 50 % tasseling						Days to 50 % silking					
	Crosses	m	d	h	i	j	l	m	d	h	i	j	l
1	BML-6 x BML-10	70**±0	3**±0.57	-3.2**±1.45	-6**±1.15	4.05**±1.04	12.5**±2.91	74**±0	3**±0.61	-7.95**±1.81	-12**±1.21	4.05**±1.07	19.9**±3.62
2	BML-6 x BML-13	70**±0.13	-3.5**±0.28	-10.7**±1.09	-9**±0.77	-2**±0.8	11.4**±1.98	74.5**±0.06	-4**±0.22	-16.35**±1.39	-18**±0.52	-2.55**±0.84	26.7**±2.75
3	BML-6 X CM-131	71**±0.13	-1.5**±0.08	-0.35±1.16	-3**±0.54	0.15±0.97	4.7**±2.13	74**±0.26	-1.6±0.96	2±1.44	-2±1.06	1.6±0.96	2±2.25
4	BML-7 x BPPTI-38	76**±0	-0.5±0.08	-16.8**±1.22	-19**±0.16	-0.4±1.1	27.6**±2.44	77.5**±0.06	-0.5**±0.08	-10.95**±1.17	-13**±0.3	-0.55±1.02	17.9**±2.31
5	BML-7 x CM-131	72**±0.2	0.50**±0.08	-0.6±1.48	-0.1±1.05	-0.1±1.0	1.2±2.36	75**±0.26	`0.50**±0.08	-4.8**±1.42	-5**±1.05	-0.2±5.6	5.6**±2.21
6	BML-10 x BML-13	65.03**±0.38	2**±0	-8.38**±0.88	-8.1**±1.55	2.45**±0.83	36.63**±2.64	68.53**±0.32	1**±0	-7.53**±1.68	-8.1**±1.29	**1.4±0.84**	32.93**±2.5
7	BML-13 x BPPTI-34	62.5**±0.19	-4**±0	-7.65**±1.11	-2**±0.78	-4.05**±0.79	25.3**±1.76	64.5**±0.19	-4.00**±0	-6.75**±1.14	-2**±1.78	-4.05**±0.83	27.5**±1.84
8	BML-13 x CM-119	70.5**±0.32	-2**±0	-5.65**±1.6	-6**±1.3	-2.05**±0.88	13.3**±2.28	73**±0.26	-2**±0	-4.4**±1.46	-4**±1.04	-1.9**±0.9	6.8**±2.31
9	BML-13 x CM-131	70**±0	-3**±0	-3.35**±0.95	-2**±0	-2.85**±0.94	4.7**±1.18	74**±0.13	-3**±0	-11.45**±1.06	-10**±0.52	-2.85**±0.91	12.9**±1.93

		Days to maturity						Plant height (cm)					
		m	d	h	i	j	l	m	d	h	i	j	l
1	BML-6 x BML-10	110**±0	1**±0.01	-6.3**±0.916	-8**±0.2	2.2**±0.83	4.6*±1.8	200.55**±3.834	10.6**±3.449	43.21*±20.76	35*±16.816	22.81**±3.945	-80.62*±31.913
2	BML-6 x BML-13	107**±0.13	2.5**±0.48	4.2**±1.38	3**±1.1	4.2**±0.96	-4.4±2.61	193.28**±3.83	-27.77**±3.34	77.77**±17.07	46.71**±16.72	-15.41**±3.91	-28.68±21.48
3	BML-6 X CM-131	107**±0.13	-1.5**±0.08	2.7**±1.08	1±0.54	-0.3±0.93	-1.4±1.96	228.48**±2.22	-15.5**±5.55	-19.26±14.47	-53.03**±14.23	5.95±5.79	71.8**±24.5
4	BML-7 x BPPTI-38	107**±0	1**±0.16	5.2**±1.13	6**±0.32	0.7±1.04	-2.4±2.26	227.96**±2.66	24.47**±5.14	11.34±20.74	-34.91±14.81	-14.27**±5.48	3.43±37.16
5	BML-7 x CM-131	107**±0	-2.5**±0.4	-11.8**±1.23	-11**±0.8	-3.8**±0.96	27.6**±2.47	232.48**±3.17	-13.37**±4.94	25.78±16.54	-5.98±16.1	-14.62**±5.29	48.5*±24.68
6	BML-10 x BML-13	105.53**±0.19	1**±0	0.86±1.11	-0.13±0.77	1.5±0.79	12.13**±1.76	**201.95**±1.94**	28**±3.88	-64.55**±12.69	-69.9**±10.99	28.15**±4.45	167.3**±21.52
7	BML-13 x BPPTI-34	107.5**±0.06	-2*±0	-1±0.9	-2**±0.26	-2**±0.85	10**±1.76	197**±3.37	-5.27±4.72	30.65±17.56	4.55±16.47	-26.67**±5.13	-5.3±26.22
8	BML-13 x CM-119	107.5**±0.19	1**±0	-12.5**±1.17	-12**±0.78	1±0.81	27**±1.93	183.61**±2.95	-18**±3.74	96.78**±14.6	85.53**±13.98	-9.55**±4.74	-24.04±20.86
9	BML-13 x CM-131	108**±0.13	-3*±0	-5.5**±1.06	-6**±0.52	-3.5**±0.9	13**±1.91	170.96**±3.39	6.8±3.09	88.43**±17.47	90.53**±14.9	15.89**±3.65	-7.54±25.87

		Ear height (cm)						Ear length (cm)					
		m	d	h	i	j	l	m	d	h	i	j	l
1	BML-6 x BML-10	100.23**±2.06	-5.77**±1.87	10.3±11.2	3.41±9.01	-3.27±2.03	-55.94**±17.33	15.23**±0.28	1.58**±0.43	7.11**±1.51	1.79±1.43	0.65±0.44	-5.64**±2.27
2	BML-6 x BML-13	82.8**±2.2	-4.15±2.69	60.84**±10.48	42.3**±10.35	-0.4±2.79	-35.69**±14.34	14.23**±2.29	-1.47**±0.46	8.66**±1.63	4.15**±1.48	-2.6**±0.47	-8.78**±2.56
3	BML-6 X CM-131	113.26**±2.48	-16.92**±4.58	-26.87±13.92	-55.81**±13.53	-9.18*±4.65	75.47**±21.85	16.65**±0.31	1.45**±0.5	1.73±1.82	-3.94**±1.6	1.08*±0.52	3.15±2.94
4	BML-7 x BPPTI-38	104.23**±1.7	5±2.62	42.66**±12.4	16.96*±8.61	6.49*±2.74	-59.46**±21.79	15.81**±0.33	0.56±0.6	2.3±1.9	-5.24**±1.8	-0.64±0.61	7.37±3.02
5	BML-7 x CM-131	109.03**±2.64	-18.95**±3.11	35.56**±12.55	-2.23±12.25	-11.95**±3.24	5.94±17.19	16.22**±0.34	0.86*±0.44	7.29**±1.89	0.07±1.62	0.75±0.47	-1.17±2.97
6	BML-10 x BML-13	104.18**±3.08	4.92*±2.46	-94.63**±13.51	-98.18**±13.27	6.17*±2.6	139.7**±16.56	14.9**±0.38	-0.66±0.4	-0.36±2.11	-3.48±1.75	-0.85±0.41	-2.7±3.28
7	BML-13 x BPPTI-34	87.2**±1.52	-6.02±3.34	-3.45±9.64	-17.65±9.06	-14.02**±3.43	40.9±16.12	15.38**±0.4	0.77±0.59	4.21±2.22	-3.57±2.02	0.37±0.59	2.57±3.43
8	BML-13 x CM-119	75.48**±1.34	1.67±2.88	74.46**±8.39	74.61**±7.89	6.93**±3.03	-72.45**±13.94	14.93**±0.29	1.63**±0.33	8.75**±1.49	2.58±1.36	1.51**±0.35	-10.11**±2.17
9	BML-13 x CM-131	78.16**±1.22	-12.5**±3.19	28.43**±10.25	25.43**±8.05	-8.5**±3.31	16.46±18.66	14.27**±0.2	0.5±0.54	10.8**±1.45	5**±1.37	1.26±0.56	-9.49**±2.53

(cont'd)

Table 1. Gene effects for grain yield and yield components in nine crosses of maize.

	Crosses	Ear girth (cm)						Number of kernels per ear					
		m	d	h	i	j	l	m	d	h	i	j	l
1	BML-6 x BML-10	12.87**±0.18	0.46±0.24	5.77**±0.89	1.61±0.87	0.36±0.26	-3.8**±1.29	370.4**±15.59	57*±26.5	828.04**±86.1	542.7**±81.85	32.24±26.73	-767.29**±134.1
2	BML-6 x BML-13	12.39**±0.18	0.02±0.29	2.82*±1.18	0.26±0.94	-0.3±90.3	-3.69±1.98	459.48**±11.01	1.62±22.31	116.81±82.79	-83.58±62.7	-28.38±22.55	-61.96±146.9
3	BML-6 X CM-131	13.55**±0.16	0.82**±0.31	1.68±1.04	-2.28**±0.9	0.64*±0.32	0.54±1.75	532.91**±18.29	42.82±27.57	221.33*±99.67	-67.71±91.63	25.56±27.77	-159.13±153.9
4	BML-7 x BPPTI-38	13.4**±0.2	-0.18±0.29	0.83±1.03	-3.46**±1	-1.43**±0.31	2.36±1.52	444.61**±8.93	-49.62±9.45	78.92±77.95	-192.96*±68.9	-82.6**±29.53	253.27±143.1
5	BML-7 x CM-131	13.45**±0.14	-0.54*±0.23	3.52**±0.77	-0.93±0.73	-1.02**±0.25	0.45±1.2	450.45**±13.91	-49.7**±14.86	154.3*±71.8	-161.3*±63.09	-55.21**±15.05	364**±106.5
6	BML-10 x BML-13	12.79**±0.2	0.81**±0.24	2.49*±1.17	-1.01±0.96	0.48±0.26	-1.23±1.83	464.83**±15.63	24.4±18.06	-111.27±96.86	-357.03**±72.23	**19.14±18.2**	455.22**±160.6
7	BML-13 x BPPTI-34	11.92**±0.15	0.92**±0.26	3.9**±0.86	-0.49±0.79	0.45±0.27	-0.19±1.37	377.35**±12.21	75.7**±21.16	310.75**±71.22	43±64.64	50.95*±21.24	-70.91±114.6
8	BML-13 x CM-119	12.3**±0.16	0±0.3	5.6**±1.01	1.31±0.9	-0.09±0.31	-4.04**±1.67	435.2**±15.75	62.5*±25.6	509.1**±95.77	177.3*±81.22	53.01*±25.7	-381.8**±157.4
9	BML-13 x CM-131	12.55**±0.13	-0.31±0.23	5.89**±0.79	2.03**±0.7	-0.07±0.24	-5.98**±1.3	432.06**±11.29	-28.47±23.59	335.84**±81.46	130.18*±65.31	-15.72±23.69	-438.35**±142.9

	Crosses	Number of kernels per row						Number of kernel rows					
		m	d	h	i	j	l	m	d	h	i	j	l
1	BML-6 x BML-10	28.21**±1.11	3.42*±1.43	36.09**±5.41	17.48**±5.3	1.92±1.44	-41.9**±7.6	14.9**±0.32	0.4±0.37	6.47**±1.58	2±1.51	-0.26±0.39	-7.74**±2.22
2	BML-6 x BML-13	30.78**±0.7	2.12±1.26	15.25**±5.11	-1.88±3.78	0.19±1.26	-18*±8.99	14.6**±0.23	-1.2**±0.44	1.72±1.53	-0.8±1.3	-1.91**±0.45	-5.05±2.59
3	BML-6 X CM-131	33.15**±1.01	3.8*±1.53	22.00**±5.41	0.6±5.09	2.81±1.54	-20.2*±8.21	16.2**±0.3	-0.8*±0.37	1.07±1.56	-2.4±1.42	-1.46**±0.4	-6.15**±2.3
4	BML-7 x BPPTI-38	30.4**±0.66	4.17±2.16	10.63**±5.33	-11.35*±5.08	1.84±2.16	5.14±9.61	14.5**±0.25	-13.87**±2.77	28.98**±5.67	24.15**±5.64	-14.5**±2.77	-53.6**±11.2
5	BML-7 x CM-131	32.15**±0.69	-1.2±0.86	9.57**±3.55	-11.5**±3.25	-1.52±0.87	4.66±5.24	15.4**±0.22	-0.4±0.22	0.78±1.15	-4*±1.02	-0.56±0.26	0.84±1.67
6	BML-10 x BML-13	31.76**±1.09	-0.02±1.1	-10.87±5.51	-20.41**±4.91	-0.45±1.11	-6.11±8	14.66**±0.19	0.2±0.23	3.91**±1.16	-1.46±0.91	0.14±0.25	-0.9±1.89
7	BML-13 x BPPTI-34	31.8**±0.8	1.42±1.24	18.86**±4.21	-5.65±4.07	-0.11±1.24	-13.7*±6.3	12.8**±0.22	1.8**±0.34	3.32*±1.29	0.4±1.14	1.92**±0.35	-1.84±2.04
8	BML-13 x CM-119	30.78**±0.78	3.97*±1.37	32.74**±4.57	8.01±4.16	3.41*±1.38	-32.6**±7.37	14.2**±0.21	0.07±0.09	5.71**±1.33	1.6±1.1	-0.07±0.35	-8.23**±2.21
9	BML-13 x CM-131	31.23**±0.63	0.17±1.39	24.84**±4.27	6.61±3.76	1.11±1.39	-38.6**±7.34	14.1**±0.13	-1.4*±0.33	4.19**±1.16	0.8±0.86	-1.35*±0.34	-7.18**±2.12

	Crosses	100 Kernal weight (gm)						Grain yield/plant (gm)					
		m	d	h	i	j	l	m	d	h	i	j	l
1	BML-6 x BML-10	23.25**±0.48	**-1.27±0.87**	5.14±2.87	-0.85±2.6	-3.56**±0.89	11.92±4.66	104**±6.07	-11.87*±4.82	172.25**±28.88	50.15±26.14	-28.37**±4.88	1.9±39.57
2	BML-6 x BML-13	23.1**±0.77	1.4±1.1	32.32**±4.39	21.6**±3.79	-1.42±1.12	-25.05**±6.98	102.33**±4.9	-11.37±6.76	194.01**±31.16	107.01**±23.81	-27.87**±6.81	-175.36**±52.27
3	BML-6 X CM-131	25.6**±0.56	3.6**±1.13	15.38**±3.68	5.6±3.2	2.12±1.15	0.44±6.24	153.26**±7.27	14.5*±6.88	46.78±37.65	-74.96*±32.17	10.75±6.94	105.36*±55.97
4	BML-7 x BPPTI-38	29.3**±0.69	-5.2**±1.58	1.48±4.3	-11.6**±4.2	-7.87**±1.6	16.64**±7.15	137.06**±4.91	29.87**±8.57	72.63*±29.42	-80.51**±26.07	17.12±8.6	160.06**±48
5	BML-7 x CM-131	29.45**±0.87	4**±1.15	13.83**±4.55	2.2±4.18	3.17**±1.18	-7.07±6.8	160.83**±5.91	20.77**±7.22	127.46**±30.25	-22.68±27.73	23.02**±7.28	3.33±44.51
6	BML-10 x BML-13	31.2**±0.67	5.22**±0.7	-10.43**±3.62	-17.65**±3.03	4.69**±0.73	4.87±5.57	142.95**±6.85	11.77±6.19	-48.24±35.06	-128.35**±30.08	11.77±6.22	53.09±51.61
7	BML-13 x BPPTI-34	24.7**±0.72	0.8±0.91	14.92**±3.58	2±3.41	-0.17±0.94	-3.05±5.14	103.66**±4.74	17.42*±7.55	133.63**±26.73	2.48±24.26	13.67±7.58	35.66±42.15
8	BML-13 x CM-119	29.8**±0.63	5.2**±1.17	5.44±4.25	-8.8*±3.46	4.5*±1.19	1.91±7.28	120.9**±4.74	24.67**±5.57	170**±26.51	44.85*±22	23.92**±5.61	-118**±41.61
9	BML-13 x CM-131	30.46**±0.44	4.6**±0.78	19.73**±2.52	-1.46±2.37	5.94**±0.81	6.65±3.99	108.68**±3.01	21.37±10.36	268.26**±24.42	145.51**±23.98	34.12**±10.4	-221.26**±44.15

For plant height, four hybrids exhibited significant '*d*' and '*h*' components. Two hybrids *viz.,* BML-6 x BML-10 and BML-13 x CM-131 recorded significant *d, h, i, j* components. Similar results were reported by Gamble, 1961 for dominance effects for this trait. Therefore, a breeding strategy which utilizes both additive and non-additive gene action such as family selection with intermating may be suitable for improvement of these populations as suggested by Hettairachi *et al.,* 2009. The hybrid BML-6 x BML-10 also exhibited high mean value for plant height and can be utilized for fodder purpose.

For ear length, four crosses for '*d*' and five crosses for '*h*' exhibited positive significance with higher magnitude for dominance variance. The crosses *viz.,* BML-6 x BML-10, BML-7 x CM-131 and BML-13 x CM-119 exhibited positive significance for *d* and *h* components. The most suitable known breeding procedure for the improvement of such trait is reciprocal recurrent selection which utilizes all kinds of gene effects. Cross BML7 x CM-131 also exhibited high mean value for this trait. Hence these crosses can be utilized for hybrid development.

Two crosses, BML-10 x BML-13 and BML-13 x CM-34 exhibited positive significance effects for '*d*' and '*h*' in case of ear girth. Jyothi *et al.,* 2009 showed dominant gene effects solely played a predominant role in the inheritance of ear girth.

The cross, BML-6 x BML-10 exhibited positive significant effects for *d, h* and *i* components pertaining to kernels per ear and kernels per row. Since '*d*' and '*i*' components are significant, desirable pure lines can be selected from early generations. The cross, BML-6 x CM-131 exhibited positive significance for '*h*' component coupled with high mean value for kernels per ear and kernels per row. Therefore, this cross can be utilized for heterosis breeding.

Only one cross, BML-13 x BML-34 exhibited positive significance for d and h components for kernel rows. This cross can be utilized for isolating purelines as additive variance is fixable and can also be utilized for heterosis breeding. Similar results were reported

by Jyothi *et al.,* 2009 for kernels per row and kernel rows.

Three crosses *viz.,* BML-6 x CM-131, BML-7 x CM-131 and BML-13 CM-131 recorded positive significance for d and h components for 100 kernel weights with higher magnitude for dominance effect.

Six crosses exhibited positive significance for additive variance and seven crosses for dominance variance for grain yield under stressed conditions. Five crosses expressed positive significance for both '*d*' and '*h*' components. The magnitude of dominance was higher than additive effect and varied between crosses. Thus, it is evident that dominance effect primarily governed yield. Therefore, a breeding procedure which utilizes both additive and dominance variance such as reciprocal recurrent selection can be used for developing hybrids and isolating promising lines for grain yield. Two crosses *viz.,* BML-13 x CM-119 and BML-13 x CM -131 exhibited significant *d, h*, and *i* components. Therefore, these crosses can be utilized for isolating desirable lines in the early generation of yield and also can be exploited for heterosis breeding as '*h*' component is of higher magnitude. Four crosses exhibited complementary epistasis for '*h*' component and therefore these crosses can be used for hybrid development.

CONCLUSION

In this investigation, generation mean analysis revealed that the crosses with additive '*d*' gene action could be improved by progeny selection in early generations whereas 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-13 x CM-131 for flowering, BML-6 x BML-10 for plant height and ear length, kernels per ear and kernels per row, BML-13 x CM-34 for ear girth and kernel rows, BML-13 x CM - 131 for 100 kernel weight and grain yield recorded significant positive standard heterosis and significant '*d'* and '*h'* components. These can be exploited as desirable single crosses

commercially and for further breeding programmes.

REFERENCES

Alamnie Atanaw, Mruthunjaya Wali, Salimath C, Jagadeesh PM, R (2006). Combining ability and heterosis for grain yield and ear characters in maize. *Karnataka Journal of Agriculture Science.* 19 (1):13-16

Arora D, Jindal SK, Ghai TR (2010). Quantitative inheritance for fruit traits in inter varietal crosses of okra (Abelmoschus esculentus L.Moench). *Electron. J. Plant Breed.* 1:1434-1442.

Abadi JM, Khorasani SK, Sar BS, Movafeg S, GolbashiM (2011). Estimation of combining ability and gene effects in forage maize (*Zea mays* L.) using line x tester crosses. *J Physiol Breed*.1 (1):57-67.

Gamble EE (1962). Gene effects in corn (*Zea mays* L.). II Relative importance of gene effects for plant height and certain component attributes of yield. *Can. J. Plant Sci.* 42: 349-358.

Darrah LL, Hallauer AR (1972). Genetic effects estimated from generation means in four diallel sets of maize inbreds. *Crop Sci.* 12(5): 615-621.

Hayman BI, Mather R (1955). The description of genetic interaction in continuous variation. Biometrics. 11: 69-82.

Hayman BI (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity.* 12: 271-90.

Hettiarachchi K, Prasanna BM, Rajan A, Singh ON, Gowda KTP, Pant SK,Sangit Kumar.(2009). Generation mean analysis of turcicum leaf blight resistance in maize.*Indian J. Genet.* 69 (2): 102-108.

Hassan Sher, Muhammad Iqbal, Kiramat Khan, Muhammad Yasir, Hameedur Rahman, (2012). Genetic analysis of maturity and flowering characteristics in maize (*Zea mays* L.). *Asian Pac J Trop Biomed.* 2(8): 621-626.

Iqbal M, Khan K, Sher H, Rahman H (2011). Genotypic and phenotypic relationship between physiological and grain yield related traits in four maize (*Zea mays* L.) crosses of subtropical climate. *J Sci Res Essays*.6 (13): 2864-2872.

Jyoti Kumari, Gadag RN, Singh RD (2009). Quantitative inheritance of yield and related attributes in sweet corn (*Zea mays* L.). *Crop Research*. 38 (1, 2& 3): 170-175.

Mather K, Jinks JL (1971). *Biometrical Genetics*, 2nd edition. Chapman and Hall, London.

Sofi P, Rather AG, Venkatesh S (2006). Detection of epistasis by generation mean analysis in maize hybrids. *Pak J Biol Sci*. 9 (10):1983-1986.

Saleem M, Shahzd K, Javid M, Ahmad A (2002). Genetic analysis for various quantitative traits in maize (*Zea mays* L.) inbred lines. *Int J Agric& Biol*. 4 (3); 379-382.

Tollenaar M, Ahmadzadeh MA, Lee EA. (2004). Physiological basis of heterosis for grain yield in maize.*Crop Sci*. 44:2086-2094.