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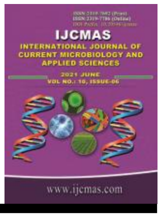

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Combining Ability and Heterosis for Kernel Yield and Yield Attributes in Maize (*Zea mays* L.)

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ABSTRACT

Analysis of 45 cross combinations made in a half diallel mating and studied in *Rabi*, 2016-17 for yield and yield components revealed that both additive and non-additive type of gene actions with predominance of non-additive gene action was found to be important for days to 50% tasseling, days to 50% silking, plant height, SPAD chlorophyll meter reading (SCMR), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, 100 kernel weight and kernel yield per plant. The crosses *viz*., BML15×PDM1474, BML7×DFTY, and BML15×PDM1452 were considered as outstanding crosses as they have recorded significant positive heterosis and sca effects in the desirable condition for most of the yield contributing characters and hence can be recommended for commercial cultivation after extensive testing under different environments and locations. All other cross combinations involving good×poor, poor×good or poor×poor may be handled through heterosis breeding while the cross combinations with good×good combiners through recurrent selection programmes to develop high yielding hybrids and isolate improved inbred lines, respectively.

Keywords

Multi-parent hybrids, heterosis, cross-pollinated crop, biological feasibility

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Introduction

Maize (*Zea mays* L.) is a highly cross-pollinated crop and the scope for exploitation of hybrid vigour will depend on the direction and magnitude of heterosis, biological feasibility and the type of gene action involved. The magnitude of heterosis provides information on the extent of genetic diversity of parents involved in developing superior F_1's so as to exploit hybrid vigour. Single cross hybrids are the most desirable as the breeding and seed production is much easier than the multi-parent hybrids (Vasal *et al*., 1995). This necessitates identification of superior inbreds for further enhancing productivity of hybrids. Gene action studies facilitates decision making of a suitable breeding procedure for genetic improvement of various quantitative traits (Jinks and Hayman, 1963) (Reza *et al.*,2004 and Begum, *et al.*, 2013). Diallel cross analysis provides the estimates of genetic parameters *viz*., combining ability and dominance relationship of the parents used for the first filial generation with or without reciprocals. The present investigation involving 45 cross combinations derived through diallele mating design was carried to identify the superior hybrid combinations, gene action governing different yield components and the magnitude of heterosis for yield and yield components based on combining ability studies.

Materials and Methods

Ten diverse maize inbred lines were crossed in all possible combinations without reciprocals. Inbreds and their F_1 hybrids were tested in a RBD with three replications during *Rabi*, 2016-17at Agricultural Research Station, Perumallapalli. Each genotype was planted in a row of 5 meter length. The spacing between row to row was 60 cm and plant to plant was 20 cm. A fertilizer dose of 120 N, 80P_2O_5, 60 K_2O kg/ha was applied. All the best agronomic management practices and plant protection measures were followed in raising a healthy crop. Observations were recorded on five randomly selected plants from each plot for plant height (cm), SPAD chlorophyll meter readings, cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, 100 kernel weight (g) and kernel yield per plant (g). Days to 50% tasseling and days to 50% silking were recorded on whole plot basis. SPAD chlorophyll meter reading (SCMR) on third leaf was measured with a SPAD -502 chlorophyll meter (Minolta Co Ltd, Osaka, Japan). Analysis of variance and mean comparison of characters were done using SAS software. Diallel cross analysis (Model I and Method IV) was followed for performing partitioning the sum of squares of genotypes in to general and specific combining ability and to estimate their effects for different cross combinations, respective standard errors and genetic components of variances using the formulae given by Griffing (1956). Heterosis expressed as per cent increase of F_1 hybrid over standard check (Standard heterosis) was computed for developmental characters, kernel yield and yield components using the formulae (Turner, 1953 and Hayes *et al.*, 1985).

Results and Discussion

Combining ability and Components of Genetic variances

Data on partitioning of genotypic variance in to mean sum of squares of GCA and SCA and components of genetic variance were presented in Table 1.

Mean performance, *sca* effects and heterosis computed over standard check (DHM 117; BML2×BML6) in respect of top 20 single cross hybridsfor days to 50% tasseling, days to 50% silking, plant height (cm), SPAD chlorophyll meter reading (SCMR), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, 100 kernel weight (g) and kernel yield per plant (g) was presented in Table 2.

Mean sum of squares due to general combining ability (GCA) and specific combining ability SCA) were significant for days to 50% tasseling (7.66** and 4.11**), days to 50% silking (10.83** and 5.99**), plant height (335.63** and 296.56**), SPAD chlorophyll meter reading (20.62** and 7.27**), cob length (5.94** and 1.88**), cob girth (3.01** and 1.01**), number of kernel rows per cob(3.63** and 0.74**), number of kernels per row(28.00** and 6.52**), 100 kernel weight (14.71** and 4.15**) and kernel yield per plant (1196.97** and 308.83**), respectively. The mean sum of squares of GCA includes the additive and additive×additive genetic portion while SCA represents the non-additive genetic portion of the total variance arising largely from dominance and epistatic deviations. The significant mean sum of squares due to GCA and SCA obtained in the present investigation indicates that both additive and non-additive gene action are involved in the expression of all the characters studied. Similar findings in maize were also reported by Iqbal *et al.,* (2007) and Hefney (2010).

The estimates of genetic components of variance computed to find out which type of gene action is more important for the above characters revealed the greater the magnitude of non-additive genetic component of variance (σ^2 sca) than additive component (σ^2 gca) suggesting that non-additive component is predominant for days to 50% tasseling (3.61** and 0.90**), days to 50% silking (5.33** and 1.27**), plant height (290.90** and 35.62**), SPAD chlorophyll meter reading (6.34**and 2.46**), cob length (1.48** and 0.70**), cob girth (0.99** and 0.36**), number of kernel rows per cob(0.50** and 0.42**), number of kernels per row(3.20** and 3.08**), 100 kernel weight (4.01**and 1.78**) and kernel yield per plant (265.69** and 144.23**), respectively. Further, the ratio of σ^2 gca/σ^2 scaless than one for all the characters studied also supported the greater importance of non-additive genetic variance.

These results are in agreement with the findings of Amer *et al.,* (2005), El- Hosary and El- Badway (2001), El- Hosary *et al.,* (2000) and Sedham *et al.,* (2007) in maize. It is evident from these results that heterosis breeding would be beneficial to utilize dominance gene effects for days to 50% tasseling, days to 50% silking, plant height, SPAD chlorophyll meter reading (SCMR), cob length (cm), cob girth, number of kernel rows per cob, number of kernels per row, 100 kernel weight and kernel yield per plant.

Mean performance, *sca* effects and Standard heterosis

Significant *sca* effects and heterosis either positive or negative was recorded for all the characters studied. *Percent* heterosis varied from character to character and from cross to cross.. Heterosis over standard check is considered either to accept or reject a hybrid variety for commercial cultivation. Negative heterosis is desirable for days to 50% tasseling and silking for development of hybrids for early duration.

The extent of heterosis depends on the magnitude of non-additive gene action and genetic diversity of parental lines involved. The magnitude of *sca* effects and heterosis was found to be low for days to 50 % tasseling and silking, SPAD chlorophyll meter reading, cob length, cob girth and number of kernel rows per cob compared to other characters. This may be due to the fact that greatest possible number of loci with dominant loci along with dominant alleles imparts vigour, size, yield, disease resistance and tolerance to environmental factors

Among the top 20 crosses, 12 and 15crosses were found to be significantly superior during season when compared to standard check (DHM 117; BML 6x BML 7) for days to 50% tasseling and 50% silking. Four crosses *viz.,* BML7×DFTY (-0.884* and -0.981); BML15×PDM1452(-1.926** and -1.690**); BML15×1474 (1.343** and 1.481**) and BML2X BML7(1.884** and -1.981) recorded significant negative *sca* effects and negative heterosis.

Table.1 Anova for Combining Ability for Kernel Yield and Yield Components in Maize

S. No	CHARACTER (S)	GCA (D.F=9)	SCA (D.F=35)	σ^2gca	σ^2 sca	σ^2gca/σ^2sca
1.	Days to 50% tasseling	7.66**	4.11**	0.90	3.61	0.25
2.	Days to 50% silking	10.83**	5.99**	1.27	5.33	0.24
3.	Plant Height (cm)	335.63**	296.56**	35.62	290.90	0.12
4.	SPAD Chlorophyll Meter Readings	20.62**	7.27**	2.46	6.34	0.39
5.	Cob length (cm)	5.94**	1.88**	0.70	1.48	0.47
6.	Cob girth (cm)	3.01**	1.01**	0.36	0.99	0.40
7.	Number of kernel rows per cob	3.63**	0.74**	0.42	0.50	0.85
8.	Number of kernels per row	28.00**	6.52**	3.08	3.20	0.96
9.	100 kernel weight (g)	14.71**	4.15**	1.78	4.01	0.44
10.	Kernel yield per plant (g)	1196.97**	308.83**	144.23	265.69	0.54

*Significant at 5% level, **Significant at 1% level

Table.2 Mean *per se* performance, sca effects and standard heterosis for kernel yield and yield components in maize

S. No	HYBRID (s)	Days to 50% Tasseling			Days to 50% Silking			Plant Height (cm)			SPAD Chlorophyll Meter Readings			Cob Length (cm)		
		Mean	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**
1	BML2×BML6	63.33	1.324**	0.00	66.33	1.060*	0.51	191.20	-1.232	4.37	49.33	-1.868**	-0.47	17.12	-0.584	-0.10
2	BML2×BML7	60.33	-1.884**	-4.74**	63.67	-1.981**	-3.54**	183.53	-0.866	0.18	53.45	2.724**	7.84**	18.40	0.877**	7.39*
3	BML2×Heypool	62.00	0.449	-2.11*	67.00	1.977**	1.52	190.00	-1.07	3.71	53.52	0.867*	7.98**	18.94	0.494	10.54**
4	BML6×DFTY	60.67	-1.009**	-4.21**	64.33	-0.273	-2.53*	193.33	-1.218	5.53	52.53	-0.02	5.99**	18.07	-0.304	5.45
5	BML6×PDM1416	60.33	-1.301**	-4.74**	63.67	-0.940*	-3.54**	183.33	-12.841**	0.07	50.27	0.224	1.41	18.33	1.311**	7.00*
6	BML6×PDM1452	61.33	-0.093	-3.16**	62.33	-2.023**	-5.56**	195.93	-1.409	6.95*	49.95	-0.736	0.77	17.18	-0.449	0.29
7	BML6×PDM1474	60.67	-0.843*	-4.21**	64.00	-0.481	-3.03**	208.33	12.828**	13.72**	53.65	1.205**	8.24**	19.43	1.138**	13.42**
8	BML7×DFTY	61.00	-0.884*	-3.68**	64.00	-0.981*	-3.03**	178.00	-8.518*	-2.84	53.69	1.605**	8.31**	19.12	0.927**	11.60**
9	BML7×PDM1452	62.33	0.699	-1.58	65.67	0.935*	-0.51	190.98	1.671	4.25	48.07	-2.147**	-3.03	17.30	-0.154	0.97
10	BML15×Heypool	62.33	0.449	-1.58	66.33	0.769	0.51	191.67	6.716	4.62	50.40	-1.471**	1.68	18.40	0.144	7.39*
11	BML15×PDM1452	59.67	-1.926**	-5.79**	63.67	-1.690**	-3.54**	173.29	-13.174**	-5.41	53.13	3.162**	7.19**	19.10	1.537**	11.48**
12	BML15×PDM1474	60.33	-1.343**	-4.74**	64.00	-1.481**	-3.03**	176.60	-8.030*	-3.60	53.26	1.532**	7.45**	19.24	1.016**	12.32**
13	DFTY×Heypool	62.00	0.782*	-2.11*	64.67	0.31	-2.02*	190.00	-3.189	3.71	53.58	-0.422	8.10**	19.48	0.367	13.72**
14	DFTY×PDM1452	60.67	-0.259	-4.21**	64.00	-0.148	-3.03**	201.47	6.768	9.97**	53.38	1.280**	7.70**	19.53	1.109**	14.01**
15	DFTY×PDM1474	63.33	2.324**	0.00	66.67	2.394**	1.01	183.00	-9.868**	-0.11	52.83	-1.029*	6.59**	18.83	-0.254	9.92**
16	Heypool×PDM1452	61.00	0.032	-3.68**	64.33	0.227	-2.53*	199.93	3.953	9.13**	53.60	1.462**	8.14**	17.41	-0.971**	1.60
17	Heypool×PDM1474	60.33	-0.718*	-4.74**	64.00	-0.231	-3.03**	195.53	1.39	6.73*	53.19	-0.704	7.32**	18.03	-1.008**	5.25
18	PDM1416×PDM1474	60.67	-0.301	-4.21**	64.00	-0.273	-3.03**	190.07	-4.425	3.75	50.20	-1.151**	1.28	17.18	-0.559	0.27
19	PDM1428×PDM1474	62.00	-0.634	-2.11*	64.67	-1.440**	-2.02*	194.00	-1.35	5.90	51.53	-1.125**	3.97*	17.17	-0.586	0.23
20	PDM1452×PDM1474	62.00	1.241**	-2.11*	65.67	1.644**	-0.51	206.55	10.894**	12.75**	52.93	0.939*	6.79**	19.00	0.651*	10.89**
	Standard Check	**63.33**	**0.95***	**0.00**	**66.00**	**0.81**	**-6.60****	**183.20**	**-5.95**	**0.00**	**49.57**	**-1.09****	**0.00**	**17.13**	**-0.27**	**0.00**
	Mean/SE(g_i)/S.E	**61.32**	**0.363**	**-3.19**	**64.65**	**0.417**	**-2.05**	**190.84**	**3.625**	**4.17**	**52.12**	**0.49**	**5.16**	**18.36**	**0.324**	**7.18**

Table.2 Contd.

S. No	HYBRID (S)	Cob Girth (cm)			Number of Kernel Rows per Cob			Number of Kernels per Row			100 Kernel Wight (g)			Kernel Yield per Plant (g)			GCA status of inbred lines
		Mean	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	**Mean**	***sca* effects**	**SH**	
1	BML2×BML6	14.52	-0.601**	0.37	14.13	-0.439	0.00	37.00	-1.745	-3.48	34.20	0.175	3.85*	143.85	5.801	19.45**	G×P
2	BML2×BML7	16.00	1.065**	10.60**	14.37	-0.01	1.65	41.00	1.880*	6.96	35.53	1.128*	7.89**	142.73	8.850**	18.52**	G×P
3	BML2×Heypool	16.08	0.558**	11.18**	15.67	0.532*	10.85**	41.00	0.88	6.96	36.30	0.732	10.22**	150.10	9.313**	24.64**	G×G
4	BML6×DFTY	15.12	-0.216	4.49*	14.90	0.051	5.42	40.00	-0.12	4.35	34.87	-0.115	5.87**	138.90	0.221	15.34**	P×G
5	BML6×PDM1416	16.04	1.424**	10.85**	14.83	0.776**	4.95	39.00	1.921*	1.74	35.77	2.516**	8.60**	137.57	17.561**	14.23**	P×P
6	BML6×PDM1452	14.50	-0.558**	0.23	14.27	-0.258	0.94	38.67	-0.287	0.87	33.20	-0.732	0.81	140.25	4.601	16.46**	P×P
7	BML6×PDM1474	16.08	0.661**	11.15**	15.67	0.560*	10.85**	41.67	1.255	8.70*	36.25	0.868*	10.08**	145.83	3.051	21.10**	P×G
8	BML7×DFTY	15.77	0.620**	8.99**	15.33	0.680**	8.49**	43.00	2.505**	12.17**	36.27	0.905*	10.12**	146.70	11.520**	21.82**	P×G
9	BML7×PDM1452	14.80	-0.072	2.30	14.07	-0.262	-0.47	39.00	-0.329	1.74	35.00	0.688	6.28**	136.07	4.166	12.99**	P×P
10	BML15×Heypool	15.70	0.335	8.53**	15.10	0.179	6.84*	39.67	-0.787	3.48	35.40	-0.066	7.49**	143.90	11.186**	19.49**	P×G
11	BML15×PDM1452	15.81	0.795**	9.29**	15.00	0.525*	6.13*	41.67	2.171*	8.70*	36.51	2.143**	10.87**	144.73	15.132**	20.18**	P×P
12	BML15×PDM1474	16.10	0.724**	11.29**	15.94	0.883**	12.78**	43.00	2.046*	12.17**	37.90	2.077**	15.08**	143.77	6.782*	19.38**	P×G
13	DFTY×Heypool	15.92	0.179	10.02**	15.23	-0.179	7.78**	41.67	0.171	8.70*	36.53	0.008	10.93**	143.20	0.753	18.91**	G×G
14	DFTY×PDM1452	16.18	0.795**	11.87**	15.57	0.601*	10.14**	41.67	1.13	8.70*	36.40	0.971**	10.53**	143.40	4.065	19.08**	G×P
15	DFTY×PDM1474	14.70	-1.049**	1.61	14.40	-1.148**	1.89	41.00	-0.995	6.96	36.50	-0.378	10.84**	151.43	4.615	25.74**	G×G
16	Heypool×PDM1452	14.72	-0.746**	1.73	15.13	0.046	7.08*	39.67	-0.662	3.48	35.90	0.425	9.01**	138.80	-0.368	15.26**	G×P
17	Heypool×PDM1474	15.83	0.01	9.45**	15.67	-0.002	10.85**	41.67	-0.12	8.70*	36.30	-0.628	10.22**	145.77	-0.784	21.04**	G×G
18	PDM1416×PDM1474	14.27	-0.762**	-1.38	14.03	-0.723**	-0.71	41.33	2.380*	7.83*	34.07	-1.084**	3.44	138.73	10.688**	15.20**	P×G
19	PDM1428×PDM1474	15.07	0.342	4.15*	14.37	-0.248	1.65	37.33	-1.329	-2.61	34.67	-0.327	5.26**	140.85	7.994*	16.96**	P×G
20	PDM1452×PDM1474	16.12	0.643**	11.41**	15.93	0.710**	12.74**	41.33	0.505	7.83*	36.61	0.781*	11.17**	142.40	-1.039	18.25**	P×G
	Standard Check	**14.47**	**-0.35**	**0.00**	**14.13**	**-0.08**	**0.00**	**38.33**	**-0.58**	**0.00**	**32.93**	**-0.93***	**0.00**	**120.43**	**-10.82****	**0.00**	
	Mean/SE(g_i)/S.E	**15.47**	**0.18**	**6.91**	**14.98**	**0.256**	**5.99**	**40.52**	**0.929**	**5.70**	**35.71**	**0.361**	**8.43**	**142.95**	**3.345**	**18.70**	

*Significant at 5% level, **Significant at 1% level

Out of 20 top yielding crosses eight have recorded significant negative sca effects while four have recorded positive sca effects. Sixteen crosses recorded significant negative heterosis, while four crosses recorded significant positive heterosis for days to 50% tasseling.

Two cross combinations DFTY×PDM1474 (1.50 and -3.07) and PDM1452×PDM 1472 (1.27 and -2.85) registered significant positive *sca* effects but significant negative heterosis, respectively. Eight crosses*viz*., BML2×PDM 1474, BML6×PDM 1452, BML15×Heypool, DFTY×Heypool, DFTY×PDM1428, DFTY×PDM1452, PDM1416×PDM1474 registered non-significant *sca* effects and significant negative standard heterosis which is in desirable direction. For days to 50% silking 15of the top 20 crosses were found significantly early to silking over the standard check. Six crosses recorded significant negative *sca* effects while five have recorded significant positive *sca* effects. Fourteen crosses have recorded significant negative heterosis over standard check for days to 50% silking.

The cross combinations BML6×PDM1474, DFTY×PDM1452 and PDM1452×PDM1474 recorded significant higher mean value over standard check for plant height during *rabi*. Two crosses BML6×PDM1474 and PDM1452×PDM1474 recorded positive *sca* effects for plant height while five crosses viz., BML6 x PDM 1416,BML 7x DFTY, BML 15x PDM 1452, BML 15x PDM 1474 and DFTYxPDM 1474 have recorded significant negative sca effects. Five crosses BML6xPDM1474, DFTYx PDM 1452, HEYPOOLx PDM1452, HEYPOOLx PDM 1474 and PDM 1452x PDM 1474 recorded significant positive heterosis for plant height over standard check. Two crosses viz., BML6x PDM1474, PDM 1452x PDM1474 recorded significant positive values for both sca and heterosis. Of the top 20 crosses, 13 crosses have registered high mean performance over the standard check during Rabi for SPAD chlorophyll meter readings. Nine crosses registered significant positive *sca* effects while six have recorded significant negative sca effects. A total of 14 crosses have recorded positive and significant heterosis over check. The crosses viz., BML2 x BML7, BML2xHEYPOOL, BML6x PDM1474, BML7x DFTY, BML15X PDM1452, BML15X PDM1474, DFTYx PDM1452 and PDM 1452 x PDM 1474 recorded significant positive heterosis for this trait.

Fourteen cross combinations recorded significantly higher mean values over standard check for cob length during Rabi. Seven crosses recorded significant positive *sca* effects while two have recorded significant negative *sca* effects. Ten crosses have recorded significant positive heterosis. Nine cross combinations recorded significant positive sca effects and heterosis for cob length during the season.

High mean, positive significant *sca* effects and significant positive heterosis was observed in BML2×BML7, BML2x HEYPOOL, BML6×PDM1416, BML6×PDM1474, BML7 × DFTY, BML15×PDM1452, BML15× PDM 1474, DFTY×PDM1452 and PDM1452 xPDM 1474 for cob girth over the standard check during Rabi. A total of nine crosses showed high mean performance and positive significant *sca* effects while 14 crosses have recorded significant positive heterosis.

Eleven crosses registered significant higher mean values for number of kernel rows per cob. The cross combinations *viz*., BML2×HEYPOOL, BML6×PDM1474, BML 7x DFTY BML15x PDM 1452, BML15x PDM 1474, PDM 1452x PDM 1474, DFTY x PDM 1452 registered high mean, significant positive *sca* effects and heterosis during Rabi over the standard check. Four crosses BML2×Heypool, BML2×PDM1474, DFTY× Heypool and Heypool×PDM1474 exhibited high mean performance, non-significant *sca* effects but significant positive heterosis. A total of 10 and11 crosses have recorded significant positive sca effects and heterosis, respectively.

Fornumber of kernels per row thirteen crosses have recorded higher mean values during Rabi over the standard check. Thirteen crosses for positive significant sca effects and nine crosses for significant positive heterosis were found superior over standard check. The cross combinations *viz*., BML7×DFTY, BML15×PDM1452 and BML15×PDM1474, DFTYx PDM 1474 recorded significant positive *sca* effects and heterosis over standard check for number of kernels per row.

Six crosses *viz*., BML2×BML7, BML6× PDM11416,, BML6×PDM1474, BML7x DFTY, BML15×PDM1452, BML15× PDM1474, BML1452×PDM1474, DFTY x PDM 1452 of the top 20 exhibited high mean performance, significant positive *sca* effects and positive significant heterosis during over standard check. A total of nine crosses and 18 crosses recorded significant positive heterosis and *sca* effects were recorded for 100 kernel weight during Rabi.

Among the top yielding crosses, nine exhibited significant positive *sca* effects while all crosses showed significant positive heterosis for kernel yield per plant when compared with standard check. High mean, high positive and significant heterosis and significant positive *sca* effects were registered byBML2×Heypool, BML2×BML7, and BML6×PDM1416, BML7x DFTY, BML15× Heypool, BML15×PDM 1452, BML15×PDM 1474, PDM 1428×PDM 1452 and PDM 1452x PDM 1474 cross combinations for grain yield during Rabi. High heterosis for yield of maize was also reported by El- Badway *et al.*, (2000), Shafey *et al.*, (2004), Kanta *et al.*, (2005), Alamnic *et al.*, (2006), El-Hosary *et al.*, (2006), Hefney (2007) and Sedhom *et al.*, (2007).

The magnitude and extent of heterosis in desired direction is of importance in deciding economical importance of heterosis. High heterosis for grain yield had contribution from high heterosis of yield components (Moneam *et al.,* 2008). In present study, three crosses *viz*; BML7×DFTY, BML15×PDM1452 and BML15×PDM1474 were heterotic for kernel yield over standard check. In addition these cross combinations also recorded, high *per se*performance, significant positive heterosis and *sca* effects for most of the yield contributing characters *viz*., days to 50% tasseling, days to 50% silking, SPAD chlorophyll meter reading, cob length, cob girth, number of kernel rows per cob, number of kernels per row and 100 kernel weight. These outstanding cross combinations involved good×poor or poor×poor general combiners as parents. Hence, these three cross combinations can be put for immediate commercial cultivation after extensive testing for their performance under different locations and environments.

The crosses with yielding potential involving good×good general combiners *viz*., DFTY×PDM1474, DFTY×Heypool and BML2×Heypool and which recorded significant positive heterosis over standard check significant or non-significant *sca* effects and low magnitude of heterosis for all other yield contributing characters may be handled through population improvement programme so as to accumulate favourable genes and to develop improved inbred lines and hybrids. The cross combinations *viz*., BML2×BML7, BML2×PDM1428, DFTY×PDM1452, BML6 ×PDM1452, BML6×PDM1474, BML15× Heypool, DFTY×PDM 1428, Heypool ×

PDM1452, PDM1416×PDM1474, PDM1428 ×PDM1474 and PDM1452 ×PDM1474 involving either good×poor, poor×good, poor×poor combinations possessing high mean performance, significant positive heterosis and significant or non-significant *sca* effects may be handled by heterosis breeding to exploit hybrid vigour and develop high yielding hybrids.

Additive and non-additive type of genetic variance were found to be governing days to 50% tasseling, days to 50% silking, plant height, SPAD chlorophyll meter reading (SCMR), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, 100 kernel weight and kernel yield per plantwith predominance of non-additive gene action. The magnitude of standard heterosis was found to be low for developmental characters, cob length, cob girth, number of kernel rows per cob compared to number of kernels per row, 100 kernel weight, plant height and kernel yield per plant. The crosses *viz*., BML7×PDM1474, BML15×PDM1452 and BML15×PDM1474 which involved poorxgood combinations coupled significant positive sca effects and positive heterosis for most of the yield contributing characters are considered as outstanding crosses which can be recommended for commercial cultivation after extensive testing under different environments and locations. Four crosses viz; BML 2x Heypool, DFTY x Heypool, DFTY x PDM 1474 and Heypool x PDM 1474 which involved high x high general combiners with high mean either significant or non-significant sca effects and significant positive heterosismay be handled through recurrent selection programme so as to accumulate desirable alleles and to isolate improved hybrids/inbred lines. All other cross combinations involving good×poor, poor×good or poor×poor may be handled through heterosis breeding to exploit hybrid vigour and to develop improved hybrids.

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