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Determination of Combining Ability and Heterosis of Grain Yield Components for Maize Mutants Based on Line×Tester Analysis

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ABSTRACT

Determination of combining abilities and heterosis of parental lines is very important in selecting the mutant lines and in deciding breeding strategies for maize hybrid production. New 46 mutant lines were crossed to 3 tester lines in a lines×testers mating design. Around 138 F1 hybrids, including the 46 parental lines and 3 tester lines were evaluated at Arjasari, West Java, Indonesia for estimation of combining abilities and heterosis of new mutant lines for yield and its components and identification of hybrid combinations based on crosses of selected mutant lines with testers. Combining ability effects revealed that none of the mutant line possessed desirable General Combining Ability (GCA) effects for all the traits studied. Mutant line M5DR 16.1.1. was found to have the highest positive and highly significant GCA effect for grain yield followed by mutant lines M5DR 9.1.3, M5 DR 4.8.8, M5 DR 3.1.2, M5 DR 18.4.1 and M5BR 153.1.2. The estimates of specific combining ability demonstrated various cross combinations having significant positive Specific Combining Ability (SCA) effects. The highest magnitude of desirable SCA effects for grain yield/plant was detected in M5 DR 16.2.1×DR 4 followed by M5BR 153.6.1×DR 6, M5BR 153.1.2×DR 4, M5DR 9.1.3×DR 8, M5DR 4.8.8×DR 4, M5DR 3.1.2×DR 6, M5DR 3.1.2×DR 8 and M5DR 18.4.1×DR 8. Not all the crosses exhibited significant positive heterosis over mid parent for grain yield, however, the cross combination M5BR 153.1.2×DR 4 followed by M5DR 3.1.2×DR 6, M5DR 3.1.2×DR 8, M5DR 1.6.3×DR 8, M5DR 4.8.8×DR 4 and M5DR 18.4.1×DR 8 revealed higher magnitude of economic heterosis for grain yield. So, the crosses M5 DR 16.2.1×DR 4 and M5BR 153.1.2×DR 4 can be utilized for developing high yielding hybrid varieties as well as for exploiting hybrid vigor.

Key words: General combining ability, specific combining ability, yield, maize, mutant, line×tester analysis

INTRODUCTION

Maize is an important staple food in Indonesia. However, maize production is affected by global climate change which caused depletion of soil and groundwater, increase of temperatures and evapotranspiration and eventually increased incidence of drought (Cassman, 1999; Hillel and Rosenzweig, 2002). Development of drought tolerant maize is important to sustain maize production.

Mutation is a very valuable tool to develop simple and desirable traits in a well-adapted variety. Some advantages of using mutation in developing new varieties include: (1) Basic genotype of the variety is usually only slightly altered, while the improved trait(s) is added, (2) Shorter time to breed the improved variety than when hybridization is used to achieve the same result (Sigurbjornsson, 1977). Mutation has been successfully applied to improve the following traits: Yield, flowering and ripening time, adaptability, plant type and growth habit, resistance to lodging and stem breakage, shattering and shedding resistance, tolerance to temperature, drought, heat and salinity, disease and pest resistance and quality (Aatsveit *et al.*, 1977). Ruswandi *et al.* (2014) developed new mutant lines using gamma irradiation. They reported some maize mutant lines showing early maturity and also drought tolerance. Follow up studies are needed to evaluate their combining ability to utilize them in maize breeding program, particularly maize hybrids formation.

The effects of combining ability, both General Combining Ability (GCA) and Specific Combining Ability (SCA) are important indicators of potential value for assessing inbred lines in hybrid combinations as a step to develop hybrid varieties in maize (Abdel-Moneam *et al.*, 2014; Hallauer, 1990). Ceyhan (2003) mentioned that the information about parents genetic structure and their combining ability are one of the most important criteria for identifying high yielding hybrids. Furthermore, Izhar and Chakraborty (2013) explained that heterosis and combining ability are prerequisite for formulating hybrid breeding programmes and for developing a good economically viable hybrid maize variety. Combining ability analysis is useful to assess the potential inbred lines and to identify the nature of gene action involved in various quantitative characters.

Differences in GCA effects is attributed to additive and epistatic genetic effects in the base population, while differences in SCA effects is attributed to non-additive genetic variance including dominance and epistatic genetic effects (Falconer, 1981). Sprague and Tatum (1942) proposed that the importance of general combining ability was relatively more than specific combining ability for unselected inbred lines, while specific combining ability was more important than general combining ability for previously selected lines. They also stated that the general combining ability is largely due to the additive effect of genes while in specific combining ability dominance or epistatic effects of genes are commonly involved.

The line×tester analysis method is promoted by Kempthorne (1957) to estimate combining ability. This method is a powerful tool to estimate general and specific combining ability effects and to select desirable parents and crosses (Kamara *et al.*, 2014). The design has been widely used in maize by several workers (Sharma *et al.*, 2004). Joshi *et al.* (2002) used line×tester design in white seed colour early maturing maize inbred lines for estimating combining ability of yield and yield contributing characters. Izhar and Chakraborty (2013) reported their investigation using the method to determine the nature and magnitude of gene action and heterosis for yield and other important traits in maize over two environments. Kamara *et al.* (2014) used the method to estimate GCA and SCA effects of some maize inbred lines for grain yield and other agronomic traits under two nitrogen fertilizer levels. Rahman *et al.* (2013) also reported their investigation using line×tester method to estimate combining ability for grain yield and yield related traits in maize variety Sarhad-White. Rovaris *et al.* (2014) estimated the combining ability of the parents and identify promising white corn genotypes and their white corn hybrids for agronomic traits, yield and grits quality using line×tester method. Legesse *et al.* (2009) successfully examined combining ability of highland transition maize inbred lines for grain yield and other desirable traits, determined heterotic groups of germplasm of the inbred lines and identified promising hybrid

crosses using line×tester analysis. The present investigation was carried out to estimate combining abilities and heterosis of new Indonesian mutant lines for yield and other important traits in maize and to identify and select superior hybrid combinations based on crosses of selected mutant lines with testers.

MATERIALS AND METHODS

Genetic materials: Genetic material evaluated in the study included 46 mutant lines, 138 single cross hybrids derived from line×tester crosses of 46 mutant lines to three tester lines and 3 tester lines. Crosses were made during 2013 and the evaluation of genotypes in experimental trails are performed in rainy season of 2014 at the experimental plots of Faculty of Agriculture, Padjadjaran University, in Arjasari, Bandung, West Java, Indonesia.

Field evaluation: The evaluation of genotypes was laid on a completely random block design (Petersen, 1994), with two replicates and one hundred and seventy eight genotypes as treatment. The genotypes included 36 mutant lines, 3 tester lines and 138 F1 hybrids. The experimental plot consisted of single rows, 5 m long, with 0, 75 m between rows and between plots and 0, 20 m within rows. During the vegetation, the standard crop management practices were applied. The plots were harvested by hand.

The yield component and grain yield per plant was measured on 15 randomly chosen competitive plants in each replicate. The yield components include plant height, ear diameter, number of ear per row, number of grain per ear, weight of 1000 seeds and ear weight per plant.

Statistical analysis: Analysis of variance for line×tester was done following Singh and Chaudhary (1979), where mutant lines, tester lines and hybrids were treated as fixed factor. Line×tester method was applied to estimate GCA and SCA (Kempthorne, 1957). The significance of hybrids, GCA and SCA mean squares were estimated using F test.

RESULTS AND DISCUSSION

Analysis of variance: Analysis of variance to test the significance of all studied traits is presented in Table 1. Results in Table 1 showed that mean squares were significant for most of studied traits.

Table 1: Means square of different parameters of test crosses derived from mutant lines

Source	df	PH	ED	RE	GE	Y
Repln	1	8.88*	24.04*	0.09	20.37*	2.67
Genotype	186	1.85*	2.70*	2.34*	1.70*	1.60*
Cross	137	1.46*	2.21*	2.56*	1.34*	1.36*
Line (c)	45	1.89*	3.09*	3.49*	1.68*	1.91*
Tester (c)	2	1.53	13.78*	23.62*	7.09*	5.07*
L×T (c)	90	1.25	1.52*	1.63*	1.04	1.00
Parent	48	2.68*	3.70*	1.71*	2.43*	2.28*
Line (p)	45	2.63*	3.76*	1.65*	2.40*	2.19*
Tester (p)	2	5.01*	4.02*	3.50*	2.93	4.28*
L(P) v T(P)	1	0.20	0.40	0.67	2.82	2.30
CrovsPAR	1	15.27*	21.79*	2.49	15.88*	2.79

*Significant at the 0.05 probability level, PH: Plant height, ED: Ear diameter, RE: Number of row per ear, GE: Number of grain per ear and Y: Grain yield per plant

Table 2: Proportional contribution of lines, testers and line×tester interaction to total variance of test crosses derived from mutant lines

Parameters	Contributions (%)		
	Lines	Testers	Line×tester
Plant height	32.35	1.59	66.06
Ear diameter	45.89	9.09	45.02
Rows numbers per ear	44.76	13.46	41.78
Grain numbers per ear	41.28	7.73	51.00
Grain yield per plant	46.12	5.45	48.43

The source of variation for the entries was partitioned into Crosses (C), Parents (P) and crosses versus parents (C vs. P). Significant differences for crosses were detected for all the studied traits, indicating the tested top crosses varied from each other for such traits. The parent was significant for all the studied traits. Crosses versus parents (C vs. P) were significant for all the studied traits except number of Row per Ear (RE), Ear Weight per Plant (EWP) and Grain Yield per plant (Y). The mean squares due to Lines (L), Testers (T) and (L×T) interaction were significant for most of studied traits except plant height and ear weight per plant.

This indicates that the mutant lines behaved differently in their respective top crosses and greater diversity exists among the testers. Meanwhile, the significant of (L×T) interaction suggested that inbred lines performed differently according to the tester which they crossed. These results are in agreement with those obtained by Mendoza *et al.* (2000), Mosa (2010), Aly *et al.* (2011), El-Hosary and El-Gammaal (2013), Konak *et al.* (2001), Kamara *et al.* (2014), Singh and Singh (1998) and Tanner and Smith (1987). Based on estimates, higher contribution of line×tester in relation to line and tester as presented in Table 2, implied the greater importance of non-additive gene effects in inheritance of grain yield and it's component traits. The earlier findings of Vasal *et al.* (1992), Joshi *et al.* (1998) and Izhar and Chakraborty (2013) showed also similar results. Predominance of greater magnitude non-additive genetic component of variance relative to additive in present study favors production of hybrid cultivars. Debnath *et al.* (1988), Sanghi *et al.* (1983), Roy *et al.* (1998), Das and Islam (1994) and Izhar and Chakraborty (2013) also reported occurrence of non-additive gene action for grain yield and its components in maize.

GCA effects: The analysis of combining ability effects revealed that none of the mutant line parents possessed desirable GCA effects for all the traits studied (Table 3-8). However, mutant line M5DR 16.1.1. was found to have the highest positive and highly significant GCA effect for grain yield followed by mutant lines M5DR 9.1.3, M5 DR 4.8.8, M5 DR 3.1.2, M5 DR 18.4.1 and M5BR 153.1.2. These mutant line parents also showed significant positive GCA effect and simultaneously possessed high mean value indicating that the per se performance of the mutant line parents could prove as a useful index for combining ability. Similar result were also observed by Roy *et al.* (1998), Hussain *et al.* (2003) and Izhar and Chakraborty (2013). The mutant line M5DR 16.1.1 exhibited highest positive and significant GCA value for various yield components viz., plant height, ear diameter, number of row per ear, number of grain per ear, therefore this mutant line is a good general combiner for these traits. The mutant lines with desirable GCA should be extensively used in the crossing program to exploit maximum genetic variability. Furthermore, Rahman *et al.* (2013) explained that lines with greater specific combining ability effects could be used for hybrid development while those having greater general combining ability could be used effectively for synthetic cultivar development.

Table 3: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for plant height

Mutants	Parent mean	GCA	DR 4		DR 6		DR 8	
			Plant height	SCA	Plant height	SCA	Plant height	SCA
M5 DR 1.1.3	243.50	-22.02	194.00	-39.07	233.34	22.37	233.50	16.70
M5 DR 1.2.3	226.00	0.53	233.00	-22.62	248.34	14.82	247.17	7.81
M5 DR 1.2.12	226.33	-7.13	219.00	-28.95	242.50	16.65	244.00	12.31
M5 DR 1.6.3	196.50	-8.91	211.67	-34.51	233.33	9.26	255.17	25.25
M5 DR 3.1.2	220.00	-4.58	246.17	-4.34	235.00	6.59	232.00	-2.25
M5 DR 3.1.4	238.84	-4.52	223.50	-27.06	250.50	22.04	239.33	5.03
M5 DR 3.6.1	234.34	-4.08	238.67	-12.34	226.67	-2.24	249.33	14.58
M5 DR 3.6.2	231.34	-9.08	234.84	-11.18	223.84	-0.07	241.00	11.25
M5 DR 4.1.3	213.00	-24.74	240.84	10.49	178.50	-29.74	233.34	19.25
M5 DR 4.8.8	220.67	1.81	250.17	-6.73	235.00	0.20	247.17	6.53
M5 DR 5.5.1	195.17	2.53	251.50	-6.12	246.17	10.65	236.84	-4.52
M5 DR 7.1.2	233.67	4.15	249.17	-10.06	248.84	11.70	241.33	-1.64
M5 DR 7.1.9	219.34	-11.08	239.00	-5.01	217.00	-4.91	237.67	9.92
M5 DR 7.3.1	230.84	2.42	250.67	-6.84	236.17	0.76	247.34	6.09
M5 DR 7.3.2	170.84	-24.02	237.50	6.43	203.67	-5.29	213.67	-1.14
M5 DR 7.4.1	227.50	-7.91	248.67	1.49	209.00	-16.07	245.50	14.59
M5 DR 7.4.2	237.84	-3.80	247.50	-3.79	219.17	-10.02	248.83	13.80
M5 DR 8.5.2	225.50	-9.13	235.00	-10.95	207.67	-16.19	256.83	27.14
M5 DR 8.5.3	220.33	0.70	242.83	-12.96	230.84	-2.85	255.33	15.81
M5 DR 8.6.3	185.84	-15.80	222.67	-16.62	210.84	-6.35	246.00	22.97
M5 DR 8.8.1	194.17	5.59	230.50	-30.18	301.50	62.92	211.67	-32.75
M5 DR 9.1.3	221.83	2.53	249.83	-7.79	230.50	-5.02	254.17	12.81
M5 DR 9.1.5	234.17	-19.19	240.00	4.10	211.34	-2.46	218.00	-1.64
M5 DR 9.4.1	218.50	-11.35	243.34	-0.40	211.34	-10.30	238.17	10.69
M5 DR 10.2.2	184.83	-5.58	233.17	-16.34	229.34	1.93	247.67	14.42
M5 DR 10.2.9	183.50	-12.30	225.50	-17.29	241.67	20.98	222.84	-3.69
M5 DR 12.3.1	192.50	-16.85	234.34	-3.90	225.50	9.37	216.50	-5.47
M5 DR 12.3.2	167.00	1.26	245.67	-10.68	237.84	3.59	247.17	7.09
M5 DR 14.1.1	215.00	-2.35	230.34	-22.40	240.83	10.20	248.67	12.20
M5 DR 14.2.2	219.17	-20.13	230.34	-4.62	204.67	-8.18	231.50	12.81
M5 DR 14.3.1	208.67	-5.86	239.00	-10.23	232.67	5.54	237.67	4.70
M5 DR 14.3.8	174.84	-0.30	239.33	-15.46	233.00	0.31	253.67	15.14
M5 DR 16.1.1	234.00	278.20**	223.83	560.50**	229.17	-282.00**	238.50	-278.50**
M5 DR 16.2.1	231.50	-4.69	244.83	-5.57	250.84	22.54	217.17	-16.97
M5 DR 18.2.1	210.50	-10.13	240.17	-4.79	231.50	8.65	224.84	-3.86
M5 DR 18.3.1	213.17	-4.96	251.00	0.88	245.84	17.81	215.17	-18.69
M5 DR 18.4.1	206.50	7.31	249.33	-13.07	253.83	13.54	245.67	-0.47
M5 DR 18.8.1	217.17	-0.46	242.34	-12.29	241.17	8.65	242.00	3.64
M5 BR 153.1.2	199.67	-1.24	240.50	-13.34	238.00	6.26	244.67	7.08
M5 BR 153.2.2	215.50	0.53	235.67	-19.95	250.33	16.81	242.50	3.14
M5 BR 153.3.2	213.17	-6.52	222.34	-26.23	239.34	12.87	245.67	13.36
M5 BR 153.4.1	217.67	-13.47	221.50	-20.12	231.33	11.81	233.67	8.31
M5 BR 153.6.1	213.17	-4.35	216.84	-33.90	250.50	21.87	246.50	12.03
M5 BR 153.7.1	223.34	-9.19	230.50	-15.40	231.67	7.87	237.17	7.53
M5 BR 153.10.2	202.17	3.15	244.50	-13.73	247.34	11.20	244.50	2.53
M5 BR 153.13.1	163.34	-4.97	243.00	-7.12	240.00	11.98	229.00	-4.86

**Significant at the 0.01 probability level

Table 4: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for ear diameter

Mutants	Parent mean	GCA	DR 4		DR 6		DR 8	
			Ear diameter (cm)	SCA	Ear diameter (cm)	SCA	Ear diameter (cm)	SCA
M5 DR 1.1.3	45.72	2.13*	42.55	-1.75	45.94	1.04	46.79	0.70
M5 DR 1.2.3	40.52	-0.25	42.55	0.63	42.42	-0.10	43.18	-0.53
M5 DR 1.2.12	44.73	0.03	38.20	-4.00*	44.64	1.84	46.15	2.16
M5 DR 1.6.3	40.60	1.30	39.68	-3.79*	44.42	0.35	48.69	3.43*
M5 DR 3.1.2	42.53	1.55	44.20	0.48	44.17	-0.15	45.18	-0.33
M5 DR 3.1.4	45.85	-0.52	39.00	-2.65	44.03	1.78	44.30	0.87
M5 DR 3.6.1	43.37	0.39	42.00	-0.55	43.42	0.26	44.63	0.29
M5 DR 3.6.2	45.00	-1.39	40.60	-0.18	40.47	-0.91	43.65	1.09
M5 DR 4.1.3	38.20	-1.56	40.99	0.38	38.72	-2.49	44.50	2.11
M5 DR 4.8.8	42.72	2.28*	45.90	1.45	44.87	-0.18	44.97	-1.27
M5 DR 5.5.1	38.75	0.15	44.12	1.79	42.40	-0.52	42.84	-1.27
M5 DR 7.1.2	41.08	-0.79	42.24	0.85	42.67	0.69	41.62	-1.55
M5 DR 7.1.9	45.77	-0.10	41.47	-0.60	42.53	-0.13	44.58	0.73
M5 DR 7.3.1	40.47	-2.37*	42.19	2.39	41.12	0.72	38.47	-3.11
M5 DR 7.3.2	36.55	-3.27**	40.70	1.81	37.50	-1.99	40.87	0.19
M5 DR 7.4.1	42.67	-0.84	42.62	1.29	40.62	-1.31	43.14	0.02
M5 DR 7.4.2	45.52	1.36	44.44	0.91	41.47	-2.65	47.05	1.74
M5 DR 8.5.2	44.85	0.22	42.64	0.25	42.07	-0.92	44.85	0.68
M5 DR 8.5.3	40.78	-1.42	41.95	1.20	39.54	-1.81	43.14	0.60
M5 DR 8.6.3	39.92	0.48	41.50	-1.14	44.93	1.69	43.89	-0.54
M5 DR 8.8.1	43.27	-2.72**	39.99	0.54	40.59	0.54	40.15	-1.08
M5 DR 9.1.3	48.55	1.69	43.82	-0.05	42.05	-2.41	48.10	2.45
M5 DR 9.1.5	43.63	-1.45	41.14	0.41	40.45	-0.87	42.97	0.46
M5 DR 9.4.1	41.17	-2.52**	38.15	-1.49	41.17	0.92	42.00	0.57
M5 DR 10.2.2	36.82	1.25	44.32	0.90	43.82	-0.20	44.50	-0.70
M5 DR 10.2.9	43.15	-0.58	39.47	-2.12	42.08	-0.11	45.60	2.23
M5 DR 12.3.1	37.87	-0.15	41.84	-0.18	46.15	3.53*	40.45	-3.35*
M5 DR 12.3.2	39.20	3.27**	47.14	1.70	44.65	-1.38	46.90	-0.32
M5 DR 14.1.1	37.24	1.64	43.24	-0.57	46.00	1.60	44.57	-1.03
M5 DR 14.2.2	44.00	-0.20	42.18	0.21	42.40	-0.17	43.72	-0.04
M5 DR 14.3.1	38.62	-1.47	41.39	0.69	41.49	0.19	41.60	-0.88
M5 DR 14.3.8	34.94	1.14	42.62	-0.69	43.49	-0.43	46.22	1.12
M5 DR 16.1.1	43.27	5.07**	46.27	-0.97	47.45	-0.38	50.37	1.35
M5 DR 16.2.1	44.67	0.92	46.39	3.30	45.17	1.48	40.10	-4.77**
M5 DR 18.2.1	42.00	-1.33	41.83	1.00	41.59	0.15	41.47	-1.15
M5 DR 18.3.1	40.70	0.90	45.40	2.33	41.39	-2.28	44.80	-0.05
M5 DR 18.4.1	42.37	1.70	43.32	-0.56	45.37	0.90	45.32	-0.34
M5 DR 18.8.1	43.55	-1.14	40.30	-0.73	38.90	-2.73	46.27	3.46*
M5 BR 153.1.2	37.24	0.29	44.17	1.71	44.92	1.86	40.67	-3.58*
M5 BR 153.2.2	39.92	2.07*	44.02	-0.21	43.90	-0.93	47.17	1.15
M5 BR 153.3.2	46.85	-1.92*	36.39	-3.87*	43.23	2.38	43.52	1.48
M5 BR 153.4.1	42.47	-0.61	43.49	1.92	40.54	-1.63	43.05	-0.30
M5 BR 153.6.1	42.29	-2.83**	35.77	-3.57*	42.88	2.94	41.75	0.63
M5 BR 153.7.1	43.49	-0.21	42.38	0.42	44.24	1.68	41.65	-2.10
M5 BR 153.10.2	35.85	0.06	44.60	2.37	43.17	0.33	41.32	-2.70
M5 BR 153.13.1	36.59	-0.22	40.67	-1.28	42.34	-0.21	45.22	1.49

*Significant at the 0.05 probability level, **Significant at the 0.01 probability level

Table 5: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for rows number per ear

Mutants	Parent mean	GCA	DR 4		DR 6		DR 8	
			No. of rows ear ⁻¹	SCA	No. of rows ear ⁻¹	SCA	No. of rows ear ⁻¹	SCA
M5 DR 1.1.3	14.34	-0.30	13.34	-0.18	12.67	-0.23	14.34	0.41
M5 DR 1.2.3	14.00	-0.30	12.67	-0.85	13.00	0.10	14.67	0.74
M5 DR 1.2.12	13.84	-0.52	12.00	-1.29	13.34	0.66	14.34	0.63
M5 DR 1.6.3	12.34	0.98*	13.50	-1.29	14.34	0.16	16.34	1.13
M5 DR 3.1.2	14.00	-0.52	13.34	0.04	12.67	-0.01	13.67	-0.03
M5 DR 3.1.4	15.33	0.37	13.33	-0.85	13.67	0.10	15.34	0.75
M5 DR 3.6.1	13.67	0.37	14.67	0.48	13.67	0.10	14.00	-0.59
M5 DR 3.6.2	14.67	1.26**	15.00	-0.07	14.00	-0.45	16.00	0.52
M5 DR 4.1.3	13.00	-0.19	15.00	1.37	11.17	-1.84**	14.50	0.47
M5 DR 4.8.8	14.00	1.03*	14.33	-0.52	14.34	0.11	15.67	0.41
M5 DR 5.5.1	13.00	-1.41**	12.34	-0.07	11.34	-0.45	13.34	0.52
M5 DR 7.1.2	13.00	-0.63	13.67	0.49	11.67	-0.90	14.00	0.41
M5 DR 7.1.9	13.33	-0.63	13.33	0.15	13.00	0.44	13.00	-0.59
M5 DR 7.3.1	12.50	-0.69	14.00	0.87	12.17	-0.34	13.00	-0.53
M5 DR 7.3.2	13.67	-0.19	13.34	-0.29	12.34	-0.67	15.00	0.97
M5 DR 7.4.1	12.34	-0.52	13.33	0.04	12.34	-0.34	14.00	0.30
M5 DR 7.4.2	14.67	-0.19	13.33	-0.30	12.00	-1.01	15.34	1.30
M5 DR 8.5.2	13.50	0.26	13.67	-0.41	12.34	-1.12	16.00	1.52*
M5 DR 8.5.3	14.34	-1.35**	13.17	0.70	12.67	0.83	11.34	-1.53*
M5 DR 8.6.3	13.67	-0.13	13.83	0.15	14.00	0.94	13.00	-1.09
M5 DR 8.8.1	14.00	-1.08**	13.33	0.59	12.00	-0.12	12.67	-0.48
M5 DR 9.1.3	16.67	1.48**	15.67	0.37	14.67	-0.01	15.34	-0.36
M5 DR 9.1.5	13.33	-1.19**	12.00	-0.63	12.00	-0.01	13.67	0.64
M5 DR 9.4.1	12.34	0.14	13.67	-0.29	13.00	-0.34	15.00	0.63
M5 DR 10.2.2	13.34	1.59**	15.00	-0.40	15.33	0.55	15.67	-0.14
M5 DR 10.2.9	14.34	-0.02	12.50	-1.29	12.67	-0.50	16.00	1.80*
M5 DR 12.3.1	14.67	1.37**	14.00	-1.18	16.34	1.77*	15.00	-0.59
M5 DR 12.3.2	13.67	0.92*	14.67	-0.07	14.67	0.55	14.67	-0.48
M5 DR 14.1.1	13.00	-0.19	14.33	0.71	12.67	-0.34	13.67	-0.37
M5 DR 14.2.2	13.17	1.48**	16.34	1.04	13.67	-1.01	15.67	-0.03
M5 DR 14.3.1	12.67	-0.30	14.34	0.82	12.67	-0.23	13.33	-0.59
M5 DR 14.3.8	12.67	0.70	14.67	0.15	14.00	0.10	14.67	-0.26
M5 DR 16.1.1	12.34	0.81*	14.67	0.04	14.33	0.32	14.67	-0.36
M5 DR 16.2.1	13.67	-0.30	14.67	1.15	14.00	1.10	11.67	-2.25**
M5 DR 18.2.1	12.67	-1.30**	13.34	0.82	11.00	-0.90	13.00	0.08
M5 DR 18.3.1	13.34	0.03	13.67	-0.18	13.33	0.10	14.33	0.08
M5 DR 18.4.1	11.67	0.59	14.34	-0.07	14.00	0.22	14.67	-0.15
M5 DR 18.8.1	13.67	0.48	15.67	1.37	12.67	-1.01	14.34	-0.36
M5 BR 153.1.2	14.50	-0.52	13.34	0.04	12.00	-0.67	14.34	0.63
M5 BR 153.2.2	14.34	-0.19	13.00	-0.63	14.34	1.33	13.34	-0.70
M5 BR 153.3.2	14.00	0.26	13.34	-0.74	14.67	1.21	14.00	-0.48
M5 BR 153.4.1	13.67	-0.19	13.33	-0.30	12.34	-0.67	15.00	0.97
M5 BR 153.6.1	13.67	-0.24	13.50	-0.07	13.67	0.71	13.34	-0.64
M5 BR 153.7.1	14.67	-0.75	14.00	0.93	13.33	0.88	11.67	-1.81*
M5 BR 153.10.2	12.34	0.14	13.67	-0.29	13.67	0.33	14.34	-0.03
M5 BR 153.13.1	13.00	-0.41	13.33	-0.07	13.33	0.55	13.33	-0.48

*Significant at the 0.05 probability level, **Significant at the 0.01 probability level

Table 6: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for number of seeds per ear

Mutants	Parent mean	GCA	DR 4		DR 6		DR 8	
			No. of seed ear ⁻¹	SCA	No. of seed ear ⁻¹	SCA	No. of seed ear ⁻¹	SCA
M5 DR 1.1.3	444.50	-46.89	280.00	-46.64	352.50	14.05	397.50	32.59
M5 DR 1.2.3	354.50	21.11	426.00	31.36	404.00	-2.45	404.00	-28.91
M5 DR 1.2.12	410.50	-44.89	232.00	-96.64	428.50	88.05	375.50	8.50
M5 DR 1.6.3	375.00	12.95	338.50	-47.98	383.50	-14.78	487.50	62.76
M5 DR 3.1.2	387.50	14.78	343.50	-44.81	439.00	38.88	432.50	5.93
M5 DR 3.1.4	509.00	37.45	310.50	-100.50*	463.00	40.22	509.50	60.26
M5 DR 3.6.1	346.50	17.78	397.50	6.19	423.50	20.38	403.00	-26.57
M5 DR 3.6.2	466.50	42.11	458.50	42.86	416.00	-11.45	422.50	-31.41
M5 DR 4.1.3	176.50	-108.70**	345.50	80.69	194.00	-82.62	305.00	1.93
M5 DR 4.8.8	295.50	72.11*	457.00	11.36	428.00	-29.45	502.00	18.09
M5 DR 5.5.1	260.50	-21.05	381.00	28.52	357.50	-6.78	369.00	-21.74
M5 DR 7.1.2	289.50	12.45	432.50	46.52	373.50	-24.28	402.00	-22.24
M5 DR 7.1.9	447.00	25.95	380.50	-18.98	421.00	9.72	447.00	9.26
M5 DR 7.3.1	348.00	18.28	390.50	-1.31	397.00	-6.62	438.00	7.93
M5 DR 7.3.2	290.00	-77.22**	298.50	2.19	274.50	-33.62	366.00	31.43
M5 DR 7.4.1	440.00	40.61	449.00	34.86	333.50	-92.45	510.00	57.59
M5 DR 7.4.2	419.00	-6.05	333.50	-33.98	393.50	14.22	425.50	19.76
M5 DR 8.5.2	356.50	25.11	356.00	-42.64	404.00	-6.45	486.00	49.09
M5 DR 8.5.3	316.50	8.28	428.50	46.69	337.50	-56.12	429.50	9.43
M5 DR 8.6.3	312.50	4.45	376.50	-1.48	384.50	-5.28	423.00	6.76
M5 DR 8.8.1	302.00	-10.05	397.00	33.52	370.50	-4.78	373.00	-28.74
M5 DR 9.1.3	471.50	55.11	403.00	-25.64	466.50	26.05	466.50	-0.41
M5 DR 9.1.5	376.00	-43.22	351.50	21.19	286.00	-56.12	403.50	34.93
M5 DR 9.4.1	329.00	-15.55	282.50	-75.48	385.00	15.22	456.50	60.26
M5 DR 10.2.2	341.50	17.45	372.00	-18.98	412.50	9.72	438.50	9.26
M5 DR 10.2.9	380.50	-36.39	262.50	-74.64	367.50	18.55	431.50	56.09
M5 DR 12.3.1	319.50	16.28	389.00	-0.81	435.00	33.38	395.50	-32.57
M5 DR 12.3.2	161.50	25.11	411.00	12.36	404.50	-5.95	430.50	-6.41
M5 DR 14.1.1	282.50	-6.39	343.00	-24.14	395.50	16.55	413.00	7.59
M5 DR 14.2.2	394.50	-4.72	380.50	11.69	346.00	-34.62	430.00	22.93
M5 DR 14.3.1	419.50	27.45	404.50	3.52	451.50	38.72	397.00	-42.24
M5 DR 14.3.8	355.50	11.45	382.50	-2.48	383.50	-13.28	439.00	15.76
M5 DR 16.1.1	378.00	32.61	377.00	-29.14	446.50	28.55	445.00	0.59
M5 DR 16.2.1	361.50	2.61	423.50	47.36	456.50	68.55	298.50	-115.90*
M5 DR 18.2.1	301.50	-81.22**	423.00	130.70**	268.50	-35.62	235.50	-95.07
M5 DR 18.3.1	353.50	-8.89	395.00	30.36	310.00	-66.45	439.00	36.09
M5 DR 18.4.1	380.50	59.95*	441.50	8.02	432.00	-13.28	477.00	5.26
M5 DR 18.8.1	439.50	21.78	405.00	9.69	411.50	4.38	419.50	-14.07
M5 BR 153.1.2	268.00	-2.55	381.00	10.02	415.50	32.72	366.50	-42.74
M5 BR 153.2.2	412.00	14.28	411.00	23.19	430.00	30.38	372.50	-53.57
M5 BR 153.3.2	441.50	-25.22	282.00	-66.31	428.50	68.38	384.50	-2.07
M5 BR 153.4.1	261.50	-67.05*	327.50	21.02	274.50	-43.78	367.50	22.76
M5 BR 153.6.1	390.00	-0.22	306.00	-67.31	456.50	71.38	407.50	-4.07
M5 BR 153.7.1	448.50	-35.55	343.00	5.02	371.00	21.22	350.00	-26.24
M5 BR 153.10.2	241.00	-7.39	440.50	74.36	339.50	-38.45	368.50	-35.91
M5 BR 153.13.1	232.00	11.78	432.00	46.69	372.50	-24.62	401.50	-22.07

*Significant at the 0.05 probability level, **Significant at the 0.01 probability level

Table 7: Means, GCA effects of parents and SCA effects of 138 test crosses with three testers for grain yield per plant

Mutants	Parent mean		DR 4		DR 6		DR 8	
	(g)	GCA	Grain yield plant ⁻¹	SCA	Grain yield plant ⁻¹	SCA	Grain yield plant ⁻¹	SCA
M5 DR 1.1.3	102.50	-3.40	53.67	-19.93	88.84	12.43	91.00	7.50
M5 DR 1.2.3	60.84	4.10	78.34	-2.76	99.17	15.26	78.50	-12.50
M5 DR 1.2.12	85.00	-3.73	39.67	-33.60*	96.50	20.43	96.34	13.16
M5 DR 1.6.3	97.50	4.27	61.67	-19.60	81.00	-3.07	113.84	22.66
M5 DR 3.1.2	90.50	18.71*	84.83	-10.88	104.84	6.32	110.17	4.55
M5 DR 3.1.4	116.67	8.99	60.84	-25.15	104.34	15.54	105.50	9.61
M5 DR 3.6.1	83.34	6.27	70.84	-12.43	86.00	-0.07	105.67	12.50
M5 DR 3.6.2	98.34	-3.79	67.33	-5.88	75.84	-0.18	89.17	6.05
M5 DR 4.1.3	30.00	-23.62*	62.84	9.46	35.67	-20.51	74.33	11.05
M5 DR 4.8.8	78.67	21.93*	104.84	5.90	96.67	-5.07	108.00	-0.84
M5 DR 5.5.1	54.17	4.82	84.67	2.85	81.50	-3.12	92.00	0.28
M5 DR 7.1.2	66.67	-0.56	80.84	4.40	75.50	-3.74	85.67	-0.67
M5 DR 7.1.9	92.50	6.71	75.17	-8.54	86.67	0.16	102.00	8.39
M5 DR 7.3.1	61.17	-0.90	75.00	-1.10	82.50	3.60	83.50	-2.50
M5 DR 7.3.2	59.00	-29.51**	53.00	5.51	44.67	-5.62	57.50	0.11
M5 DR 7.4.1	100.84	1.10	100.67	22.57	54.34	-26.57	92.00	4.00
M5 DR 7.4.2	104.17	1.93	92.00	13.07	80.67	-1.06	76.83	-12.01
M5 DR 8.5.2	85.84	4.71	81.17	-0.54	89.50	4.99	87.17	-4.45
M5 DR 8.5.3	56.00	-13.96	72.50	9.46	48.50	-17.34	80.83	7.88
M5 DR 8.6.3	62.67	2.93	87.00	7.07	76.17	-6.56	89.33	-0.51
M5 DR 8.8.1	81.50	-10.01	69.17	2.18	80.17	10.37	64.34	-12.56
M5 DR 9.1.3	107.50	20.38*	95.67	-1.71	90.34	-9.84	118.84	11.55
M5 DR 9.1.5	90.00	-16.90	59.67	-0.43	55.50	-7.40	77.83	7.83
M5 DR 9.4.1	73.67	-14.68	44.00	-18.32	78.17	13.04	77.50	5.28
M5 DR 10.2.2	65.34	5.83	88.34	5.51	75.67	-9.96	97.17	4.44
M5 DR 10.2.9	80.50	-11.29	53.00	-12.71	62.33	-6.18	94.50	18.89
M5 DR 12.3.1	45.83	-3.90	72.00	-1.10	81.17	5.27	78.84	-4.17
M5 DR 12.3.2	40.67	13.32	89.00	-1.32	88.83	-4.29	105.84	5.61
M5 DR 14.1.1	57.34	6.77	74.34	-9.43	97.83	11.26	91.84	-1.83
M5 DR 14.2.2	90.34	-15.90	67.67	6.57	54.84	-9.07	73.50	2.50
M5 DR 14.3.1	101.33	-0.51	82.17	5.68	82.00	2.71	78.00	-8.39
M5 DR 14.3.8	69.00	4.38	82.83	1.46	64.84	-19.34	109.17	17.89
M5 DR 16.1.1	80.50	17.93	91.00	-3.93	96.50	-1.23	110.00	5.16
M5 DR 16.2.1	86.67	4.38	111.34	29.96	95.50	11.32	50.00	-41.28*
M5 DR 18.2.1	70.84	-16.79	76.17	15.96	66.33	3.32	50.84	-19.28
M5 DR 18.3.1	83.67	5.77	104.84	22.07	62.00	-23.57	94.17	1.50
M5 DR 18.4.1	88.33	30.43**	98.17	-9.27	111.84	1.60	125.00	7.66
M5 DR 18.8.1	99.67	1.27	74.34	-3.93	84.00	2.93	89.17	1.00
M5 BR 153.1.2	31.50	9.49	104.50	18.01	99.34	10.04	68.34	-28.06
M5 BR 153.2.2	76.00	7.60	99.67	15.07	81.84	-5.57	85.00	-9.50
M5 BR 153.3.2	107.17	-9.90	47.67	-19.43	90.50	20.60	75.84	-1.17
M5 BR 153.4.1	45.00	-20.73*	68.67	12.40	42.83	-16.24	70.00	3.83
M5 BR 153.6.1	91.67	-5.57	50.00	-21.43	102.00	27.77	75.00	-6.34
M5 BR 153.7.1	86.17	-0.34	76.33	-0.32	95.50	16.04	70.84	-15.72
M5 BR 153.10.2	36.67	-3.07	93.33	19.40	72.00	-4.73	69.17	-14.67
M5 BR 153.13.1	27.84	-4.96	81.17	9.12	70.17	-4.68	77.50	-4.45

*Significant at the 0.05 probability level, **Significant at the 0.01 probability level

Table 8: Heterosis of 138 test crosses with three testers for plant height, ear diameter and ear numbers per row

Mutants	Plant height			Ear diameter			Rows numbers per ear		
	DR 4	DR 6	DR 8	DR 4	DR 6	DR 8	DR 4	DR 6	DR 8
M5 DR 1.1.3	-14.51	7.98	9.03	-7.18	5.62	9.76*	-8.05	-7.33	8.87
M5 DR 1.2.3	6.80	19.78	20.32	-1.61	3.72	7.88	-11.61	-3.70	12.81
M5 DR 1.2.12	0.31	16.87	18.69	-15.77**	3.80	9.54*	-15.80*	-0.61	10.97
M5 DR 1.6.3	4.05	21.16	33.83	-8.33	8.50	21.51**	-0.02	13.16	34.25**
M5 DR 3.1.2	14.41	15.01	14.61	-0.11	5.42	10.11*	-6.98	-6.19	5.15
M5 DR 3.1.4	-0.48	17.19	12.98	-15.05**	1.08	3.77	-11.13	-3.53	12.22
M5 DR 3.6.1	7.34	7.17	18.96	-5.97	2.59	7.67	3.49	2.47	9.08
M5 DR 3.6.2	6.34	6.59	15.82	-10.74*	-6.19	3.27	2.25	1.19	19.99**
M5 DR 4.1.3	13.78	-11.12	17.30	-2.61	-2.55	14.49**	8.42	-14.12*	16.00*
M5 DR 4.8.8	16.08	14.82	21.91	3.51	6.85	9.35	-0.03	6.19	20.50**
M5 DR 5.5.1	24.04	28.27	24.65	4.14	5.97	9.43	-10.84	-12.81	6.68
M5 DR 7.1.2	12.24	17.84	15.33	-2.96	3.63	3.26	-1.19	-10.27	12.00
M5 DR 7.1.9	11.25	6.37	17.61	-9.59*	-2.27	4.53	-4.79	-1.25	2.65
M5 DR 7.3.1	13.64	12.59	19.01	-2.39	0.61	-3.84	3.05	-4.55	6.12
M5 DR 7.3.2	24.62	13.31	20.15	-1.36	-3.62	7.42	-5.88	-7.48	16.89*
M5 DR 7.4.1	13.59	0.44	19.08	-3.83	-3.22	4.95	-1.28	-2.62	15.06*
M5 DR 7.4.2	10.45	2.78	17.74	-2.86	-4.43	10.64*	-9.13	-13.26*	15.00*
M5 DR 8.5.2	7.84	0.28	25.18	-6.11	-2.31	6.30	-2.98	-6.91	25.49**
M5 DR 8.5.3	12.77	12.88	26.04	-3.29	-3.63	7.41	-9.22	-7.30	-13.92*
M5 DR 8.6.3	12.41	12.60	32.73	-3.36	10.68*	10.47*	-2.38	5.01	1.31
M5 DR 8.8.1	13.97	57.51	11.70	-10.38*	-3.98	-3.02	-7.01	-11.11	-2.58
M5 DR 9.1.3	15.62	12.30	25.00	-7.29	-6.37	9.21*	-0.03	-1.15	6.98
M5 DR 9.1.5	7.99	-0.04	4.06	-8.18	-4.71	3.32	-14.29*	-8.85	7.94
M5 DR 9.4.1	13.49	3.81	18.10	-12.44**	-0.13	4.08	1.20	2.62	23.28**
M5 DR 10.2.2	18.01	22.80	33.99	7.05	12.22*	16.56**	7.12	16.42*	23.70**
M5 DR 10.2.9	14.51	29.87	21.00	-11.43*	-0.31	10.30*	-13.81*	-7.30	21.51**
M5 DR 12.3.1	16.34	18.32	14.75	-0.20	16.63**	4.52	-4.55	18.09**	12.51
M5 DR 12.3.2	30.21	33.74	40.50	10.68*	10.97*	19.13**	3.51	9.99	14.28*
M5 DR 14.1.1	8.31	19.32	24.39	3.92	17.19**	16.10**	3.58	-2.58	9.32
M5 DR 14.2.2	7.26	0.37	14.60	-6.24	-0.55	4.66	17.37**	4.49	24.54**
M5 DR 14.3.1	14.08	17.11	20.80	-2.15	3.86	6.46	4.88	-1.27	8.09
M5 DR 14.3.8	24.27	28.20	41.06	5.36	14.13**	24.12**	7.33	9.10	18.91**
M5 DR 16.1.1	392.30**	8.44	13.89	3.69	12.25*	21.66**	8.65	13.12	20.57**
M5 DR 16.2.1	10.82	19.40	4.32	2.36	5.11	-4.75	3.49	4.99	-9.08
M5 DR 18.2.1	14.14	15.99	13.74	-4.90	-0.12	1.72	-2.43	-14.28*	5.41
M5 DR 18.3.1	18.54	22.36	8.13	4.77	0.98	11.67*	-2.37	1.23	13.12
M5 DR 18.4.1	19.63	28.47	25.55	-1.94	8.48	10.65*	8.87	13.52	23.94**
M5 DR 18.8.1	13.37	18.85	20.40	-9.96*	-8.28	11.38*	10.57	-5.01	11.71
M5 BR 153.1.2	17.32	22.57	27.26	6.17	14.43**	5.94	-8.57	-12.73*	8.19
M5 BR 153.2.2	10.68	23.88	21.15	2.51	8.15	18.73**	-10.36	4.88	1.27
M5 BR 153.3.2	5.00	19.12	23.45	-21.60**	-1.88	0.76	-6.98	8.63	7.69
M5 BR 153.4.1	3.50	13.86	16.11	-1.66	-3.18	5.00	-5.91	-7.48	16.89*
M5 BR 153.6.1	2.40	24.68	23.87	-18.95**	2.64	2.05	-4.71	2.49	3.92
M5 BR 153.7.1	6.30	12.46	16.21	-5.25	4.38	0.34	-4.55	-3.63	-12.51
M5 BR 153.10.2	18.55	26.57	26.36	9.02	11.94*	9.61	1.20	7.87	17.81*
M5 BR 153.13.1	30.06	36.36	31.54	-1.48	8.75	18.80**	-3.65	2.54	6.64

*Significant at the 0.05 probability level, **Significant at the 0.01 probability level

SCA effects: An important assessment of the results with respect to specific combining ability effects showed that none of the cross combinations exhibited desirable significant SCA effects for all the characters. The estimates of specific combining ability based on line×tester analysis demonstrated various cross combinations having significant positive SCA effects (Table 4, 5, 6 and 7). The highest magnitude of desirable SCA effects for grain yield/plant was detected in M5 DR 16.2.1×DR 4 followed by M5BR 153.6.1×DR 6, M5DR 14.3.8×DR 8, M5BR 153.1.2×DR 4, M5DR 9.1.3×DR 8, M5DR 4.8.8×DR 4, M5DR 3.1.2×DR 6, M5DR 3.1.2×DR 8, M5DR 1.6.3×DR 8 and M5DR 18.4.1×DR 8. Beck *et al.* (1990), Singh and Mishra (1996), Choudhary *et al.* (2000), Prakash and Ganguli (2004), Aly *et al.* (2011), Izhar and Chakraborty (2013), Rahman *et al.* (2013) and Kamara *et al.* (2014) also reported high positive specific combining ability effects along with high per se performance for grain yield. The cross combination M5DR 18.2.1×DR 4 followed by M5BR 153.6.1×DR 6, M5BR 153.6.1×DR 6, M5DR 16.2.1×DR 4, M5DR 16.2.1×DR 6, M5DR 18.4.1×DR 8, M5DR 4.8.8×DR 8 and M5DR 3.2×DR 6 was a good specific combiner for number of seed per ear. The cross combination M5 DR 12.3.1×DR 6 was the best specific combiner followed by M5DR 16.1.1×DR 8, M5DR 18.4.1×DR 6, M5DR 12.3.2×DR 4 and M5DR 1.6.3×DR 8 for ear diameter. The cross combination M5DR 1.6.3×DR 8 was the best specific combiner followed by M5DR 16.1.1×DR 8, M5DR 18.4.2×DR 8 for number of rows per ear. The superiority of crosses as parents could be explained on the basis of interaction between positive alleles from good combiners and negative alleles for the poor combiners as parents (Izhar and Chakraborty, 2013).

Heterosis: The high yield of such crosses would be non-fixable and thus could be exploited for heterosis breeding. Not all the crosses exhibited significant positive heterosis over mid parent for grain yield (Table 7-9). The cross combination M5BR 153.1.2×DR 4 followed by M5DR 3.1.2×DR 6, M5DR 3.1.2×DR 8, M5DR 1.6.3×DR 8, M5DR 4.8.8×DR 4 and M5DR 18.4.1×DR 8 revealed high

Table 9: Heterosis of 138 test crosses with three testers for number of grain per ear and grain yield per plant

Mutants	Grain No. ear ⁻¹			Grain yield plant ⁻¹		
	DR 4	DR 6	DR 8	DR 4	DR 6	DR 8
M5 DR 1.1.3	-8.05	-7.33	8.87	-52.99**	6.07	0.18
M5 DR 1.2.3	-11.61	-3.70	12.81	-16.07	57.61	12.14
M5 DR 1.2.12	-15.80*	-0.61	10.97	-62.37**	28.67	17.36
M5 DR 1.6.3	-0.02	13.16	34.25**	-44.77**	-0.31	28.87
M5 DR 3.1.2	-6.98	-6.19	5.15	-21.57	34.84	29.86
M5 DR 3.1.4	-11.13	-3.53	12.22	-49.83**	14.87	7.75
M5 DR 3.6.1	3.49	2.47	9.08	-32.27	15.95	30.05
M5 DR 3.6.2	2.25	1.19	19.99**	-39.93*	-7.14	0.47
M5 DR 4.1.3	8.42	-14.12*	16.00*	-19.35	-24.92	36.18
M5 DR 4.8.8	-0.03	6.19	20.50**	2.53	34.57	36.85
M5 DR 5.5.1	-10.84	-12.81	6.68	-5.93	36.78	38.00
M5 DR 7.1.2	-1.19	-10.27	12.00	-16.02	14.68	17.49
M5 DR 7.1.9	-4.79	-1.25	2.65	-31.15	10.06	18.84
M5 DR 7.3.1	3.05	-4.55	6.12	-19.78	30.78	19.01
M5 DR 7.3.2	-5.88	-7.48	16.89*	-42.65*	-27.96	-16.77
M5 DR 7.4.1	-1.28	-2.62	15.06*	-11.17	-34.47	2.22
M5 DR 7.4.2	-9.13	-13.26*	15.00*	-20.00	-4.63	-16.18
M5 DR 8.5.2	-2.98	-6.91	25.49**	-23.30	18.67	5.65

Table 9: Continue

Mutants	Grain No. ear ⁻¹			Grain yield plant ⁻¹		
	DR 4	DR 6	DR 8	DR 4	DR 6	DR 8
M5 DR 8.5.3	-9.22	-7.30	-13.92*	-20.26	-19.83	19.60
M5 DR 8.6.3	-2.38	5.01	1.31	-7.69	19.33	25.97
M5 DR 8.8.1	-7.01	-11.11	-2.58	-33.28	9.44	-19.91
M5 DR 9.1.3	-0.03	-1.15	6.98	-18.00	4.74	27.32
M5 DR 9.1.5	-14.29*	-8.85	7.94	-44.71*	-28.39	-7.98
M5 DR 9.4.1	1.20	2.62	23.28**	-55.89**	12.74	1.42
M5 DR 10.2.2	7.12	16.42*	23.70**	-7.58	16.12	34.49
M5 DR 10.2.9	-13.81*	-7.30	21.51**	-48.63**	-14.32	18.37
M5 DR 12.3.1	-4.55	18.09**	12.51	-16.11	46.48	26.14
M5 DR 12.3.2	3.51	9.99	14.28*	6.91	68.14	76.64
M5 DR 14.1.1	3.58	-2.58	9.32	-18.83	59.94	34.56*
M5 DR 14.2.2	17.37**	4.49	24.54**	-37.39*	-29.40	-13.27
M5 DR 14.3.1	4.88	-1.27	8.09	-27.65	-1.40	-13.57
M5 DR 14.3.8	7.33	9.10	18.91**	-14.97	-3.23	47.36
M5 DR 16.1.1	8.65	13.12	20.57**	-11.79	32.65	37.79
M5 DR 16.2.1	3.49	4.99	-9.08	4.79	25.94	-39.70
M5 DR 18.2.1	-2.43	-14.28*	5.41	-22.54	-2.34	-32.22
M5 DR 18.3.1	-2.37	1.23	13.12	0.08	-16.59	15.66
M5 DR 18.4.1	8.87	13.52	23.94**	-8.33	45.87	49.26
M5 DR 18.8.1	10.57	-5.01	11.71	-34.07*	2.03	-0.20*
M5 BR 153.1.2	-8.57	-12.73*	8.19	32.84	105.90**	23.50
M5 BR 153.2.2	-10.36	4.88	1.27	-1.24	16.08	9.56
M5 BR 153.3.2	-6.98	8.63	7.69	-59.08**	5.13	-18.60
M5 BR 153.4.1	-5.91	-7.48	16.89*	-19.61	-22.13	12.75
M5 BR 153.6.1	-4.71	2.49	3.92	-54.02**	30.21	-12.20
M5 BR 153.7.1	-4.55	-3.63	-12.51	-27.99	26.35	-14.31
M5 BR 153.10.2	1.20	7.87	17.81*	14.87	41.63	19.42
M5 BR 153.13.1	-3.65	2.54	6.64	5.64	51.16	44.86

*Significant at the 0.05 probability level, **Significant at the 0.01 probability level

magnitude of economic heterosis for grain yield. Significant percentage of heterosis for grain yield in maize was also reported by Lonquist and Gardner (1961), Gerrish (1983) and Rahman *et al.* (2013). The cross combination M5DR 1.6.3×DR 8 followed by M5DR 4.8.8×DR 8, M5DR 16.1.1×DR 8, dan M5DR 18.4.1×DR 8 revealed positive and significant heterosis for ear diameter, number of grain per ear, number of rows per ear and plant height. Most crosses showing significant positive SCA effect and highest magnitude of economic heterosis for grain yield involved DR 6 and DR 8 as testers. According to Rahman *et al.* (2013), the promising crosses were identified as overall high general combiners and these could be utilized for development of either the synthetic varieties or an elite breeding population by allowing thorough mixing among them to achieve new genetic recombination and then subjecting the resultant population to recurrent selection.

CONCLUSION

There was genetic variability among mutant maize line populations and the top cross hybrids assessed for all the studied traits. The following stood out for general combining ability of mutant line M5DR 16.1.1, M5DR 9.1.3, M5 DR 4.8.8, M5 DR 3.1.2, M5 DR 18.4.1 and M5BR 153.1.2 to

grain yield, number of grain per ear and number of rows per ear. The following hybrid combinations were outstanding M5 DR 16.2.1×DR 4, M5BR 153.6.1×DR 6, M5DR 14.3.8×DR 8, M5BR 153.1.2×DR 4, M5DR 9.1.3×DR 8, M5DR 4.8.8×DR 4, M5DR 3.1.2×DR 6, M5DR 3.1.2×DR 8, M5DR 1.6.3×DR 8 and M5DR 18.4.1×DR 8. These promising crosses that were identified as overall high general combiners could be utilized for development of either the synthetic varieties or an elite breeding population by allowing thorough mixing among them to achieve new genetic recombination and then subjecting the resultant population to recurrent selection.

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