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RESEARCH PAPER

Combining ability and heterosis study for grain yield and yield attributing traits in maize (*Zea mays* L.)

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Abstract: An investigation was carried out to estimate combining ability and heterosis in maize (*Zea Mays* L.) at Maize Research Centre and Seed Farm, Devihosur during 2020-21. Combining ability analysis using line × tester design was conducted among inbred lines by crossing 20 lines with three testers. Significant general and specific combining ability variances were observed for all the characters studied. The significant estimates of GCA and SCA variances suggested the importance of both additive and non-additive gene actions for the expression studied traits. The lines *viz*., DMIL 211, DMIL 212 and DMIL 168 and tester DMIL 031 were identified as best general combiners for grain yield. Heterosis estimation was carried out using three commercial checks GPMH 1101, 900 MG and NK 6240. Among sixty crosses, DMIL 212 × DMIL 031, DMIL 117 × DMIL 021, DMIL 145 × DMIL 031, DMIL 151 × DMIL 021 and DMIL 168 × DMIL 031 exhibited highest significant SCA effects and high heterosis over checks for grain yield. These hybrids need to be further evaluated across locations and over seasons to select best hybrids for commercial exploitation.

Key words: Additive, Combining ability, Heterosis, Hybrids

Introduction

Maize (*Zea mays* L.) is the third most important cereal crop after rice and wheat in the world. Globally, maize is known as “Queen of cereals” because of its highest genetic potential among cereals. Maize is becoming an important crop in the rice-based cropping system. Maize continues to expand rapidly at an average rate of 20% per year in terms of productions. A combination of high market demand with comparatively low cost of production and high yield has generated tremendous interest among the farmers in maize cultivation. Day by day it is gaining popularity in the country due to huge demand, particularly for poultry feed industry. During 2018-19 India produced 27.8 million tons of maize in 9.2 million ha area. The average productivity during the period of 2018-19 has increased by 5.42 times and reached 2.96 t/ha in India. However, this was still much lesser than the global average productivity 5.75 t/ha (Anon., 2019). The acreage and production of maize have an increasing tendency with the introduction of exotic hybrids due to high yield potentials. Being a C_4 plant, it is physiologically more efficient with higher grain yield and wider adaptation over a range of environmental conditions. Due to the growing demand for the dairy and meat products in developing countries and the decline in rice production in China and India, maize has been projected the most important future crop by 2030 (Chandana *et al.,* 2016).

Combining ability estimation are important genetic attributes for maize breeders in anticipating improvement in productivity via hybridization and selection. Maize exhibits heterosis for all traits and the extent of heterosis vary significantly depending on the choice of parents and the trait(s) measured. Combining ability studies provide information on the genetic mechanisms controlling the inheritance of quantitative traits and enable the breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes. In Biometrical genetics two types of combining abilities are considered *i.e.,* general combining ability (GCA) and specific combining ability (SCA). General combining ability refers to the average performance of the genotype in a series of hybrid combinations and is a measure of additive gene action whereas specific combining ability is the performance of a parent in a specific cross in relation to general combining ability (Sharief *et al*., 2009).

Heterosis and combining ability are prerequisites for developing a good economically viable maize hybrid. The phenomenon of heterosis has been exploited extensively in crop breeding, leading to significant increase in yield.

Therefore, the present investigation on tester line× tester mating design was undertaken for isolating superior parent lines and thereby to identify better combining parents to obtain suitable hybrids and determine percent of heterosis using standard commercial checks.

Material and methods

The experimental material for the present investigation comprised of 20 newly developed elite inbred lines *viz.,* DMIL 207, DMIL 208, DMIL 209, DMIL 210, DMIL 211, DMIL 212, DMIL 217, DMIL 218, DMIL 115, DMIL 107, DMIL 117, DMIL 118, DMIL130, DMIL 142, DMIL 145, DMIL 148, DMIL 151, DMIL 162, DMIL 168 and DMIL 174 and three testers *viz.,* DMIL 011, DMIL 021 and DMIL 031. The list of inbred lines and their pedigree were presented in Table 1. These twenty elite inbred lines of maize were crossed with three testers in line x tester mating design to generate 60 single cross hybrids during *kharif* 2020-21 at Maize Research Centre and Seed Farm, Devihosur.

Evaluation of F1 hybrids was done by raising 60 single cross hybrids along with twenty inbreds, three testers and three checks *viz.,* GPMH 1101, 900 M and NK 6240 during *summer* 2021 in Randomized complete block design (RCBD) with three

Table 1. The list of maize parental lines and their pedigree

Sl. No.	Lines	Pedigree	Source
1	DMIL-207	CML411 × CML468-X-X-X-4	Maize Research Centre and Seed Farm, Devihosur
2	DMIL-208	CML411 × CML468-X-X-X-10	
3	DMIL-209	CML411 × CML468-X-X-X-17	
4	DMIL-210	NK6240 × CML412-X-X-X-4	
5	DMIL-211	NK6240 × CML412-X-X-X-5	
6	DMIL-212	NK6240 × CML412-X-X-X-8	
7	DMIL-217	NK6240 × NE 1412004-X-X-X-5	
8	DMIL-218	NK6240 × NE 1412004-X-X-X-11	
9	DMIL-115	CML337 × CML338-X-X-X-14	
10	DMIL-107	CML337 × CML338-X-X-X-19	
11	DMIL-117	CML337 × CML338-X-X-X-20	
12	DMIL-118	CML337 × CML338-X-X-X-21	
13	DMIL-130	CML337 × CML338-X-X-X-22	
14	DMIL-142	NK6240 × CML 412-X-X-X-15	
15	DMIL-145	NK6240 × CML 413-X-X-X-16	
16	DMIL-148	NK6240 × CML 413-X-X-X-17	
17	DMIL-151	NK6240 × CML 413-X-X-X-18	
18	DMIL-162	NK6240 × CML 451-X-X-X-14	
19	DMIL-168	NK6240 × CML 451-X-X-X-15	
20	DMIL-174	NK6240 × CML 451-X-X-X-17	
	TESTERS	Source	
1	DMIL-011	900M Gold × NEI-004	Maize Research Centre and Seed Farm, Devihosur
2	DMIL-021	NS × 052030	
3	DMIL-031	NK 6240 × CML412	

replications to estimate the combining ability and heterosis in maize at Maize Research Centre and Seed Farm, Devihosur. Each genotype was planted in three rows with plot size 3.0 x 1.2 meters. The spacing between rows and plants maintained 60cm and 30cm respectively. One plant per hill was maintained and recommended package of practices was followed to raise a healthy crop.

Observations were recorded on five randomly selected plants in each replication for twelve characters such as days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent dry husk, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, shelling percentage, hundred grain weight(g) and grain yield (q/ha). Combining ability and heterosis analysis was carried out according to formulae given by Kempthorne (1957) and Talukder *et al.,* 2016, using WINDOSTAT (edition 9.1). Percent heterosis was calculated by using the following formula.

Heterosis over check (standard heterosis) = (F1-CC/CC) ′ 100
Where, F1 = Mean performance of F1, CC = Mean performance of the best commercial check

Results and discussion

The analysis of variance for combining ability revealed highly significant differences among the parents and hybrids for all the characters studied presented in Table 2 and Table 3. It was observed that for all twelve characters, the mean sum of squares of replication was found to be non-significant which are considered under investigation. The mean sum of squares

Table 2. Analysis of variance for different quantitative characters of maize

Source of variation Character	Replications	Parents	Females	Males	Females vs Males	Parent vs Crosses	Crosses	Error
Df	2	22	19	2	1	1	59	164
Days to 50 per cent tasseling	4.76	18.90**	17.27**	7*	73.6**	186.97**	7.46**	1.81
Days to 50 per cent silking	0.88	13.72**	9.39**	14.25**	94.77**	129.19**	7.63**	1.94
Days to 75 per cent dry husk	21.86	102.61**	22.67	580.19**	666.40**	10.52	20.32	22.98
Plant height (cm)	23.59	185.87*	142.51*	124.35**	1328.83**	15135.92**	397.50**	104.99
Ear height (cm)	46.10	166.44**	103.07**	85.68*	1631.97**	9087.48**	175.48*	30.29
Cob length (cm)	0.77	2.66*	2.98*	2.88*	4.86*	284.88**	7.12**	1.21
Cob girth (cm)	0.01	0.35**	0.39**	0.30*	0.31*	7.04**	0.28**	0.07
No. of Kernel rows per ear	0.07	0.49**	2.35*	1.77	0.74	80.57**	3.87**	0.61
No. of Kernels per row	5.28	24.23**	16.82**	14.41*	204.62**	137.15**	38.24**	4.96
Shelling percentage	7.83	39.76*	42.52*	19.08	28.58	729.69**	19.95	17.56
100 seed weight (g)	0.66	17.07**	18.60**	9.40*	17.42*	1345.04**	36.86**	4.30
Grain yield (q/ha)	40.53	90.44*	95.08*	107.12**	178.4**	63598.83**	464.84**	44.74

*, ** - Significant at 5 % and 1 % level of probability, respectively

Table 3. Analysis of variance for combining ability for yield and yield related traits.

Sources	d.f.	Days to 50 per cent tasseling	Days to 50 per cent silking	Days to 75 per cent dry husk	Plant height (cm)	Ear height (cm)	Cob length (cm)
Crosses	59	7.463**	7.63**	20.32**	397.50**	175.48**	7.12**
Line	19	10.98*	8.27*	16.55**	455.07**	288.12*	10.01*
Tester	2	41.77**	52.23**	10.27**	607.33**	318.58*	26.64*
Line x Tester	38	3.89*	4.97**	22.72**	357.66**	111.62**	4.65**
Error	118	2.03	0.27	1.10	106.98	19.35	1.43

Sources	d.f.	Cob girth (cm)	Number of kernel rows per cob	Number of kernels per row	Shelling percentage (%)	Hundred grain weight (g)	Grain Yield (q/ha)
Crosses	59	0.28**	3.87**	38.24**	19.95*	36.86**	464.84**
Line	19	0.51*	4.72*	54.43*	30.09*	66.70*	644.28**
Tester	2	0.20*	7.10*	276.88**	72.99*	20.16*	552.57**
Line x Tester	38	0.18**	3.26**	17.59**	12.08	22.81**	370.51**
Error	118	0.03	0.64	3.90	13.34	4.492	46.67

*, ** - Significant at 5 % and 1 % level of probability, respectively

for parents and crosses were highly significant for all the characters except days to 75 per cent dry husk maturity under the study indicating the presence of considerable genetic differences among selected parental lines and hybrids which were developed from them.

The knowledge of additive and non-additive gene action is essential for plant breeder which is useful for the development of superior hybrids in plant breeding programme. The combining ability analysis enables the partitioning of genotypic variation of the hybrids into variation due to general combining ability (main effects) and specific combining ability (interaction effects). In the genotypes studied, estimates of variance due to SCA were higher than GCA variance indicating the predominance of non-additive gene action except days to 50 per cent tasseling and days to 75 per cent dry husk presented in Table 4. The role of additive and non-additive gene action for grain yield and its component traits had been reported earlier by Meenakshi *et al.* (2017) and Rajesh *et al.* (2018).

Estimates of GCA effects revealed that no line was observed to be good combiner for all the traits. Best lines and testers with significant GCA effects in the desirable direction for each character are presented in Table 5. out of twenty inbred lines eight lines *viz.,* DMIL 210, DMIL 211, DMIL 212, DMIL 107, DMIL 142, DMIL 151, DMIL 168 and DMIL 031 were good general combiners for grain yield. Among them, DMIL 168 was the best combiner with highest gca effects in positive direction. Apart from this, it was a good general combiner for plant height, Ear height, number of kernel rows per cob, number of kernels per row, shelling percentage and hundred grain weight characters in positive direction. Among testers, DMIL 031 recorded significant gca effects for most of the traits in desirable direction. It recorded positive GCA effects for Plant height, number of kernels per cob, number of kernels per ear and hundred grain weight proving to be a best combiner in producing heterotic hybrids. However, these lines and testers should be evaluated further to confirm their superiority. Best crosses with significant

Table 4. Estimates of component of variances for yield and yield related traits

Characters	σ^2 GCA	σ^2 SCA	σ^2 GCA/ σ^2 SCA
Days to 50 per cent tasseling	0.71	0.69	1.02
Days to 50 per cent silking	0.82	1.01	0.81
Days to 75 per cent dry husk	0.27	0.08	3.30
Plant height (cm)	12.35	84.22	0.146
Ear height (cm)	7.91	27.11	0.29
Cob length (cm)	0.006	0.03	0.17
Cob girth (cm)	0.01	1.14	0.165
Number of kernel rows per cob	0.15	0.88	0.17
Number of kernels per row	1.65	4.20	0.39
Shelling percentage (%)	1.13	6.17	0.18
Hundred grain weight (g)	0.98	1.82	0.54
Grain yield (q/ha)	16.04	108.59	0.14

Table 5. Best lines and testers with significant GCA effects in the desirable direction

Characters	Lines	Testers
Days to 50 per cent tasseling	DMIL 142 -2.06**	DMIL 011 -0.68**
Days to 50 per cent silking	DMIL 142 -1.58**	DMIL 011 -0.80**
Days to 75 per cent dry husk	DMIL 209 -4.20**	DMIL 011 -0.47
Plant height (cm)	DMIL 107 16.30**	DMIL 031 3.63**
Ear height (cm)	DMIL 212 9.14**	DMIL 012 2.21**
Cob length (cm)	DMIL 210 1.46**	DMIL 012 0.57**
Cob girth (cm)	DMIL 218 0.70**	DMIL 011 0.04**
Number of kernel rows per cob	DMIL 212 1.27**	DMIL 031 0.39**
Number of kernels per row	DMIL 168 3.59**	DMIL 021 1.40**
Shelling percentage (%)	DMIL 168 3.87**	DMIL 011 1.26*
Hundred grain weight (g)	DMIL 117 5.07**	DMIL 031 0.59
Grain yield (q/ha)	DMIL 168 19.58**	DMIL 031 2.79**

*, ** - Significant at 5 % and 1 % level of probability, respectively

SCA effects in desirable direction for each characters are presented in Table 6. The cross combinations *viz.,* DMIL 209 x DMIL 021, DMIL 210 x DMIL 011, DMIL 210 x DMIL 031, DMIL 212 x DMIL 031, DMIL 217 x DMIL 021, DMIL 218 x DMIL 021, DMIL 115 x DMIL 011, DMIL 117 x DMIL 021, DMIL 130 x DMIL 011, DMIL 145 x DMIL 031, DMIL 151 x DMIL 021, DMIL 168 x DMIL 011, DMIL 168 x DMIL 031 and DMIL 174 x DMIL 011 recorded significant positive *sca* effects for grain yield indicating good specific combinations. These results are in agreement with results obtained by Panda *et al.* (2017) and Kapoor *et al.* (2014). Therefore, recurrent selection for specific combining ability could be followed in the segregating generations.

Heterosis:

Maturity characters

Maturity is an important attribute of a genotype which affects economic yield directly or indirectly. The components *i.e.,* days to 50 per cent tasseling, days to 50 per cent silking and days to 75 per cent dry husk defines the maturity of a genotype. These maturity characters also influenced by environmental factors. However, Maturity characters are critical for designing hybrids for early or late maturity to suit different cropping strategies.

DMIL 145 × DMIL 021 and DMIL 117 × DMIL 021 crosses recorded lowest negative heterosis for days to 50 per cent tasseling over the check NK 6240. DMIL 142 × DMIL 031 and DMIL 130 × DMIL 031 crosses recorded lowest negative heterosis for days to 50 per cent silking over check NK 6240 and DMIL 142 × DMIL 031 cross recorded lowest negative heterosis for days to 75 per cent dry husk over check NK 6240. The cross combinations, DMIL 211 × DMIL 031 and DMIL 107 × DMIL 021 manifested highest positive heterosis for plant height over NK 6240 and DMIL 212 × DMIL 031 and DMIL 115 × DMIL 031 manifested highest positive heterosis for ear height these results are in Correspondance with the results of Umar *et al.* (2015) and Owusu (2017).

Yield characters

Grain yield is a complex quantitative character which is influenced by other ancillary and environmental factors. Comprehensive study is difficult for such of the traits and it is the ultimate objective in majority of the crop plants on which plant breeding experiments are centered around.

DMIL 148 × DMIL 021 and DMIL 211 × DMIL 021 were two best crosses with high significant positive heterosis for cob length over check NK 6240. For cob girth, DMIL 107 × DMIL 031 and DMIL 142 × DMIL 021 crosses recorded highest positive heterosis over check NK 6240. Crosses, DMIL 212 × DMIL 031 and DMIL 145 × DMIL 031 recorded high positive heterosis for number of kernel rows per cob. The cross combinations DMIL 117 × DMIL 021 and DMIL 145× DMIL 031 recorded high positive heterosis for number of kernel rows per row. DMIL 209 × DMIL 011 and DMIL 168 × DMIL 011 recorded high positive heterosis for shelling percentage. For hundred grain weight DMIL 145 × DMIL 031 and DMIL 117 × DMIL 031 recorded highest positive heterosis over check NK 6240. Earlier workers including Gazala *et al.* (2017) and Dhoot *et al.* (2017) reported considerable positive heterosis for these traits. Five hybrids *viz.,* DMIL 212 × DMIL 031, DMIL 117 × DMIL 021, DMIL 145 × DMIL 031, DMIL 151 × DMIL021 and DMIL 168

Table 6. Best crosses with significant SCA effects in the desirable direction

Sl. No	Characters	Crosses		
1	Days to 50 per cent tasseling	DMIL 151 × DMIL 031 -2.45**	DMIL 212 × DMIL 021 -2.31**	DMIL 145 × DMIL 011 -2.14**
2	Days to 50 per cent silking	DMIL 211 × DMIL 031 -2.19**	DMIL 145 × DMIL 011 -2.70**	DMIL 107 × DMIL 021 -2.05**
3	Days to 75 per cent dry husk	DMIL 168 × DMIL 031 -7.44**	DMIL 212 × DMIL 011 -6.62**	DMIL 142 × DMIL 011 -5.68**
4	Plant height (cm)	DMIL 211 × DMIL031 25.74**	DMIL 207 × DMIL 021 21.64**	DMIL 174 × DMIL 011 18.25**
5	Ear height (cm)	DMIL 211 × DMIL 031 9.19**	DMIL 209× DMIL 011 10.65*	DMIL 174 × DMIL 011 9.45*
6	Cob length (cm)	DMIL 211 × DMIL 021 2.10**	DMIL 210 × DMIL 011 1.96**	DMIL 142 × DMIL 031 1.78**
7	Cob girth (cm)	DMIL 168 × DMIL 031 0.52**	DMIL 151 × DMIL 011 0.50**	DMIL 107 × DMIL 021 0.50**
8	Number of kernel rows per cob	DMIL 145 × DMIL 031 2.36**	DMIL 162 × DMIL 011 2.04**	DMIL 148 × DMIL 011 1.41**
9	Number of kernels per row	DMIL 145 × DMIL 031 5.56**	DMIL 174 × DMIL 021 5.15**	DMIL 210 × DMIL 011 3.74**
10	Shelling percentage (%)	DMIL 117 × DMIL 021 8.26**	DMIL 145 × DMIL 031 7.89**	DMIL 168 × DMIL 011 7.25**
11	Hundred grain weight (g)	DMIL 145 × DMIL 031 5.77**	DMIL 210 × DMIL 011 3.56**	DMIL 168 × DMIL 011 2.47**
12	Grain yield (q/ha)	DMIL 212 × DMIL 031 13.93**	DMIL 117 × DMIL 021 17.65**	DMIL 145× DMIL 031 16.66**

*, ** - Significant at 5 % and 1 % level of probability, respectively

× DMIL 031 showed significant positive standard heterosis for grain yield indicating their ability to respond to high input management. Similar observations were also reported by Varalakshmi and Wali (2017) and Anilkumar *et al.* (2018).

Majority of hybrids showed significant positive heterosis over mid parent and over better parent heterosis. Twenty seven hybrids showed significant heterosis over check GPMH 1101, seven hybrids showed positive heterosis over 900M GOLD and NK 6240. These top performing hybrids DMIL 168 × DMIL 021, DMIL 168 × DMIL 031, DMIL 151 × DMIL 021, DMIL 145 × DMIL 031, DMIL 117 × DMIL 021, DMIL 212 × DMIL 031 and DMIL 168 × DMIL 011 had significant positive SCA effects and it was found that grain yield per hectare was predominately governed by non-additive gene action. these crosses could be further exploited for hybrid breeding program.

Conclusion

The present study resulted in the identification of top 5 promising hybrids *viz.,* DMIL 212 × DMIL 031, DMIL 117 × DMIL 021, DMIL 145 × DMIL 031, DMIL 151 × DMIL 021 and DMIL 168 × DMIL 031. which were found to possess significantly high *per se*, heterosis and SCA effects for grain yield. Identification of suitable parental lines for future breeding programme also effected by identifying the parents DMIL 168, DMIL 211, DMIL 212 and DMIL 145 which having significant general combining ability for the grain yield.

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