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RESEARCH PAPER

Studies on combining ability and identification of single cross hybrids for grain yield and its component traits of maize (*Zea mays* L.)

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Abstract: An investigation was carried out to estimate combining ability and heterosisin maize (*Zea mays* L.) at the University of Agricultural Sciences, Dharwad during 2018. Combining ability analysis using line × tester design was conducted in inbred lines by crossing 15 lines with three testers. The variance ratio (ratio of GCA to SCA) revealed that the expressions of traits under this study were predominantly controlled by non-additive gene action. The lines *viz*., DMIL 3, DMIL 30 and DMIL 35 and tester DMIL 58 were identified as best general combiners for grain yield. Among crosses, DMIL 30 × DMIL 58, DMIL 17 × DMIL 58 and DMIL 35 × DMIL 58exhibited highest significant SCAeffects 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: Combining ability, Heterosis, Hybrids, Line × tester

Introduction

Maize has been the subject of genetic study for more than a century and has offered tremendous insight into genetics, breeding and evolution. Maize (*Zea mays* L.) is world's third most important cereal crop after rice and wheat. It is the only cultivated species with greater economic importance in the tribe Maydeae of the family Poaceae and plays an enormous role in food and nutritional security worldwide. Being a C4 plant, maize is physiologically more efficient, has higher grain yield potential 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 to be the most important future crop by 2030 (Salvi *et al.,* 2007).

In any hybrid breeding programme choosing appropriate parents is important to exploit significant heterosis for economic traits. So, selection should be based on *per se* performance and combining ability of the parents. The genetic architecture of yield can be better understood through the application of biometric principles. Of several biometrical methods to generate information on the combining ability status of parental lines, is line × tester developed by Kempothorne (1957). This analysis provides reliable information on magnitude of additive and non-additive components based on general and specific combining ability effects of parents and their hybrid combinations.

Combining ability studies provide information on the relative importance of GCA and SC Avariance, help to assess the nature of gene action and to identify superior parental lines for their *per se* performance. This investigation was carried out to determine the nature and magnitude of gene action and heterosis for yield and other important traits in maize.

Material and methods

Segregating materials were received from Directorate of Maize Research (DMR), New Delhi and now it is Indian Institute of Maize Research (IIMR), Ludhiana. These segregating materials are selfed for further generations and 15 elite inbred lines *viz.,* DMIL 1, DMIL 3, DMIL 5, DMIL 7, DMIL 8, DMIL 11, DMIL 12, DMIL 15, DMIL 17, DMIL 18, DMIL 29, DMIL 30, DMIL 33, DMIL 34 and DMIL 35 and three testers *viz.,* DMIL 42, DMIL 48 and DMIL 52 were selected in F_6 generation based on their *per se* performance, grain quality, pollen shedding ability and uniformity. The list of inbred lines and their pedigree are presented in Table 1. The 15 elite inbred lines of maize were crossed with three testers in line × tester mating design to generate 45 single cross hybrids during summer 2018 at the Main Agriculture Research Station, University of Agricultural Sciences, Dharwad.

Table 1.Maize parental lines and their pedigree

Sl. No.	Lines	Pedigree
	Females	
1	DMIL 1	NK 6240-13-48-51-107
2	DMIL 3	NK 6240-13-176-48-138
3	DMIL 5	900 M-14-57-50-178
4	DMIL 7	900 M-14-127-78-93
5	DMIL 8	CML 425 × HKI PCBT 3-10-27-38-100
6	DMIL 11	CML 561 × CML 543-10-28-57-4
7	DMIL 12	HKI 586-1 × CML 114-10-28-53-10
8	DMIL 15	HKI 86-1 × CML 114-23-10-50-4
9	DMIL 17	CML 337 ×CML 412-13-8-25-10
10	DMIL 18	NK 3240-29-52-68-120
11	DMIL 29	CML 561 × CML 543-15-45-72-89-114
12	DMIL 30	900 M-19-136-42-53
13	DMIL 33	CML 425 × HKI PCBT 5-15-36-55-97
14	DMIL 34	HKI 586-5 × CML 114-19-37-71-5
15	DMIL 35	CML 337 ×CML 412-6-17-45-51
	Testers (Males)	
1	DMIL 48	NK 6240 × CML 338- ×- × - × -10-4
2	DMIL 52	CM 430 × CML 431- ×- ×- ×-15-5
3	DMIL 58	CML 411 × CML 468- ×- ×- ×- 10- 3

Evaluation of F_1 hybrids was done by raising 45 single cross hybrids along with 15 inbreds, three testers and three checks *viz.,* GH 0727, 900 M and NK 6240 during *kharif* 2018 in randomized complete block design with two replications. Each genotype was planted in two rows with plot size 3.0 × 1.2 m. The spacing between rows and plants was maintained at 60 and 30 cm, respectively. One plant per hill was maintained and recommended package of practices was followed to raise a healthy crop. Observations 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, ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, shelling percentage, hundred kernel weight and grain yield. Combining ability and heterosis analysis was carried out according to formulae given by Kempthorne (1957) and Talukder *et al.* (2016), through computer generated program, Windostat (Edition 9.1).

Results and discussion

The analysis of variance for combining ability revealed highly significant differences among the parents and hybrids for all the characters studied (Tables 2 and 3). Partitioning of crosses into lines, testers and line × tester revealed that the variance due to lines and line × tester was significant for all the characters that indicated genetic difference among them. For testers, significance was found for all characters except days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent dry husk and ear height. The estimates of variance due to SCA were higher than GC Avariance indicating the predominance of non-additive gene action for these characters (Table 4). The role of non-additive gene action for grain yield and its component traits had been reported earlier by Dhoot *et al.* (2017) and Rajesh *et al.* (2018).

Estimates of GCA effects revealed that no line proved 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. Only three out of fifteen inbred lines *viz.,* DMIL3, DMIL 30 and DMIL 35 were good general combiners for grain yield. Among them, DMIL 30 was the best with

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

Source of variation character	Replications	Parents	Female	Male	Females vs Male	Parent vs Crosses	Crosses	Error
Degrees of freedom	1	17	14	2	1	1	44	62
Days to 50 per cent tasseling	5.19	13.64**	12.96**	4.66**	41.08**	97.22**	5.56**	1.74
Days to 50 per cent silking	3.24	11.64**	10.26**	4.66**	45**	96.66**	5.87**	2.22
Days to 75 per cent dry husk	2.12	19.89**	23.74**	0.5	4.672**	0.35	15.5**	3.09
Plant height (cm)	15.29	286.94**	284.49**	83.72**	727.62**	394.47**	294.97**	75.51
Ear height (cm)	32.99	217.75**	184.85**	65.05**	983.73**	4318.34**	137.6**	58.06
Cob length (cm)	0.2	2.52*	2.98*	0.3*	0.5*	102.85**	5.1**	0.87
Cob girth (cm)	0.03	0.24**	0.28**	0.04*	0.05*	4.16**	0.19**	0.017
No. of kernel rows per ear	1.01	0.62**	0.61**	1.04*	0.01	33.88**	2.71**	0.58
No. of kernels per row	6.02	26.9**	22.59**	7.12*	126.84**	98.59**	28.86**	7.39
Shelling percentage	8.08	50.33**	53.5**	35.6**	35.39**	217.55**	24.66**	7.53
100 kernel weight (g)	0.34	16.49**	18.62**	0.23	19.29**	647.97**	28.99**	5.86
Grain yield (q/ha)	79.77	107.48**	120.96**	61.44*	10.91*	376..43**	302.18**	27.22

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

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

Sources	Degrees of freedom	Days to 50 per cent tasselling	Days to 50 per cent silking	Days to 75 per cent dry husk	Plant height (cm)	Ear heigh t (cm)	Cob length (cm)	Cob girth (cm)	Number of kernel rows per cob	Number of kernels per row	Shelling (%)	Hundred kernel weight (g)	Grain yield (q/ha)
Crosses	44	5.56 **	5.87**	15.50**	294.97**	137.60**	5.10**	0.19**	2.71**	28.86**	24.66**	28.99**	301.34**
Line	14	6.04**	6.57**	13.92*	303.06**	244.26 **	8.608 *	0.20**	3.29**	37.55**	33.09**	49.01**	498.93*
Tester	2	3.67	2.63	29.37	212.61**	188.77	5.76**	0.33**	2.85**	84.09 **	13.40**	130.24 **	172.88*
Line × Tester	28	5.46**	5.75**	15.30**	296.81**	80.61**	3.30 **	0.18**	2.41**	20.57**	21.25**	11.75**	211.72**
Error	62	1.74	2.22	3.09	75.51	58.06	0.87	0.02	0.58	7.39	7.53	5.86	27.22

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

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	0.002	2.68	0.0007
Days to 50 per cent silking	0.0023	2.84	0.0008
Days to 75 per cent dry husk	0.0038	7.63	0.0004
Plant height (cm)	-0.0351	146.67	-0.0002
Ear height (cm)	1.08	39.52	0.028
Cob length (cm)	0.03	1.64	0.02
Cob girth (cm)	0.0003	0.09	0.003
Number of kernel rows per cob	0.0057	1.20	0.004
Number of kernels per row	0.15	10.27	0.015
Shelling percentage (%)	0.06	9.76	0.006
Hundredkernel weight (g)	0.32	5.71	0.057
Grain yield (q/ha)	1.71	106.02	0.016

highest GCA effects in positive direction. Apart from this, DMIL 30 proved to be a good general combiner for plant height, cob length, number of kernel rows per cob, number of kernels per row and hundred grain weight. Among testers, DMIL 58 showed significant GCA effects for most of the traits studied. It recorded positive GCA effects for ear height,number of kernels per cob 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 SCA effects in desirable direction for each character are presented in Table 6. The cross combinations *viz.,* DMIL 17× DMIL 58, DMIL 30

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

Sl. No.	Characters	Lines	Testers
1	Days to 50 per cent tasseling	DMIL 5 -1.44**	DMIL 52 -0.34
2	Days to 50 per cent silking	DMIL 5 -1.22**	DMIL 52 -0.26
3	Days to 75 per cent dry husk	DMIL 18 -2.47**	DMIL 52 -0.84
4	Plant height (cm)	DMIL 30 16.47**	DMIL 52 1.80*
5	Ear height (cm)	DMIL 33 11.74**	DMIL 58 2.71**
6	Cob length (cm)	DMIL 12 2.21**	DMIL 52 0.48**
7	Cob girth (cm)	DMIL 8 0.28**	DMIL 48 0.10**
8	Number of kernel rows per cob	DMIL 35 1.25**	DMIL 58 0.23*
9	Number of kernels per row	DMIL 30 2.31**	DMIL 58 1.64
10	Shelling percentage (%)	DMIL 1 2.92**	DMIL 52 0.41
11	Hundred grain weight (g)	DMIL 30 5.97**	DMIL 58 2.26**
12	Grain yield (q/ha)	DMIL 30 21.82**	DMIL 58 2.79**

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

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

Sl. No.	Characters	Crosses		
1	Days to 50 per cent tasseling	DMIL 18 × DMIL 52 -2.48**	DMIL 7 × DMIL 48 -2.35**	DMIL 34 × DMIL 48 -2.18**
2	Days to 50 per cent silking	DMIL 30 × DMIL 52 -3.07**	DMIL 34 × DMIL 48 -2.48**	DMIL 7 × DMIL 48 -2.32**
3	Days to 75 per cent dry husk	DMIL 35 × DMIL 52 -6.65**	DMIL 3 × DMIL 58 -4.75**	DMIL 5 × DMIL 48 -3.92**
4	Plant height (cm)	DMIL 3 × DMIL58 20.69**	DMIL 11 × DMIL 48 18.89**	DMIL 17 × DMIL 52 17.63**
5	Ear height (cm)	DMIL 3 × DMIL 48 12.86**	DMIL 30× DMIL 48 8.68*	DMIL 11× DMIL 58 7.28*
6	Cob length (cm)	DMIL 3 × DMIL 48 1.85**	DMIL 7 × DMIL 52 1.67**	DMIL 1 × DMIL 52 1.61**
7	Cob girth (cm)	DMIL 3 × DMIL 58 0.45**	DMIL 5 × DMIL 48 0.45**	DMIL 11 × DMIL 52 0.45**
8	Number of kernel rows per cob	DMIL 35 × DMIL 58 2.12**	DMIL 30 × DMIL 58 1.80**	DMIL 18 × DMIL 52 1.41**
9	Number of kernels per row	DMIL 15 × DMIL 48 6.20**	DMIL 3 × DMIL 48 5.15**	DMIL 7 × DMIL 52 4.55**
10	Shelling percentage (%)	DMIL 8 × DMIL 52 5.14**	DMIL 33 × DMIL 58 4.80**	DMIL 8 × DMIL 48 3.83**
11	Hundred grain weight (g)	DMIL 34 × DMIL 58 4.70**	DMIL 35 × DMIL 58 4.34**	DMIL 15 × DMIL 48 3.92**
12	Grain yield (q/ha)	DMIL 17 × DMIL 58 22.03**	DMIL 30 × DMIL 58 16.14**	DMIL 35× DMIL 58 13.43**

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

Table 7. Best single cross hybrids based on mean, SCA effects, and standard heterosis for grain yield

Hybrid	Mean (q/ha)	sca effect	Standard heterosis (%) Over GH 0727	Over NK -6240	Over 900 M	Type of cross
DMIL 30 × DMIL 58	106.23	16.14**	42.92**	15.97**	12.06**	H x H
DMIL 17 × DMIL 58	103.78	22.03**	39.62**	13.30**	9.47*	L x H
DMIL 35 × DMIL 58	103.19	13.43**	38.83**	12.65**	8.85*	H x H
DMIL 30 × DMIL 48	99.13	1.63	33.36**	8.22*	4.57	H x L
DMIL 3 × DMIL 48	95.93	7.84*	29.06**	4.73	1.19	H x L

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

× DMIL 58, DMIL 35 × DMIL 58, DMIL 12 × DMIL 52, DMIL 34 × DMIL 52, DMIL 8 × DMIL 48, DMIL 3 × DMIL 48 and DMIL 11 × DMIL 58 showed significant positive SCA effects for grain yield indicating good specific combinations and these single cross hybrids were obtained from parents with low × high, high × high, high × high, low × low, low × low, low × low, high × low and low × high GCA effects implying that grain yield is governed by both additive and epistatic gene actions. These results are in agreement with the results of Panda *et al.* (2017) and SCA Kapoor *et al*. (2014). Cross combination DMIL 35 × DMIL 58 exhibited significant positive SCA effect on number of kernels per row and hundred grain weight. In addition, DMIL 3× DMIL 48 and DMIL 35 × DMIL 58 cross combinations exhibited significant SCA effects for ear length and number of kernel rows per cob, respectively. The crosses with significant SCA effects involved parents with low × low or high × highGCA effects indicating the presence of non-allelic interactions. This suggests that, recurrent selection for specific combining ability could be followed in the segregating generations. DMIL 8 × DMIL 58 and DMIL 5 × DMIL 58 crosses recorded lowest negative heterosis for days to 50 per cent tasseling and days to 50 per cent silking over the check NK 6240. The cross combinations, DMIL 30 × DMIL 58 and DMIL 30 × DMIL 48 manifested highest positive heterosis for plant height and ear height over NK 6240 and these results are in agreement with the results of Umar *et al.* (2015) and Owusu *et al.* (2017). DMIL 12 × DMIL 52 and DMIL 8 × DMIL 58were two best crosses with highly significant positive heterosis over checks for cob length and cob girth, respectively. The crosses, DMIL 35 × DMIL 58 and DMIL 17 × DMIL 58 revealed higher positive heterosis for number of kernel rows per cob and number of kernels per row over check NK 6240, respectively. The cross combinations DMIL 7 × DMIL 48 and DMIL 35 × DMIL 58 were identified as best crosses for shelling percentage and hundred grain weight, respectively. Earlier Gazala *et al.* (2017) and Dhoot *et al.* (2017) reported considerable positive heterosis for these traits. Three hybrids *viz.,* DMIL 17 × DMIL 58, DMIL 30 ×DMIL 58 and DMIL 35 × DMIL 58 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).

Conclusion

Success of maize breeding depends onthe development of high yielding hybrids using suitable inbred lines. The present study resulted in the identification of top 5 promising hybrids *viz.,* DMIL 30 × DMIL 58, DMIL 17 × DMIL 58, DMIL 35 × DMIL 58, DMIL 30 × DMIL 48 and DMIL 3 × DMIL 48 which were found to possess significantly high *per se*, heterosis and SCA effects for grain yield. Among the parental lines, DMIL 3, DMIL 30, DMIL 35 and DMIL 58 showed significant general combining ability for the grain yield. Hence, cross-combinations with desirable SCA effects and better yield performance would be tested in multi-location trial to identify better-performing cross(es) among them. Additionally, these superior crosses were identified as overall good general combiners and these could be utilized for development of either the synthetics varieties or an elite breeding population by allowing through mixing among them to achieve new genetic recombination and then subjecting the resultant population to recurrent selection.

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