

RESEARCH PAPER

Combining ability analysis for grain yield and its component traits in maize (*Zea mays* L.)

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Abstract: The present investigation was carried out at Botany garden, University of Agricultural Sciences, Dharwad, with the view of assessing the combining ability, nature of gene action with respect to yield and its related traits during *kharif* 2019. A total of ten newly developed inbred lines were crossed in half diallel mating system to derive forty-five single cross hybrids. The ratio of GCA to SCA revealed that the expressions of traits under the study were predominantly controlled by non-additive gene action. The lines *viz.*, DMIL 17 and DMIL 30 were identified as best general combiners with better mean performance for grain yield. Among crosses, DMIL 7 × DMIL 30, DMIL 11 × DMIL 15 and DMIL 5 × DMIL 8 exhibited highest significant SCA effects 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, Diallel, Heterosis, Maize

Introduction

Maize (*Zea mays* L.) is one of the world's third most important cereal crop after rice and wheat. It is a member of grass family poaceae and is highly cross pollinated crop. It has assumed greater significance due to its demand for food, feed and industrial utilization. Globally, maize is known as "Queen of cereals" because of its highest genetic potential among cereals. Maize has been the subject of genetic study for more than a century and has offered tremendous insight into genetics, breeding and evolution. Being a C₄ plant, it is physiologically more efficient, 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 (Salvi *et al.*, 2007).

Hybrid cultivars have played a vital role in increasing acreage and productivity of maize. In any hybrid breeding programme choosing appropriate parents is important to exploit significant heterosis for economic traits. The genetic architecture of yield can be better understood through the application of biometric principles which give information on the combining ability status of parental lines. One of the techniques widely used is diallel mating design developed by Griffing (1956). 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. So, selection should be based on per se performance and combining ability of the parents.

Combining ability is the relative ability of a genotype to transmit its desirable performance to its crosses. Combining ability analysis is not only the quickest method of understanding the genetic nature of quantitatively inherited traits, but also gives essential information about the selection of parents which in turn throws better segregants. The variance due to general combining ability (GCA) is usually considered to be an indicator of the extent of additive type of gene action,

whereas specific combining ability (SCA) is taken as the measure of non-additive type of gene actions in heterosis breeding. The best combinations with general combining ability of individual lines are helpful to get more desirable recombinants which enables for further improvement of the crop. Hence, this investigation was carried out to determine the nature, magnitude of gene action and combining ability analysis for yield and other important traits in maize.

Material and methods

The present research work was carried out during *rabi* 2018 at Seed Farm, Devihosur, Haveri and *kharif* 2019 at Botany garden, University of Agricultural Sciences, Dharwad. The materials used during the course of experimentation comprised of ten newly developed elite inbred lines *viz.*, DMIL 1, DMIL 3, DMIL 5, DMIL 7, DMIL 8, DMIL 11, DMIL 15, DMIL 17, DMIL 30 and DMIL 35. The list of inbred lines and their pedigree were presented in Table 1. The ten elite inbred lines of maize were crossed in diallel mating fashion to generate forty-five single cross hybrids.

Evaluation of F₁ hybrids was done by raising forty-five single cross hybrids along with parents and three checks *viz.*, GH 0727, CP 818 and NK 6240 during *kharif* 2019 in Randomized Complete Block Design (RCBD) with three replications to estimate the combining ability in maize at Botany garden, University of Agricultural Sciences, Dharwad. Each genotype was planted in two rows with plot size 4.0 x 1.2 meters. The spacing between rows and plants maintained 60cm and 20cm, 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 maturity, 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 kernel weight (g) and grain yield (q/ha). Combining ability and heterosis analysis was carried out by adopting Model-1, Method-2 formulae given by Griffing (1956) through computer generated program, WINDOSTAT (edition 9.1).

Results and discussion

Recently in India, research strategies are being diverted to produce single cross hybrids to achieve quantum jump in production and productivity of maize. In the present study, The analysis of variance revealed highly significant differences among the parents and hybrids for all the characters studied presented in Table 2 which indicated the presence of adequate genetic differences among selected parental lines and F₁s. Parents vs hybrids exhibited significant mean sum of squares and significant values for all the traits except for days to 50 per cent silking and plant height which revealed the presence of substantial heterosis in resultant F₁ hybrids.

The inbred lines need to be examined for their combining ability, in order to produce the heterotic hybrids. The estimates of combining ability will give GCA and SCA components along with the characteristic gene action. Parent’s estimates of gca effects help to identify the superior parents to be used to generate

superior cross combinations. Whereas, the sca effects reflect which cross combination is suitable for commercial exploitation as a hybrid variety and the ratio of gca/sca variance indicates the gene action governing the concerned trait. In the present study, the analysis of variance for combining ability indicated that the mean squares due to parents, hybrids and parents vs hybrids were significant for all the characters except for days to 50 per cent silking and plant height. The estimates of variances for combining ability revealed the presence of higher SCA variance than GCA variance reflecting the superiority of non-additive gene action in the expression of traits under investigation (Table 3). The ratio of gca/sca variance was less than unity which indicated the predominance of dominance variance in control of studied traits. These results are fostering to exploit heterosis. The role of non-additive gene action for grain yield and its component traits had been reported earlier by Kanagarasu *et al.* (2010) and Kuselan *et al.* (2017). Contrarily, Ojo *et al.* (2007) reported that the additive gene action was more important for grain yield than non-additive gene action.

From the results it is evident that gca effects varied in their magnitude for different characters. No line was observed to be good combiner for all the traits. Best lines with significant gca effects in the desirable direction for each character are presented

Table 1. The pedigree and features of maize parental lines

Sl. No.	Lines	Pedigree	Features
1	DMIL 1	NK 6240-13-48-51-107	Medium tall plant, moderate <i>per se</i> performance and good kernel color
2	DMIL 3	NK 6240-13-176-48-138	Thick stem, erect leaves and absence of tassel
3	DMIL 5	900 M-14-57-50-178	Good kernel color and thick stem
4	DMIL 7	900 M-14-127-78-93	High <i>per se</i> performance, erect leaves and medium tall plant
5	DMIL 8	CML 425 × HKI PCBT 3-10-27-38-100	Medium tall, moderate <i>per se</i> performance and absence of tassel
6	DMIL 11	CML 561 × CML 543-10-28-57-4	High <i>per se</i> performance, medium tall and good seed color
7	DMIL 15	HKI 86-1 × CML 114-23-10-50-4	Good kernel color, thick stem and absence of tassel
8	DMIL 17	CML 337 × CML 412-13-8-25-10	Late maturity, moderate <i>per se</i> performance and tall plant
9	DMIL 30	900 M-19-136-42-53	Late maturity and high test weight
10	DMIL 35	CML 337 × CML 412-6-17-45-51	High <i>per se</i> performance, late maturity and thick stem

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

Sl. No.	Sources of variation Characters	Replication	Treatments	Parents	Hybrids	Parents v/s Hybrids	Error
	Degrees of freedom (df)	2	54	9	44	1	108
1	Days to 50 per cent tasseling	0.006	13.003**	19.615**	11.267**	29.900**	2.265
2	Days to 50 per cent silking	5.988	10.057**	11.393**	9.879**	5.867	2.371
3	Days to 75 per cent dry husk maturity	4.145	15.154**	16.800**	12.779**	104.836**	3.639
4	Plant height (cm)	11.499	766.341**	1160.908**	702.711**	14.933	13.431
5	Ear height (cm)	26.315	241.576**	352.504**	206.058**	806.003**	60.366
6	Cob length (cm)	0.009	5.856**	12.262**	4.102**	25.364**	0.759
7	Cob girth (cm)	0.005	0.216**	0.297**	0.180**	1.057**	0.011
8	Number of kernel rows per cob	0.996	2.563**	5.125**	2.054**	1.864*	0.393
9	Number of kernels per row	0.198	46.134**	90.933**	37.967**	2.308*	0.568
10	Shelling percentage	0.842	14.337**	11.271*	14.590**	30.829*	4.892
11	100 kernel weight (g)	1.023	74.856**	94.700**	55.827**	733.527**	17.023
12	Grain yield / plot (kg)	0.242	3.323**	3.368**	2.981**	17.974**	0.108
13	Grain yield / ha (q)	46.481	957.118**	971.446**	862.874**	4974.923**	34.354

*, ** - 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% tasseling	Days to 50% silking	Days to 50% dry husk maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob girth (cm)	Number of kernel rows per cob	Number of kernels per row	Shelling per centage	100 kernel weight (g)	Grain yield / plot (kg)	Grain yield (q/ha)
Parents	9	19.615**	11.393**	16.800**	1160.908**	352.504**	12.262**	0.297**	5.125**	90.933**	11.271*	94.700**	3.368**	971.446**
Hybrids	45	11.267**	9.879**	12.779**	702.711**	206.058**	4.102**	0.180**	2.054**	37.967**	14.590**	55.827**	2.981**	862.874**
Parents vs Hybrids	1	29.900**	5.867	104.836**	14.933	806.003**	25.364**	1.057**	1.864*	2.308*	30.829*	733.527**	17.974**	4974.923**
Error	108	2.265	2.371	3.639	13.431	60.366	0.759	0.011	0.393	0.568	4.892	17.023	0.108	34.354
σ^2_{gca}		0.735**	0.381**	0.876**	28.512**	8.968**	0.233**	0.010**	0.1145**	1.017**	0.407**	2.715**	0.172**	49.493**
σ^2_{sca}		2.532**	2.159**	2.503**	232.735**	50.962**	1.480**	0.059**	0.519**	15.786**	2.800**	16.616**	0.873**	250.321**
$\sigma^2_{gca/\sigma^2_{sca}}$		0.290	0.177	0.350	0.123	0.176	0.157	0.165	0.280	0.064	0.146	0.163	0.197	0.198
σ^2_A		1.469	0.763	1.753	57.024	17.935	0.465	0.019	0.291	2.034	0.815	5.431	0.344	98.987
σ^2_D		2.532	2.159	2.503	232.735	50.962	1.480	0.059	0.519	15.786	2.800	16.616	0.873	250.321
σ^2_{A/σ^2_D}		0.580	0.353	0.700	0.245	0.352	0.314	0.322	0.561	0.129	0.291	0.327	0.394	0.395

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

Table 4. Best lines and crosses with significant GCA and SCA effects in the desirable direction

Characters	Lines	GCA effect	Crosses	SCA effect	Mean performance
Days to 50 per cent tasseling	DMIL 7	-1.750**	DMIL 5 × DMIL 15	-4.197**	57.33
			DMIL 8 × DMIL 15	-3.141**	57.33
			DMIL 30 × DMIL 35	-2.808**	59.67
Days to 50 per cent silking	DMIL 7	-1.072**	DMIL 5 × DMIL 15	-3.667**	59.33
			DMIL 5 × DMIL 7	-2.750**	59.00
			DMIL 3 × DMIL 17	-2.639**	58.67
Days to 75 per cent dry husk maturity	DMIL 7	-1.694**	DMIL 8 × DMIL 11	-4.785**	97.00
			DMIL 5 × DMIL 7	-3.702**	97.67
			DMIL 7 × DMIL 35	-2.174*	99.33
Plant height (cm)	DMIL 17	9.753**	DMIL 7 × DMIL 30	30.882**	179.80
			DMIL 8 × DMIL 17	23.048**	183.00
			DMIL 1 × DMIL 30	22.048**	175.40
Ear height (cm)	DMIL 30	5.554**	DMIL 7 × DMIL 11	16.824**	74.20
			DMIL 3 × DMIL 8	14.463**	74.27
			DMIL 1 × DMIL 7	11.207**	71.40
Cob length (cm)	DMIL 30	0.888**	DMIL 7 × DMIL 30	2.318**	17.17
			DMIL 11 × DMIL 15	2.184**	15.23
			DMIL 1 × DMIL 11	2.074**	15.44
Cob girth (cm)	DMIL 17	0.088**	DMIL 3 × DMIL 11	0.455**	4.98
			DMIL 1 × DMIL 11	0.412**	4.94
			DMIL 1 × DMIL 3	0.308**	4.88
Number of kernel rows per cob	DMIL 17	0.930**	DMIL 15 × DMIL 35	1.429**	14.60
			DMIL 8 × DMIL 15	1.145**	14.20
			DMIL 3 × DMIL 35	0.945**	14.60
Number of kernels per row	DMIL 5	1.420**	DMIL 1 × DMIL 11	6.892**	34.80
			DMIL 1 × DMIL 15	6.876**	33.80
			DMIL 5 × DMIL 11	6.142**	36.00
Shelling percentage	DMIL 7	1.550**	DMIL 30 × DMIL 35	3.655**	86.22
			DMIL 3 × DMIL 35	3.605**	87.41
			DMIL 8 × DMIL 17	2.731*	86.12
100 kernel weight (g)	DMIL 30	3.458**	DMIL 7 × DMIL 15	11.061**	44.00
			DMIL 1 × DMIL 11	7.394**	42.00
			DMIL 8 × DMIL 35	6.686**	41.00
Grain yield (q/ha)	DMIL 17	14.776**	DMIL 7 × DMIL 30	32.030**	106.11
			DMIL 11 × DMIL 15	30.045**	97.34
			DMIL 5 × DMIL 8	29.248**	90.26

in Table 4. Among the ten lines studied for their combining ability DMIL 5, DMIL 7, DMIL 17 and DMIL 30 exhibited gca effects in desirable direction for maturity characters, plant height, ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, shelling percentage, 100 kernel weight and grain yield.

Among them, DMIL 7 recorded significant negative gca effects for days to 50 per cent tasseling, days to 50 per cent silking and days to 75 per cent dry husk maturity indicating early maturing genotype that can be further used in breeding for improvement. The parental line, DMIL 17 was the best with highest gca effects in positive direction for grain yield. Apart from this, it was a good general combiner for plant height, cob girth and number of kernel rows per cob characters in positive

direction. The lines, DMIL 30 and DMIL 5 showed significant positive gca effect for the traits ear height, cob length and hundred kernel weight, respectively. However, these lines should be evaluated further to confirm their superiority for the development of synthetic varieties. The top hybrids based on their sca effects for different traits are given in Table 4. Among the forty-five hybrids, twenty-one hybrids revealed significant positive sca effects for grain yield. The top five hybrids identified based on sca effects for yield are DMIL 7 × DMIL 30, DMIL 11 × DMIL 15, DMIL 5 × DMIL 8, DMIL 3 × DMIL 8 and DMIL 1 × DMIL 11 and these single cross hybrids had high per se performance and were obtained from crossing low, average and good general combiners which indicates that grain yield is governed by both additive and epistatic gene actions. These results are in agreement with results obtained by Talukder *et al.* (2016) and Panda *et al.* (2017). Kambe gowda *et al.* (2013) also reported high positive specific combining ability effects along

with high per se performance for grain yield. Cross combination, DMIL 7 × DMIL 30 exhibited significant positive sca effect for plant height and cob length. In addition, DMIL 7 × DMIL 11, DMIL 3 × DMIL 11, DMIL 15 × DMIL 35, DMIL 1 × DMIL 11, DMIL 30 × DMIL 35 and DMIL 7 × DMIL 15 cross combinations exhibited significant sca effects for ear height, cob girth, number of kernel rows per cob, number of kernel per row, shelling percentage and hundred kernel weight respectively. Parents of positive and significant gca effects can be exploited for the development of single cross hybrids since non-additive gene action for the traits was observed. Further they can also be used for population improvement programme through reciprocal recurrent selection.

Conclusion

The cross combination identified in the present study with significantly higher SCA will become useful in the development of commercial hybrids.

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