

Genetic analysis for yield and yield component traits in maize (*Zea mays* L.) genotypes

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Abstract: An experiment was conducted to study the genetic structure of yield and its components in diallel cross (excluding reciprocals) of maize involving 10 parents. The resultant 45 hybrids along with ten parents were raised in Randomized Block Design with three replications. Analysis of variance revealed that all the genotypes were significant for all the characters. The estimated value of average degree of dominance (H_1/D)^{0.5} revealed that over dominance (non additive gene effects) were pronounced in the inheritance of all the characters viz., days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height, ear height, ear girth, ear length, number of kernel rows per ear, number of kernels per row, 100- seed weight and grain yield per plant. The estimate of additive variance was also high but it was less than dominance variance. The distribution of positive and negative alleles were in shorter distance for days to 50 per cent silking, plant height and 100-seed weight. Dominance to recessive genes ratio $[4DH_1]^{0.5} + F/[4DH_1]^{0.5}$ ranged from one to two, indicating the excess of dominant genes against recessive genes which were not much higher. The results indicated that most of the traits were under the control of non-additive (over dominance) gene action therefore the material can easily be exploited by heterosis breeding, population improvement through reciprocal recurrent selection, bi-parental mating and diallel selective mating.

Key words: Gene effects, Hayman's ratio's, maize, grain yield

Maize is the third most important cereal food crop of the world after wheat and rice. In India, maize ranks third next to rice and wheat (Centre for Monitoring Indian Economy, 2014). Among the cereals maize is rich in starch, oil and sucrose. Globally 67 per cent of maize is used for livestock feed, 25% human consumption, industrial purposes and balance is used as seed and demand for grain is increasing world wide. Formulation of a comprehensive breeding programme for the improvement of any crop depends on the gene action involved for a particular trait to be improved. Diallel analysis is one of the useful biometrical techniques for such studies. Therefore, keeping in view the crop and the utility of diallel analysis, the present investigation was undertaken to study the type of gene action involved in respect of yield and its components.

MATERIALS AND METHODS

Ten diverse inbred lines of maize were crossed in Diallel mating design (excluding reciprocals) during

Kharif, 2011 at College Farm, College of Agriculture, Rajendranagar, Hyderabad, T.S., India. The resultant 45 hybrids along with ten parents were raised in Randomized Block Design (Punse and Sukhatme 1985) with three replications at College Farm, College of Agriculture, Rajendranagar, Hyderabad, T.S., India. Each entry was sown in a row of 4 meters length with a spacing of 75 cm between rows and 20 cm between the plants. One plant per hill was maintained. The recommended fertilizers of Nitrogen, Phosphorus and Murate of Potash were applied in the ratio of 120:80:60 kg ha⁻¹. The entire phosphorus and Murate of potash and half dose of Nitrogen was applied as basal, while remaining half dose of nitrogen in two equal split doses at knee height stage and tasseling stages. Intercultural operations like weeding and irrigation schedules were taken to protect the crop from pests and diseases, so as to raise a healthy crop. At flowering and maturity stages, observations were recorded on days to 50 per cent tasseling, days to 50 per cent silking, days to maturity,

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plant height (cm), ear height (cm), ear girth (cm), ear length (cm), number of kernel rows per ear, number of kernels per row, 100- seed weight (g) and grain yield per plant (g).

The components of genetic variance D , H_1 , H_2 , F , h^2 and E were calculated as per the method proposed by Hayman (1954). Further, genetic ratios by using significant components of variance were calculated for the characters under study.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for all the characters studied (Table 1). The genotypes exhibited highly significant differences among themselves for all the characters. The parents exhibited significant differences among themselves for all the characters indicating greater diversity in the parental lines. The hybrids exhibited significant differences, indicating varying performance of cross combinations. The parents vs hybrids which indicates average heterosis, was also significant for all traits, thus considerable average heterosis was reflected in hybrids.

Estimates of genetic components of variance revealed that both additive (D) and dominance components (H_1) were highly significant and positive for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height, ear height, ear girth, number of kernels per row, 100-seed weight and grain yield per plant. This indicates that both additive and dominant gene actions condition the above

characters. However, for all the characters dominance component (H_1) was more predominant than additive component. The significance of dominance effect was also reflected by high value of H_2 component, which indicates the proportion of positive and negative genes. It is evident that non additive gene effects were predominantly involved in the inheritance of all the traits under study. The environmental component was much lower than additive and dominance variance.

Estimates for average degree of dominance [H_1/D]^{0.5} showed that there was over dominance for all the traits studied *viz.*, days to 50 per cent tasseling (Paul and Debnath 1999), days to 50 per cent silking (Tallei and Kocha Ksarai 1999) days to maturity (El-Hosary *et al.* 1994), Plant height (Dodiya and Joshi 2002), ear height (Ram Reddy *et al.* 2011) ear girth (Jayakumar and Sundaram 2007), ear length (Mathur *et al.* 1998) number of kernel rows per ear (Gowhar *et al.* 2007), number of kernels per row (Turgut *et al.* 1995; Fahad *et al.* 2009) and 100-seed weight (Irshad *et al.* 2010; Singh *et al.* 2010; Gul *et al.* 2013; Sarac and Nedelea 2013; Hussain *et al.* 2014; Mozammil *et al.* 2015). In maize non-additive genetic variance is more often evident in controlling the inheritance of traits than additive components (Wright *et al.* 1971). In this experiment also non additive genetic component (H_1) was the major part of genetic variance for most of the yield and yield related traits.

The estimate of dominance variance (H_2) was found to be significant for all the traits indicating

Table 1
Analysis of variance for combining ability for yield and yield components in maize

Source	d.f	Days to 50% tasseling	Days to 50 % silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear girth (cm)
Replicates	2.00	2.25	1.32	2.75	143.86	103.79	0.68
Treatments	54.00	52.70**	52.38**	84.80**	2838.39**	1065.48**	7.23**
Parents	9.00	101.78**	84.83**	84.03**	1959.31**	915.90**	6.61**
Hybrids	44.00	42.78**	46.15**	61.34**	2079.24**	916.74**	5.00**
Parent Vs.Hybrids	1.00	47.85**	34.26**	1123.88**	44153.05**	8956.51**	110.53**
Error	108.00	4.25	4.28	2.44	153.58	33.03	0.45
Total	164.00	20.18	20.08	29.56	1037.48	373.85	2.69

Table 1 (cont.)

Source	d.f	Ear length (cm)	Number of kernel rows per ear	Number of kernels per row	100- Seed weight (g)	Grain yield per plant (g)
Replicates	2.00	0.40	0.63	26.71	0.21	78.66
Treatments	54.00	24.29**	4.83**	150.87**	65.31**	4658.26**
Parents	9.00	24.18**	3.57**	166.34**	86.49**	1377.85**
Hybrids	44.00	15.21**	4.89**	103.38**	52.10**	3368.81**
Parent Vs.Hybrids	1.00	425.00**	13.23**	2101.18**	456.19**	90918.20**
Error	108.00	0.63	0.56	5.27	0.57	46.63
Total	164.00	8.42	1.96	53.47	21.88	1565.48

* Significance at 5% level; ** Significance at 1% level

Table 2
Estimates of genetic parameters for different traits in maize

S.no	Genetic parameters	Days to tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear girth (cm)	Ear length (cm)	No. of kernel row per ear	No. of kernels per row	100-seed weight (g)	Grain yield per plant (g)
1	D	32.52*	26.86*	27.19*	601.97*	293.86*	2.05*	7.84*	1.00	53.56*	28.64*	443.54*
2	H ₁	49.26*	49.29*	98.97*	3666.53*	1201.42*	7.60*	27.39*	7.68*	173.59*	84.47*	5389.55*
3	H ₂	36.09*	40.12*	88.41*	3062.13*	819.30*	6.70*	24.19*	5.66*	138.13*	68.43*	5098.92*
4	h ²	5.81	4.01	148.05*	5809.79*	1178.14*	14.53*	56.02*	1.67*	276.67*	60.15*	11995.54*
5	F	30.36*	21.77	28.19*	953.05	367.74	1.88*	8.41	2.54	64.75	35.68*	273.88
6	E	1.40	1.40	0.81	51.13	11.43	0.15	0.20	0.18	1.88	0.18	15.73

Table 3
Hayman's ratio of genetic parameters for different traits in maize

S.no.	Hayman's ratios	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear girth (cm)	Ear length (cm)	No. of kernel rows per ear	No. of kernels per row	100-seed weight (g)	Grain yield per plant (g)
1	[H/D] ^{0.5}	1.23	1.35	1.90	2.46	2.02	1.92	1.86	2.76	1.80	1.71	3.48
2	H ₁ /4H ₂	0.18	0.20	0.22	0.20	0.17	0.22	0.22	0.18	0.19	0.20	0.23
3	[4DH ₁] ^{0.5} +F	2.22	1.85	1.74	1.94	1.89	1.62	1.80	2.69	2.01	2.13	1.19
4	[4DH ₁] ^{0.5} -F											
5	h ² /H ₂	0.16	0.10	1.67	1.89	1.43	2.16	2.31	0.29	2.00	0.87	2.35
6	f ²	2.49	2.53	0.00	4.84	1.61	0.09	1.80	5.46	1.51	0.12	8.78

overwhelming dominance effect of genes. The estimates of F (mean Fr over arrays) were positive for all the traits and significant only for days to 50 per cent tasseling, days to maturity, ear girth and 100-seed weight indicating that dominant genes were majorly involved in the control of these traits. The results were confirmed by $[4DH_1]^{0.5} + F/[4DH_1]^{0.5} - F$, which depicts the relative proportion of dominance and recessive alleles in parents. Since this ratio was greater than unity for all the traits studied, there was more of dominant alleles than recessive alleles in parents.

The estimated values of $H_2/4H_1$ (genes with +/- effects) in parents were less than 0.25 implying asymmetrical distribution of positive and negative alleles for all the traits. This asymmetrical distribution could have caused the inflation of dominance to over dominance. These results are in confirmation with findings of Kumar *et al.* (1999); Joshi *et al.* (1998); Umakanth *et al.* (2000); Mohammad *et al.* (2010); Khalid *et al.* (2012). The estimates of $H_2/4H_1$

and $\frac{[4DH_1]^{0.5} + F}{[4DH_1]^{0.5} - F}$ thus gave inconsistent results regarding symmetrical distribution of alleles with positive and negative effects and were not always showing equal spread of dominance and recessive alleles, respectively. This implies that dominant alleles may or may not be associated with positive effect; similarly, a recessive allele may or may not be associated with negative effect. More will be the gain in selection if proportion of dominant genes is high. From the results it was evident that, the numerical values ranged from 1.19 (grain yield per plant) to 2.69 (number of kernel rows per ear), indicating that recessive and dominant genes were not in high disproportion and most of the allele pairs might be existing in heterozygous form.

The estimated value of h^2/H_2 for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height, ear height, number of kernel row per ear, and 100-seed weight was governed by one to two gene groups. Whereas the characters ear girth, ear length, number of kernels per row and grain yield per plant was governed by two to three gene groups (Mohammad, 2014).

It is evident that the test of homogeneity (t^2) was non-significant for all the traits, indicating that diallel assumptions were fulfilled in the absence of epistasis. However, the expression of non additive component could be more because most of the genes were expected to exist in heterozygous form for many loci.

The results revealed non-additive gene action to be predominant in the inheritance of most of the traits under study and hence, there is a little scope for improvement of these traits by selection. Further, over dominance for most of the traits reveals that selection in later generations may be more effective and the selection in early generations will be more effective for the traits which govern additive gene action. Heterosis could be exploited in developing hybrids and inbreds through population improvement.

CONCLUSION

Thus in the present investigation to conclude that selection can be made for parents which possessed most dominant genes with positive effects for respective traits. The parents with positive dominant genes for earliness and high yields could be advanced for heterosis breeding programme to produce hybrids with high yield and earliness. Maximum gain could be achieved by maintaining considerable heterozygosity coupled with selection in segregating generations to enhance genetic recombination resulting in breakage of undesirable linkage, provide transgressive segregation and create broad genetic base against which maximum number of potentially functional genes may be accumulated, reassembled and expressed, leading to isolation of stable and widely adopted genotypes. Since development of intermating population is a long term approach, population improvement through methods like reciprocal recurrent selection, biparental mating and diallel selective mating as supplement to conventional breeding system is advocated for improvement of these characters in maize.

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