Research Article

Genetic Studies Involving Metric Traits in High Alitude Maize Inbred Lines under Temperate Conditions

G. Ali*, Z.A. Dar, I. Abidi , A.A. Lone., S.H. Wani., M.A. Ahangar and I. Bisati

Shere Kashmir University of Agricultural Sciences and Technology of Kashmir

Division of Genetics and Plant Breeding, Srinagar-190025

*Corresponding Author E-mail: zahoorpbg@gmail.com

ABSTRACT

The present study was carried out to generate information on gene action utilizing Hayman's component of diallel analysis. The experimental material comparised of 66 F_1s generated by crossing 12 diverse inbred lines of maize (Zea mays L.) in diallel mating design and these 66 F_1s along with 12 parents and two standard checks were evaluated in randomised complete block design in two replications at two locations namely High Altitude Rice Research Sub-station, Larnoo (E_1) and Experimental Farm of Division of Plant Breeding and Genetics, Shalimar (E_2). Analysis of variance revealed prepondance of sca variance than gca for all traits studied and the estimation of variance due to dominance deviations ($\hat{\sigma}^2{}_D$) was higher in magnitude than additive genetic variance ($\hat{\sigma}^2{}_A$) for all the traits studied in individual environments as well as pooled over environments which favours the production of hybrids. Component analysis of genetic variance for pooled analysis revealed significance of both additive (D) and dominance (H_1 and H_2). Component analysis of genetic variance revealed the significance of additive gene action for maturity traits , plant height, kernal row number, kernels per row, and 100-grain weight, whereas components of variance due to dominance deviations were significant for all the traits indicating the preponderance of non- additive gene action in the inheritance of various traits. Average degree of dominance was in over dominance range for all the characters for graphical analysis where as the gene distribution was observed to be asymmetrical for all traits except for kernels per row.

Key words: *Maize, Component analysis, Gene action, Diallel analysis*

INTRODUCTION

Maize is a versatile crop grown over a wide range of agro climatic zones. In fact, the suitability of maize to diverse environments is unmatched by any other crop. It is grown from below sea level to altitudes higher than 3000 m, and in areas with 250 mm to more than 5000 mm of rainfall per year and with a growing cycle ranging from 3 to 10 months.

In Jammu and Kashmir, the crop is cultivated over an area of 0.30 million hectares with total production of 0.59 MT and productivity of 1.96 T ha^{-1}, whereas, 0.1 million hectare area is under maize in Kashmir with production of 0.18 MT with an average yield of 1.8 T ha$^{-1(1)}$. Combining ability is an important prerequisite for developinga good economically viable hybrid maize variety. Properchoice of parents is an important criterion in order to exploit hybrid vigour. This key step depends on factors like *perse* performance of the parents and their combining ability. Combining ability is a potent tool in identifying the good combiners for hybridization especially, when a large number of parental lines are available and promising ones are to be selected on the basis of their ability to give superior cross combinations. Besides pin pointing the promising parents to be used in the development of advanced hybrids particularly when the production of such hybrids is not feasible due to some inherent problems in economic hybrid seed production, combining ability analysis has a momentous role in crop improvement as it helps in characterizing the nature and magnitude of genetic effects governing yield and its component traits.

MATERIALS AND METHODS

Twelve maize inbred lines [viz. PMI-03, PMI-48, PMI-64, PMI-67, PMI-68, PMI-69, PMI-117, PMI-118, PMI-224, PMI-298, PMI-390 and PMI-401] were crossed in a diallel mating design and all possible 66 single crosses, along with two standard checks viz., SMH-1 and C-15 were evaluated were evaluated in randomised complete block design in two replications at two locations namely High Altitude Rice Research Sub-station, Larnoo (E$_1$) and Experimental Farm of Division of Plant Breeding and Genetics, Shalimar (E$_2$).

Observations were recorded on days to 50 % tasseling, 50 % silking, plant height, ear length (cm), ear girth (cm), number of kernel rows ear^{-1}, number of kernels row^{-1}, 100 grain weight and grain yield plant^{-1} (g). Diallel component analysis[8,10] was performed with the help of statistical software Windostat version 9.1

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) for all the characters, over the environments, showed significant differences among environments, genotypes and genotype × environment interaction (Table 1). Significant genotype × environment interaction suggested the differential response of genotypes over the environments. Analysis of variance for all the characters under study in two different environments indicated significant differences among the treatments. Significant variation among the yield traits in maize was earlier reported by Hussain *et al*[11]., Haq *et al*[7]., Kumar *et al*[13]., Dawod *et al*[5]., and Sarac and Nedelea[17]. The estimates related to genetic components of variance (Table-2) revealed that estimates of additive component (D) significant for all the traits whereas the two measures of dominance component (H$_1$ and H$_2$) were significant for all the traits. This suggested the involvement of both these components in the inheritance of these traits, however greater magnitude of dominance component than its corresponding additive component of variance demonstrated greater role of dominance component in the inheritance of traits studied, which was also found while estimating variance arising due to dominance deviation through combining ability analysis by Griffing[6] approach. The distribution of alleles in the parents revealed that positive and negative alleles at these loci

are not in equal proportion in parents since H_1 exceeds H_2 and dominance gene action resulted mainly from positive gene action. Similar result have been reported by Aydin *et al*[2]., Rakesh *et al*[16].,Lata *et al*[14]., and Dar *et al*[4].

Estimation of h_2 was significant and positive for all characters except prolificacy index and shelling percentage revealing that net dominance effect over all the loci in heterozygote was significantly more and exhibited the positive direction of dominance. The non significant and positive value of h_2 exhibited by prolificacy index and shelling percentage indicated that the deviation of dominance variance resulted from both dominant and recessive alleles that were equally distributed in the parents. The value of F estimate was positive and non significant for all traits under study except kernels per row and shelling percentage thus revealing contribution of more recessive alleles towards dominance deviation. On the contrary, the value of F estimate was positive and significant for kernels per row and shelling percentage revealing higher frequency of dominant alleles in the parents for these traits.

The study of proportions of various genetic components of variance revealed that the proportion of ($H_2/4H_1$) was less then 0.25 for all the traits under study indicating asymmetrical gene distribution in the parents. The estimate of h^2/H_2 was less than unity for prolificacy index and shelling percentage indicating greater proportion recessive group of genes for these two traits and for rest of traits h^2/H_2 was more than unity indicating greater proportion of dominance group of gene. The genetic ratio KD/KR which gives the proportion of dominant and recessive alleles in the parent was greater than unity for all characters under study except for prolificacy index, ear girth and 100-grain weight where it was less than unity. This suggested that barring ear girth, 100-grain weight and prolificacy index there was higher proportion of dominant alleles in the parents for all the characters. The recessive and dominant genes where nearly equal for 100-grain weight and ear girth whereas excess of recessive genes controlled inheritance for prolificacy index. The study of proportion of average degree of dominance measured form genetic components of variance $(H_1/D)^{0.5}$ was more unity thus revealing over dominance range for all traits under study. Similar results have been reported by Kumar and Gupta[12], Rakesh[16] and Lata *et al*[14].

This dominance was due to high heterozygosity in F_1 indicating that parents selected were diverse and from different source population However, the discrepancy in the degree of dominance estimated from genetic components resulted mostly from G x E interaction or from sampling error, which subsequently had an influence on the estimation of dominance components. Further while discussing the limitations of component analysis Mather and Jinks[15] suggested that due to unequal gene distribution (if u=v=0.5, $H_2'/4H_1$ is not equal to 0.25), H_1 gets more inflated than H_2 and result is over estimation of degree of dominance secondly the component D gets also deflated in presence of additive x dominance (j type) of epistasis. This is turn causes inflation in the $(H_1/D)^{0.5}$ in diallel. Over dominance in most cases may result from a particular combination of positive and negative genes or complementary type of gene action due to correlated gene distribution, which may seriously inflate mean degree of dominance and convert partial dominance into apparent over dominance[3,9].

Table 1: Pooled analysis of variance for different characters in maize

S.No.	Source of Variation	d.f	Days to 50% anthesis	Days to 50% silking	Plant height (cm)	Ear length (cm)	Ear girth (cm)	Kernel row ear^{-1}	Kernels row^{-1}	100-grain weight (g)	Grain yield plant^{-1} (g)
1.	**Environments**	1	11400.630**	11766.210**	51405.200**	394.875**	87.789**	0.185	1409.300**	148.281**	39536.790**
2.	**Treatments**	77	63.667**	61.389**	5601.520**	17.362**	4.377**	10.748**	86.735**	60.830**	3572.761**
3.	**Parents**	11	23.324**	23.794**	4634.733**	8.063**	2.717**	15.233**	56.625**	41.460**	916.769**
4.	**Hybrids**	65	29.509**	31.660**	2523.578**	6.919**	2.446**	9.481**	56.625**	41.460**	1467.798**
5.	**Parents v. s Hybrids**	1	2727.699**	2407.375**	6302.400**	798.409**	148.175**	43.751**	3650.50**	1555.938**	169611.300**
6.	**Treatment x Environments**	77	4.414**	3.062**	638.316**	5.174**	1.422**	1.916**	19.853**	5.253**	391.461**
7.	**Parent x Environments**	11	5.415**	3.248**	505.004**	1.055*	0.471*	0.305	7.590**	2.258**	39.016
8.	**Hybrids x Environments**	65	4.079**	2.856**	634.688**	5.041**	1.496**	2.178**	18.992**	5.691**	374.551**
9.	**Parent v. s Hybrids x Environments**	1	15199**	14.456**	2340.569**	59.116**	7.083**	2.647**	210.735**	9.663**	53678.475**
10.	**Error**	154	1.144	1.312	31.850	0.491	0.237	0.354	1.908	0.901	27.189
1.	**Total**	**311**	**54.099**	**54.469**	**1726.943**	**7.104**	**1.836**	**3.318**	**31.901**	**17.285**	**1123.020**

*, ** significant at 5 and 1 per cent level, respectively

Table 2: Estimates of genetic parameters for grain yield and other attributes in maize

S. No.	Components	Days to 50% anthesis	Days to 50% silking	Plant height (cm)	Ear length (cm)	Ear girth (cm)	Kernel row ear^{-1}	Kernels row^{-1}	100- grain weight (g)	Grain yield plant^{-1} (g)
		Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled
1.	$\hat{D}$	32.195** ± 1.954	32.798** ± 1.527	825.092** ± 83.582	0.483 ± 0.690	0.047 ± 0.117	2.986** ± 0.571	4.900* ± 2.265	8.526** ± 1.185	9.524 ± 122.041
2.	$\hat{H_1}$	66.424** ± 3.910	67.419** ± 3.055	1602.572 ± 4189.434	5.091** ± 1.380	0.722** ± 0.235	2.524** ± 1.143	30.726** ± 4.531	25.773** ± 2.371	1675.770** ± 244.148
3.	$\hat{H_2}$	40.712** ± 3.256	41.183** ± 2.541	1601.246** ± 139.089	5.026** ± 1.148	0.714** ± 0.195	2.519** ± 0.951	30.726** ± 3.769	23.824** ± 1.972	1608.983** ± 203.089
4.	$\hat{h^2}$	213.90** ± 2.174	189.347** ± 1.699	17957.70** ± 92.996	63.670** ± 0.767	12.020** ± 1.309	3.900** ± 0.635	293.214** ± 2.501	128.316** ± 1.318	13415.350** ± 135.787
5.	$\hat{F}$	-59.615** ± 4.429	61.590** ± 3.461	368.679 ± 189.434	2.412 ± 1.563	0.929** ± 0.266	0.348** ± 1.295	5.611 ± 5.133	3.571 ± 2.686	300.937 ± 276.599
6.	$\hat{E}$	38.026** ± 0.542	38.746** ± 0.423	333.59** ± 23.181	2.499** ± 0.191	0.632** ± 0.032	0.821** ± 0.158	9.256** ± 0.628	1.861** ± 0.328	219.937** ± 33.848

*, ** significant at 5 and 1 per cent level, respectively. *D* – variance component due to additive genetic effects; *H* 1- variance component due to dominance deviations; *H* 2 – estimate of dominance genetic variance due to proportion of positive and negative genes; *h* 2 – net dominance effect; *F* – mean of covariance of additive and dominance effects over all the arrays; *E* – environmental component of variation.

Table 3: Proportion of components of genetic variation for different characters in maize

S.No.	Components	Days 50% anthesis	Days to 50% silking	Plant height (cm)	Ear length (cm)	Ear girth (cm)	Kernel rows ear^{-1}	Kernels row^{-1}	100- grain weight (g)	Grain yield plant^{-1} (g)
		Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled
7.	$(\hat{H}_1/\hat{D})^{1/2}$	1.436	1.434	1.394	3.245	3.909	1.044	2.504	1.739	13.265
8.	$\hat{H}_2/4\hat{H}_1$	0.153	0.153	0.249	0.246	0.247	0.249	0.250	0.231	0.240
9.	$\dfrac{(4\hat{D}\hat{H}_1)^{1/2} +\hat{F}}{(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}} = \dfrac{KD}{KR}$	0.216	0.209	0.724	0.131	-0.430	1.118	0.628	0.785	-0.087
10	$\hat{h}^2/\hat{H}_2$	5.254	4.598	11.214	12.668	16.834	1.551	9.542	5.386	8.338
11	**Heritability h^2 (n.s)**	0.030	0.043	0.419	0.141	0.258	0.442	0.225	0.473	0.233

$(H_1/D)^{1/2}$ - average degree of dominance; $H_2/4H_1$ - proportion of dominant genes with positive and negative effects; KD/ KR - proportion of dominant and recessive genes; h^2/H_2 - proportion of gene(s)/gene(s) blocks exhibiting dominance; h^2 (ns) – narrow sense heritability estimate.

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