

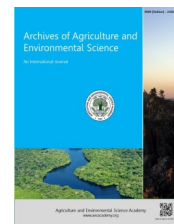


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ORIGINAL RESEARCH ARTICLE

Gene action studies in early maturing maize (*Zea mays* L.) inbred linesZ.A. Dar^{1,2}, A.A. Lone¹, G. Ali¹, I. Abidi, R.A¹. Lone, S. Gulzar¹, Abrar Yasin¹, Yusra Ali¹ and N. Yousuf¹¹Dryland (Karewa) Agricultural Research Station, Budgam, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir-190001 (J & K), INDIA²Division of Plant Breeding & Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir -190001 (J&K), INDIA

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ABSTRACT

The present investigation was aimed to investigate the gene action in early maturing maize (*Zea mays* L.) inbred lines. The experimental material comprised of 30 crosses generated by crossing six maize inbred lines in a diallel mating design during *Kharif* 2013. These 30 crosses along with standard checks viz., SMH-2 and VMH-45 were evaluated in randomized block design in three replications during *Kharif* 2014 and *Kharif* 2015. Significant variation was observed for all studied traits during both the seasons. Both additive (D) and dominance (H₁ and H₂) components of genetic variance were found significant under the study. Preponderance of non-additive gene action was observed for all traits under study. Average degree of dominance was in over dominance range for all characters. The gene distribution was asymmetrical for all traits. The value of KD / KR indicated presence of excess of dominant genes for all traits except 100-grain weight and ear girth. Heritability of most of the traits was low to medium

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INTRODUCTION

Maize (*Zea mays* L.) is a cereal crop, grown widely throughout the world in a range of agro-ecological environments that include tropics, sub-tropics and temperate regions; from sea level to 3000 m above (Morris, 2002) both under irrigated to semi-arid conditions. Having originated in Mexico, maize is now grown at least in 164 countries around the world and a tremendous choice is available as regards varieties maturing in 85 days to more than 200 days (Brink and Belay, 2006) with variability in grain colour, size and texture. Maize has a worldwide significance as food, feed and as a good source of starch, protein and oil. Many countries rely on maize as a primary staple as it meets the protein and calorie requirements of the human beings (Vasal, 2002). Hayman's approach of diallel analysis (Hayman, 1954) is most suited to determine the type of gene action, controlling the expression of plant in early generations, which is a prerequisite for genetic improvement of any crop. Knowing the gene actions governing the traits of interest, plant breeders can devise suitable strategies to develop novel germplasm (Kearsey

and Pooni, 1998). Thus, the present study was conducted over two environments, to have reliable estimates of the various components of genetic variation for traits related to in a set of elite maize lines.

MATERIALS AND METHODS

Six early maturing maize inbred lines viz. V-351, V-335, KDM-332A, KDM-347, KDM-913A and KDM-445A were crossed in a diallel mating design during *Kharif* season of 2013 and all 30 possible single crosses, along with two standard checks viz., SMH-2 and VMH-45 were evaluated in a randomized block design (RBD) with three replications during *Kharif* season of 2014 and *Kharif* season of 2015 at Dryland (Karewa) Agricultural Research Station, Budgam, Jammu and Kashmir, India. Observations were recorded on morphological traits viz., days to 50 % tasseling, 50 % silking, plant height, ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, hundred grain weight and grain yield per plant (in grams). Diallel component analysis (Hayman, 1954) 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 (*Kharif* seasons of 2015 and 2016), genotypes and genotype \times environment interaction (Table 1). Significant genotype \times 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, i.e. six parents and 30 diallel set of crosses. Significant variation among the yield traits in maize was earlier reported by Hussain *et al.* (2009), Haq *et al.* (2009), Kumar *et al.* (2012), Dawod *et al.* (2012) and Sarac and Nedelea (2013a) and Dar *et al.* (2017).

The components of genetic variation were estimated for all the characters and pooled results are presented in Table 2. Analysis of the components of genetic variance revealed that both additive (D) and dominance components (H_1 and H_2) were significant for all the traits. This finding suggested the involvement of both these dominance components (H_1 and H_2) in the inheritance of these traits, however greater magnitude of dominance component demonstrated greater role of dominance component in the inheritance of these traits. The distribution of alleles in the parents revealed that positive and negative alleles at these loci are not in equal proportion in parents as H_1 exceeds H_2 and dominance gene action resulted mainly from positive gene action. Dawod *et al.* (2012) reported relatively higher estimates of dominance components than additive component for kernel rows ear⁻¹, kernels row⁻¹ and grain yield which are in line with the present findings. Estimation of

H_2 effects was found to be significant and positive for all traits studied revealing that net dominance effect over all the loci in heterozygote was more and that too it exhibited dominance in positive direction. Value of F estimate was positive and non significant for all traits studied except kernels row⁻¹ thus revealing contribution of more recessive alleles towards dominance deviation. On the contrary, the value of F estimate was significant and positive for kernels row⁻¹ revealing higher frequency of dominant alleles in the parents for these traits. Proportions of components of genetic variations were calculated and results are presented in Table 3. The average degree of dominance indicated over-dominance for all the traits, over the environments which suggested the importance of non-additive type of gene action for all the traits. Over-dominance for ear traits and grain yield, similar to present findings was also reported by Kumar *et al.* (2012), Dawod *et al.* (2012) and Sarac and Nedelea (2013a, 2013b). The study of proportions of various genetic components of variance revealed that the proportion of ($H_2/4H_1$) was less than 0.25 for all the studied traits indicating asymmetrical gene distribution in the parents. Asymmetric distribution of genes for kernels rows ear⁻¹ was reported by Khodarahmpour (2011) which supports the present findings. Also Zare *et al.* (2011) observed values of $H_2/4H_1$ away from 0.25, showing asymmetric distribution of positive and negative dominant genes for kernel rows ear⁻¹ and kernels row⁻¹ in their study. The genetic ratio KD/KR which gives the proportion of dominant and recessive alleles in the parent was found to be greater than unity for all traits studied except for ear girth and 100-grain weight where it was less than unity. This suggested that barring ear girth and 100-grain weight there was higher proportion of dominant alleles in the parents for traits studied and the recessive and domi-

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

S.N.	Source Variation	of	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	11410.6 30**	11767.2 10**	51406. 20**	395.87 7**	86.889 **	0.195	1410.32 0**	149.29 1**	39540.790**
2.	Treatments		35	62.657* *	60.389* *	5602.5 20**	16.962 **	4.487* *	10.758* *	86.745* *	60.830 **	3576.861**
3.	Parents		5	22.364* *	23.794* *	4633.7 33**	8.083* *	2.737* *	15.233* *	55.635* *	41.463 **	919.779**
4.	Hybrids		29	28.809* *	30.670* *	2524.5 78**	6.959* *	2.476* *	9.485**	56.725* *	42.760 **	1468.898**
5.	Parents v.s Hybrids		1	2737.60 9**	2410.39 5**	6301.4 00**	799.40 9**	149.16 5**	43.851* *	3652.50 3**	1565.9 38**	169621.302* *
6.	Treatment x Environments		35	4.494**	3.072**	637.31 6**	5.178* *	1.52**	1.936**	19.873* *	5.283* *	389.46**
7.	Parent x Environments		5	5.385**	3.252**	507.00 4**	1.065* *	0.571* *	0.315	7.990**	2.358* *	39.916
8.	Hybrids x Environments		29	4.089**	2.860**	632.68 8**	5.061* *	1.516* *	2.217**	18.892* *	5.791* *	385.51**
9.	Parent v. s Hybrids x Environments		1	15199**	14.467* *	2337.5 69**	59.126 **	7.133* *	2.447**	210.735 **	9.763* *	53778.4**
10.	Error		70	1.143	1.314	31.848	0.494	0.247	0.364	1.918	0.911	27.199

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

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

S.N.	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.	$\hat{\Delta}$ D	5.55** ± 1.87	5.62** ± 1.80	11150.72** ± 86.43	1.89 ± 0.70	0.62** ± 0.12	3.72 ± 0.42	13.68** ± 2.17	10.14** ± 1.12	222.40* ± 95.55
2.	$\hat{\Delta}$ H ₁	41.68** ± 3.73	39.84** ± 3.59	2414.44* ± 152.90	11.44** ± 1.40	2.30** ± 0.24	4.05** ± 0.84	53.66** ± 4.34	30.12** ± 2.24	2290.73** ± 191.16
3.	$\hat{\Delta}$ H ₂	36.17** ± 3.11	34.06** ± 2.99	2253.81* ± 127.19	10.18** ± 1.16	2.19** ± 0.20	3.39** ± 0.70	47.31** ± 3.61	26.66** ± 1.86	2077.34** ± 159.01
4.	$\hat{\Delta}$ h ²	225.64** ± 2.08	199.12** ± 2.00	17897.58** ± 82.04	66.03** ± 0.78	12.24** ± 1.13	3.59** ± 0.47	301.95** ± 2.41	128.69* ± 1.25	14034.06* ± 106.32
5.	$\hat{\Delta}$ F	2.87 ± 4.23	2.36 ± 4.07	124.16 ± 173.23	1.37 ± 1.59	0.03** ± 0.27	0.70** ± 0.95	8.68 ± 4.92	1.17 ± 2.54	25.39 ± 216.57
6.	$\hat{\Delta}$ E	0.29 ± 0.52	0.33 ± 0.50	7.96 ± 21.20	0.12 ± 0.19	0.06 ± 0.3	0.09** ± 0.12	0.48 ± 0.60	0.23 ± 0.31	6.80 ± 26.50

*, ** 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.N.	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
2.	$(\hat{H}_1/\hat{D})^{1/2}$	2.74	2.66	1.45	2.46	1.92	1.04	1.98	1.72	3.21
3.	$\hat{H}_2/4\hat{H}_1$	0.22	0.21	0.23	0.22	0.24	0.21	0.22	0.22	0.23
4.	$\frac{(\hat{4DH}_1)^{1/2} + \hat{F}}{(\hat{4DH}_1)^{1/2} - \hat{F}} = \frac{KD}{KR}$	1.20	1.17	1.08	1.35	0.97	1.20	1.38	0.94	1.04
5.	\hat{h}^2/\hat{H}_2	6.24	5.87	7.94	6.49	5.60	1.06	6.38	4.83	6.76
6.	Heritability h^2 (n.s)	12.16	12.65	33.13	15.19	19.45	50.07	22.58	23.95	18.84

$(H_1/D)^{1/2}$ - 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/\square_2 - proportion of gene(s)/gene(s) blocks exhibiting dominance; h^2 (ns) - narrow sense heritability estimate.

nant genes where nearly equal for traits viz., 100-grain weight and ear girth. Similar to the present findings the prevalence of dominant genes for ear related traits and grain yield was reported by Zare *et al.* (2011) and Kumar *et al.* (2012). The proportion of average degree of dominance measured from genetic components of variance $(H_1/D)^{0.5}$ was more than unity thus revealing over dominance for the traits studied.

The narrow sense heritability was highest for kernel rows ear⁻¹ (50.07%) followed by plant height (33.13%), 100 grain weight (23.95%) and kernels row⁻¹ (22.58%) (Table 3). The moderate heritability for kernel rows ear⁻¹ suggested effectiveness of selection for improvement of this trait. Ear length, ear girth and grain yield plant⁻¹ exhibited low heritabilities (15.19 % 19.45 % and 18.84 %) over the seasons suggesting lower selection efficiency for these traits. Low narrow sense heritability for grain yield (~10%) was reported by Khodarahmpour (2011), and Sarac and Nedelea (2013b), which also reported relatively less genetic variation for yield in their material. Similarly, moderate narrow sense heritability estimates for kernel rows ear⁻¹ (48.4%) and kernels row⁻¹ (43.7%) were reported by Zare *et al.* (2011).

Conclusions

In conclusion, in this study the prevalence of greater magnitude of non additive genetic component of variance than additive component suggesting that heterosis breeding would be beneficial to utilize the dominance gene effects of these traits. The low narrow sense heritability of few traits viz., ear length, ear girth and gain yield plant⁻¹ suggested that selection for these traits may not be effective and reliable. However, owing to the high heritabilities of traits viz., kernel rows ear⁻¹, 100 grain weight and kernels row⁻¹ selection may be more reliable.

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