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RESEARCH PAPER

Genetic analysis to determine the nature and magnitude of genetic variances and heritability estimates in maize (*Zea mays* L.)

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Key words: Genetic parameters, Gene action, *Zea mays*.

Abstract

The F_1 hybrids along with the parents were evaluated in field for genetic analysis to determine the nature and magnitude of genetic variances and heritability estimates a in maize (*Zea mays* L.) in 2012 using RCBD with three replications. Results analysis of variance showed, based upon the results of tests, simple genetic model was fully adequate for analyzing the data set for all traits except plant height. It was observed that a and b components which are due to additive and dominant gene effects, respectively, were significant for all studied characteristics. Estimates of genetic components of variance according to Hayman (1954) revealed that the value of D is less than H_1 and H_2 indicating that dominant genetic effects for traits such as the days taken to tasseling, plant height, HI and grain yield per plant were more important than additive genetic effects. Thus the selection in later generations may be more effective. However, the values of H_1 and H_2 were $<$ D denoting that genes showing dominance effect for 100 grain weight, number of rows per ear and number of kernels per row were less important than additive genes. The 100 grain weight, number of rows per ear and number of kernels per row were under the control of additive type of gene action and so the selection in early generations will be more effective for these traits which is additively controlled.

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Introduction

Maize (*Zea mays* L.) is the sole cultivated member of genus Zea and tribe Maydeae. Maize being nutritionally, an important crop, has multiple functions in the traditional farming system, being used as food and fuel for human beings and feed for livestock and poultry. Recent projections by the International Food Policy Research Institute indicate that by 2020, the demand for maize in developing countries will overtake that for wheat and rice (Gerpacio and Pingali, 2007). Genetic effects of heritable parameters lead a plant breeder to a clear understanding of inheritance patterns of various plant traits as their relative contribution to the final grain yield. Hayman's approach is a powerful statistical technique, which provides six genetic components of variance and ratios of dominant and recessive genes in the parents to quantify their dominance order. Such information will be of tremendous help to accurately ascertain the merits of individual characters as yield promoting traits. The study of diallel analysis of the genetic traits would certainly be a valuable aid in selection and breeding for better maize hybrids and synthetics under drought conditions. The information derived may be helpful to develop selection criterion and selection of most promising inbred lines for further future breeding programmes. The present investigation was undertaken to study the type of gene action involved in respect of yield and its components.

Materials and methods

Experimental site and soil characteristics

The study was conducted at dezful research station in safi abad, in Khuzestan province, Iran (32°22′ N and 48°23′ E, 82 m above sea level) in the years 2012. The type of soil found at this location is clay loam, and its pH = 7.4 with EC = 1.2 mmhos/cm. The experimental material comprised six inbred lines of maize (CML, SD\17, SD\15, SD\3, SD\704 and SD\10). The F_1 seed along with their parental inbred lines were planted in field based on RCBD with three replications in 31 July (which was the planting date). Each plot contained 3 rows that are 75 cm apart and 6 m in length and they consisted of 30 hills, two seeds of which were sown and one seedling of which was removed at the 4 leaves stage. The experiment was irrigated after 90±5 mm evaporation from class A pan. while fertilizers were applied prior to sowing at a rate of 120 kg N ha^{-1} and 140 kg P ha^{-1}, and an additional side dressing of 120 kg N ha^{-1} was applied at the six leaves stage of maize plants. Non-experimental lines were planted to minimize the edge border effects.

Data collection

At maturity, data were recorded for the data pertaining to days taken to tasseling, , plant height, 100 grain weight, number of rows per ear, number of kernels per row and grain yield per plant. The grains produced by the selected plants used for biological yield were weighed in grams and average grain yield per plant was recoded. Grain yield trait was adjusted to 14% of grain moisture. Harvest index for each treatment was calculated in percentage by using the following formula: Harvest index (%) =(Grain yield/plant)/(Biological yield)× 100.

Statistical/Biometrical Analysis

The data pertaining to yield and its components were statistically analyzed to determine significant differences among the genotypes according to Steel *et al.* (1997). The simple additive-dominance (AD) model, proposed by Hayman (1954) and Jinks (1954) and exemplified by Mather and Jinks (1982) for diallel analysis, was employed for further investigations.

Results and discussion

Analysis of variance

ANOVA revealed highly significant genotypic variations for all characters among 21 genotypes. Mean squares for parental inbred lines and the crosses were significant at $P<0.01$ for all the characters Table 1. Adequacy test for yield and its related traits and validity of assumptions underlying the genetic model were tested by joint regression analysis and analysis of variance (Wr + Vr) and covariance (Wr - Vr). Results analysis of variance revealed that non-significant variation within the arrays (Wr - Vr) for all the characters except plant height interval that was significant at $P<0.05$. Thus, the results of the test suggested that the simple genetic model was fully adequate for all the characters except plant height. While non-significant differences at $P>0.05$ between the arrays (Wr+Vr) for the trait like plant height showed the absence of dominant effects and presence of epistasis. The joint regression analysis showed that the regression coefficient ‘b’ for all the parameters departed significantly from zero but did not deviate from unity except plant height, in this trait, regression coefficient ‘b’ non-significantly from zero but significantly from unity (Table 1). This property of the regression line suggested the presence of intra-allelic gene interaction, independent distribution of genes among the parents for this trait. The unit slope of regression lines for all the traits indicated that the assumptions underlying the additive-dominance model were met except plant height. Thus, based upon the results of three tests simple genetic model was fully adequate for analyzing the data set for all traits except plant height.

Table 1. Scaling tests for adequacy of additive-dominance model for yield and its components.

Source of variance	*df*	*Days taken to tasseling*	*Plant height (cm)*	*No. of rows/ear*	*No. of kernels/row*	*Harvest index(%)*	*100-grain Weight(g)*	*Grain yield /plant(g)*
Block	2	65.92^{*}	468.61^{*}	6.67^{*}	32.34^{*}	175.25^{**}	23.38^{*}	237.21^{**}
Wr - Vr	5	8.39^{ns}	242.15^{*}	2.59^{ns}	3.28^{ns}	37.47^{ns}	7.56^{ns}	258.67^{ns}
Error	10	7.54	72.42	1.25	6.84	21.75	4.28	371.06
Block	2	25.62^{*}	725.23^{*}	25.62^{*}	64.32^{*}	89.19^{**}	86.34^{*}	2389.53^{**}
Wr + Vr	5	62.48^{*}	356.51^{ns}	62.48^{*}	52.10^{*}	68.28^{**}	69.41^{*}	1152.24^{*}
Error	10	9.71	253.14	9.71	10.61	9.12	15.81	193.06
Joint regression(b)		0.79	0.37	0.78	0.57	0.61	0.68	0.92

ns, * and **: Not significant, significant at the 5% and 1% levels of probability, respectively.

The results of the analysis of variance of F_1 and parents data showed highly significant differences for a and b suggesting the presence of both additive and dominance genetic effects in the expression of all traits (Table 2). The significant b_1 item revealed the presence of directional dominant effects of genes. However, the b_1 item for all traits was significant except number of rows per ear, number of kernels per row and HI. Among inbred lines, asymmetrical gene distribution for all traits was evident due to the significance of the b_2 item. Also, among parents, specific gene effects for days taken to tasseling, plant height, harvest index, number of rows per ear and number of kernels per row were evident due to the significance of the b_3 (this component which is synonym with specific combinig ability variance) item. Irshad-Ul-Haq *et al.* (2010) reported that a, b, b_1, b_2 and b_3 items for all traits were significant.

Table 2. Analysis of variance of diallel Tables for the evaluated traits.

Source of variance	*df*	*Days taken to tasseling*	*Plant height (cm)*	*No. of rows/ear*	*No. of kernels/row*	*Harvest index(%)*	*100-grain Weight(g)*	*Grain yield /plant(g)*
Block	2	52.31^{**}	80.28^{**}	5.43^{*}	11.73^{*}	27.29^{*}	9.23^{*}	126.64^{**}
Genotype	20	561.98^{**}	561.98^{**}	0.97^{**}	97.41^{**}	40.97^{**}	6.98^{**}	316.89^{**}
a	5	17.73^{**}	222.38^{**}	1.89^{**}	97.41^{**}	50.86^{**}	12.20^{**}	293.51^{**}
b	15	12.62^{**}	676.32^{**}	0.28^{*}	115.28^{*}	37.68^{**}	6.06^{**}	324.67^{**}
b_1	1	40.64^{**}	8434.82^{**}	0.04^{ns}	1512.75^{ns}	8.00^{ns}	72.93^{**}	498.18^{**}
b_2	5	24.04^{**}	207.04^{**}	1.09^{**}	62.29^{**}	25.03^{*}	3.52^{**}	189.20^{**}
b_3	9	1.67^{ns}	174.98^{**}	0.24^{**}	25.53^{**}	48.01^{**}	0.09^{ns}	29.71^{ns}
Error	40	3.35	15.39	0.13	9.42	7.27	0.01	12.82
CV (%)	--	5.87	7.88	6.35	3.84	11.86	5.73	10.05

ns, * and **: Not significant, significant at the 5% and 1% levels of probability, respectively.

Genetic components of variation were estimated according to Hayman (1954) and are presented in Table 3. Estimates of genetic components of variance revealed that both additive (D) and dominance components (H_1) were highly significant and positive for the days taken to tasseling, plant height, 100 grain weight, number of rows per ear, number of kernels per row, HI and grain yield per plant. This indicated that both additive and dominant gene actions condition the above characters (Table 3). However, for traits such as the days taken to tasseling, plant height, HI and grain yield per plant, significant value of D and H revealed the importance of additive and dominant genetic effects. The value of D is less than H_1 and H_2 indicating that genes showing dominant genetic effects for traits such as the days taken to tasseling, plant height, HI and grain yield per plant were more important than additive genetic effects. The importance of dominant variation was also indicated by significant H components (H_1 and H_2). Unequal value of H_1 and H_2 displayed different distribution of dominant genes. Positive and significant value of F indicated that positive genes were more frequent. The value of $\overline{uv}$ ratio was <0.25, indicating unequal distribution of genes for the days taken to tasseling, plant height, HI and grain yield per plant among the parents. The significance of values of h^2 indicated the important effect of heterozygous loci for the days taken to tasseling, plant height, HI and grain yield per plant. The effects due to E were significant suggesting played a significant role for the expression in the development of the above four characters (Table 3). Even though the environmental component was significant it was much lower than additive and dominance variance.

Table 3. Estimation of the components of genetic variations for yield and yield components.

Parameters	*Days taken to tasseling*	*Plant height (cm)*	*No. of rows/ear*	*No. of kernels/row*	*HI(%)*	*100-grain Weight(g)*	*Grain yield /plant(g)*
D	13.70^{**}	168.76^{*}	0.59^{**}	135.56^{**}	34.21^{*}	19.29^{**}	277.39^{**}
H_1	19.84^{**}	573.99^{**}	0.58^{**}	119.43^{**}	40.13^{**}	17.41^{**}	912.20^{**}
H_2	17.75^{**}	518.45^{**}	0.29^{**}	102.38^{**}	36.25^{**}	14.96^{**}	895.64^{**}
F	4.59^{*}	65.59^{*}	0.71^{*}	41.75^{ns}	11.75^{ns}	10.36^{**}	147.23^{**}
h^2	64.42^{**}	623.28^{**}	-0.03^{ns}	25.86^{ns}	0.396^{ns}	53.73^{**}	256.39^{*}
E	2.82^{**}	5.38^{**}	0.05^{ns}	1.63^{ns}	2.62^{**}	0.62^{ns}	3.39^{*}
$(H1/D)^{0.5}$	1.45	2.89	0.99	0.88	1.07	0.95	1.81
$\overline{uv}$	0.22	0.23	0.18	0.21	0.22	0.21	0.24
h_b^2	0.74	0.89	0.78	0.74	0.84	0.85	0.68
h_n^2	0.26	0.18	0.42	0.70	0.41	0.47	0.23

ns, * and **: Not significant, significant at the 5% and 1% levels of probability, re spectively.

Estimates for mean degree of dominance $(H_1/D)0.5$ for the days taken to tasseling(1.45), plant height(2.89), HI(1.07) and grain yield per plant (1.81) were more than one indicating over dominance. This indicated, that the above four characters might be governed by over-dominance. The asymmetrical distribution of alleles as indicated by H2 was further confirmed by the facts that H1 was not equal to H2. The estimate of broad sense heritability were for the days taken to tasseling (0.74), plant height (0.89), HI (0.84) and grain yield per plant (0.68) percent and narrow sense heritability were for the days taken to tasseling (0.26), plant height (0.18), HI (0.41) and grain yield per plant (0.23) percent. These results are in accord once with the work of Watto *et al.* (2009), Bello and Olaoye (2009) and Chohan *et al.* (2012), Moradi *et al.* (2014).

Thus the investigation showed that all the above four characters character were governed by nonadditive gene action in all the cases. Hence there is little scope for improvement in these traits by selection. Heterosis could be exploited for developing inbreds and hybrids. Maximum gain could be obtained by maintaining considerable heterozygoity coupled with selection in segregating generation to enhance genetic recombination resulting in breakage of undesirable linkage, provide transgressive segregation and create a broad genetic base against which maximum number of potentially functional genes may be accumulated, reassembled and expressed, leading to isolation of stable and widely adapted 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.

Estimates of genetic components of variance revealed that both additive (D) and dominance components (H_1) were highly significant and positive for 100 grain weight, number of rows per ear and number of kernels per row. This indicated that both additive and dominant gene actions condition the all three characters (Table 3). However, the values of H_1 and H_2 were < D denoting that genes showing dominance effect were less important than additive genes. Non-significant estimates of F indicated that positive or dominant genes were not frequent. The value of $\overline{uv}$ ratio was <0.25, indicating unequal distribution of genes for 100 grain weight, number of rows per ear and number of kernels per row among the parents. The significance of values of h^2 indicated the important effect of heterozygous loci for the all three characters. Environmental variation (E) was positive and non-significant depicting that environmental variations were less important for these traits. The mean degree of dominance was < 1 signifying partial dominance in F_1 hybrid which was denoted by the regression slope. The estimate of broad sense heritability were for 100 grain weight (0.85), number of rows per ear(0.78) and number of kernels per row(0.74) percent and narrow sense heritability were for 100 grain weight (0.47), number of rows per ear(0.42) and number of kernels per row(0.70) percent. The results are in line with those of Srdic *et al.* (2007), Asefa *et al.* (2008), Zare *et al.* (2011) and Chohan *et al.* (2012) who reported that 100-grain weight and number of kernels per row were under the control of additive type of gene action.

Conclusion

Estimates of genetic components of variance according to Hayman (1954) revealed that both additive and dominant gene actions condition the above characters. The value of D is less than H_1 and H_2 indicating that genes showing dominant genetic effects for traits such as the days taken to tasseling, plant height, HI and grain yield per plant were more important than additive genetic effects However, the values of H_1 and H_2 were < D denoting that genes showing dominance effect for 100 grain weight, number of rows per ear and number of kernels per row were less important than additive genes.

It may be said that overall information obtained in the present study if practised with care can, in general, go a long way in developing promising synthetics and hybrids of maize. All the parameters, except 100 grain weight, number of rows per ear and number of kernels per row, were under the control of over-dominance type of gene action. Thus the selection in later generations may be more effective. The 100 grain weight, number of rows per ear and number of kernels per row were under the control of additive type of gene action and so the selection in early generations will be more effective for these traits which is additively controlled.

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