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ESTIMATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN GENOTYPES OF MAIZE (*Zea mays* L.)

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ABSTRACT

The objectives of the study were to estimate the magnitude of genetic variability, heritability and genetic advance for yield and contributing characters of the thirty maize genotypes. These genotypes were evaluated during *Kharif* 2016 in a randomized block design with three replications. A high genotypic and phenotypic coefficient of variation was observed for plant height followed by ear height. Low, medium and high estimates of broad sense heritability were found in different plant characters under study. Highest heritability estimates were found in plant height (94.30%) followed by ear height (90.30%) and leaf width (85.60%). Plant height (41.74%) was exhibited highest genetic advance as per cent of mean followed by ear height (39.49%), leaf width (18.71%), cob length without husk (8.27%) and 100 seed weight (7.61%). Greater magnitude of broad sense heritability coupled with higher genetic advance in characters under study provided the evidence that these plant parameters were under the control of additive genetic effects.

INTRODUCTION

Maize known as Queen of Cereals, also called corn is one of the most important cereal crops of the world. Maize distinguished botanically as *Zea mays* L., belongs to the grains family Graminae. It is grown from latitude 58N to 40S, from sea level to higher than 3000 m altitude and in areas receiving yearly rainfall of 250 to 5000 mm (Downsell *et al.*, 1996). In India maize crop stand up as the third cash crop after wheat and rice. Maize; mainly a rain fed *Kharif* crop is grown both in *Kharif* and *Rabi* season. In *Kharif*, it is sown in March-July till mid August and harvested from mid September. The major states producing maize during the *Kharif* season are Karnataka, Andhra Pradesh, Maharashtra, Madhya Pradesh, Uttar Pradesh, etc. In *Rabi*, it is sown in September-December in Bihar, Uttar Pradesh, Punjab and coastal region of Andhra Pradesh, Karnataka, etc. The growing Indian economy and changing consumer preferences, especially based on health consciousness are likely to fuel demand for maize by food, feed and other industrial users.

In the last few years, maize is increasingly being used for feed consumption. Thereby, assuming almost steady demand and reasonable price, the total maize consumption for 2016-17 for feed is likely to rise to 13000 thousand metric tonnes compared to 2015-16 estimated consumption of 12700 thousand metric tonnes. As well, based on latest market reports the poultry industry has been growing at 4-5 percent in the last few years. About 65-70% of maize produced in the country is used by the poultry, livestock, food and starch industries. The parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in a given characteristic. The efficiency with which genotypic variability can be exploited by selection depends upon heritability and the genetic advance (GA) of individual trait (Bilgin *et al.*, 2010). Heritability provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations (Bello *et al.*, 2012). Heritability coupled with high GA would be more useful in predicting the resultant effect in the selection of the best genotypes for yield and its attributing traits (Singh *et al.*, 2011). The present investigation was conducted to study the extent of genetic variability present in the available germplasm and to explore the possibility of improving them through breeding programme.

MATERIALS AND METHODS

Experimental Material

The experimental materials consisted of 30 accessions of maize (*Zea mays* L.) obtained from the my supervisor Prof. Rajesh Singh, Maize Breeder in Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (Table 1).

Experimental design and land preparation

The experiment was laid out in randomized block design. The field was divided into three homogeneous replication blocks. Thirty genotypes were randomly planted in three replications. Each entry was represented by a double row of 4 m length spaced at 75cm between the rows and 20 cm between the plants within the rows. A uniform piece of land was selected for laying out the experiment. The land was brought to the fine tilth by ploughing and harrowing.

Sowing and cultural practices

The land was prepared by ploughing followed by two cross harrowing. The basal dose of 60 kg N, 60 kg P_2O_5 and 40 kg K_2O per hectare was applied to the whole experimental area. The remaining dose of 60 kg N was applied in equal two splits at 30 and 45 days after sowing. The thinning operation was carried out 20 days after sowing. The cultural practices like plant protection and weeding were followed as and when required during the crop growth period.

Statistical Analysis

Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in following form.

Where,

r = number of replication

t = number of treatments

Estimates of variance components

The variability present in the population was estimated by measure mean, phenotypic and genotypic variance and coefficient of variation. To estimate the phenotypic and genotypic variance, genotypic and phenotypic coefficients of variation were estimated based on formula Syukur *et al.* (2012) as follow:

ó ^{2}G = [(MSG) – (MSE)] / r

ó ^{2}P = [ó^{2}G + (ó^{2}E /r)],

Where, ó^{2}G = Genotypic variance; ó^{2}P = Phenotypic variance; ó^{2}E = Environmental variance (error mean square from the analysis of variance); MSG = Mean square of genotypes; MSE = Error mean square; r = Number of replications.

Genotypic coefficient of variation (GCV) = [(ó^{2}G)$^{1/2}$ / x] × 100;

Phenotypic coefficient of variation (PCV) = [(ó^{2}P)$^{1/2}$ / x] × 100,

Where, ó ^{2}G = Genotypic variance; ó^{2}P = Phenotypic variance; is grand mean of a character.

According to the formula as described by Allard (1960) as follow:

h^2 bs = [(ó^{2}G) / (ó^{2}P)] × 100, where: h^2 bs = heritability in broad sense; ó^{2}G = Genotypic variance; ó^{2}P = Phenotypic variance.

Estimation of genetic advance

Genetic advance was calculated by the formula given by Johnson *et al.* (1955)

GA = K x (ó^{2}g/ ó^{2}p) x óp or GA = K x h^2 x óp

Where,

K = Selection differential which is 2.06 at 5 per cent selection intensity

ó^{2}g = genotypic variance

ó^{2}p = phenotypic variance

óp = phenotypic standard deviation

h^2(b.s.) = heritability broad sense

The genetic advance as percentage of the mean (GAM) was calculated as described by Johnson *et al.* (1955) as follow:

$$GAM\ (\%) = \frac{GA}{x} \times 100$$

Where, GAM = Genetic advance as percentage of the mean, GA = genetic advance, and x = grand mean of a character.

RESULTS AND DISCUSSION

In present study, 30 genotypes of maize showing wide spectrum of variation for various characters were evaluated during 2016. The experiment was conducted following Randomized Block Design with three replications at Genetics and Plant Breeding Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The characters studied were plant height (cm), days to 50% tasselling, days to 50% silking, days to 75% brown husk , ear height (cm), leaf width (cm), tassel length (cm), cob length with husk (cm), cob length without husk (cm), cob diameter (cm), 100 seed weight (g), and grain yield per plant (g).

Analysis of variance

Mean squares of the 12 characters from analysis of variance (ANOVA) are presented in (Table 2). The analysis of variance revealed highly significant differences among genotypes under study, showing variations for all twelve characters in thirty genotypes of maize. Thus, the presence of variability in present investigation indicated the ample scope of selection for these traits. Similar trends of high significant difference among the different genotypes were observed by Parimala *et al.* (2011), Pinnisch *et al.* (2012) and Patil *et al.* (2016) in maize; Kumar and Kerkhi (2015) in wheat; Parhe *et al.* (2014) and Jakhar *et*

Table 1: List of thirty maize genotypes included in the studies

S.N.	Genotype	S.N.	Genotype	S.N.	Genotype
1	CML-163	11	HKI-193-1	21	HUZM-478
2	CML-169	12	HKI-287	22	HUZM-509
3	DMR-QPM-58	13	HKI-586	23	HUZM-536
4	CML-141	14	HUZM-152	24	HUZM-1105
5	CML-161	15	HUZM-185	25	V-348
6	HKI-162	16	HUZM-211-1	26	V-351
7	HKI-164-4-(1-3)-2	17	V-25	27	HUZM-80-1
8	HUZM-53	18	V-335	28	HKI-1105
9	HUZM-88	19	V-336	29	HKI-323
10	HUZM-97-1-2	20	HUZM-242	30	HUZM-60

Table 2: Analysis of Variance (ANOVA) for twelve traits in thirty maize genotypes

Source of variation	DF	Mean sum of squares											
		PH	DTT	DTS	DBH	EH	LW	TL	CLWH	CLWOH	CD	100 SW	GY
Replication	2	194.49	11.54	13.30	14.21	18.03	0.33	13.61	7.36	0.06	0.49	1.16	61.71
Treatment	29	2396.89**	20.59**	27.70**	38.33**	341.58**	2.24**	15.74**	10.75**	6.62**	0.33**	2.60**	2.60**
Error	58	47.62	15.08	16.76	17.13	11.78	0.12	6.93	5.49	2.49	0.16	0.49	0.49

**and* Significant at 1% and 5% level of significance, respectively. Where, PH (cm) = plant height, DTT (50%) = days to 50% tasseling, DTS(50%) = days to 50% silking, DBH(75%) = days to 75% brown husk, EH(cm) = ear height, LW(cm) = leaf width, TL(cm) = Tassel Length CLWH(cm) = cob length with husk, CLWOH(cm) = cob length without husk, CD(cm) = cob diameter, 100 SW(g) = 100 seed weight, GY = grain yield per plant.

Table 3: Estimates of variability, heritability and genetics advance as per cent of mean for twelve characters in thirty maize genotype

Traits Parameter	PH	DTT	DTS	DBH	EH	LW	TL	CLWH	CLWOH	CD	100 SW	GY
Range Max	163.92	57.33	64.33	97.33	64.70	11.08	37.14	30.91	21.17	5.78	20.5	100.73
Min	74.63	42.67	48.33	76.00	30.01	6.48	24.27	18.41	12.43	3.78	15.39	70.33
Grand mean	134.09	51.86	58.43	88.88	51.98	8.56	30.94	25.72	17.44	4.38	17.35	86.29
ó^{2}p	830.70	16.92	20.40	24.19	121.72	0.83	9.87	7.24	3.87	0.22	1.19	58.46
ó^{2}g	783.09	1.83	3.65	7.07	109.93	0.71	2.94	1.76	1.38	0.058	0.70	19.22
ó^{2}e	47.62	15.08	16.76	17.13	11.78	0.119	6.93	5.49	2.49	0.159	0.496	39.24
PCV (%)	21.49	7.93	7.73	5.53	21.22	10.61	10.15	10.46	11.28	10.62	6.30	8.86
GCV (%)	20.87	2.61	3.27	2.99	20.17	9.82	5.54	5.15	6.73	5.49	4.83	5.08
ECV (%)	5.15	7.49	7.00	4.66	6.60	4.03	8.51	9.11	9.05	9.09	4.06	7.26
C.V. (%)	5.15	7.49	7.00	4.66	6.60	4.03	8.51	9.11	9.05	9.09	4.06	7.26
Heritability (%)	94.30	10.80	17.90	29.20	90.30	85.60	29.70	24.20	35.60	26.80	58.60	32.90
GA	55.97	0.919	1.66	2.96	20.53	1.60	1.92	1.34	1.44	0.26	1.32	5.18
GA as % of mean	41.74	1.77	2.85	3.33	39.49	18.71	6.22	5.23	8.27	5.85	7.61	6.00

Where, PH (cm) = plant height, DTT (50%) = days to 50% tasseling, DTS(50%) = days to 50% silking, DBH(75%) = days to 75% brown husk, EH(cm) = ear height, LW(cm) = leaf width, TL(cm) = Tassel Length CLWH(cm) = cob length with husk, CLWOH(cm) = cob length without husk, CD(cm) = cob diameter, 100 SW(g) = 100 seed weight, GY = grain yield per plant.

al. (2016) in chickpea in previous studies.

Variability components and coefficients of variation

Estimates of phenotypic variance (ó^{2}p), genotypic variance (ó^{2}g), phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 3. The maximum phenotypic variance value (830.7) was noted for the trait plant height followed by ear height (121.72) and grain yield per plant (58.46). Similarly, the genotypic variances for these characters were also high indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. The highest PCV was recorded for plant height (21.49) followed by ear height (21.22), cob length without husk (11.28), cob diameter (10.62), leaf width (10.61) and lowest for days to 75% brown husk (5.53). The trait plant height was showed highest GCV (20.87) followed by ear height (20.17), leaf width (9.82) and cob length without husk (6.73). High coefficient of variation provides great scope for the selection of desirable types. Similar findings by Rafiq *et al.* (2010) revealed presence of substantial variability for all traits studied.

Heritability and genetic advance

Heritability estimate, that provide the assessment of amount of transmissibility of genetic variability to total variability, happens to be the most important basic factor that determines the genetic improvement or response to selection. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation (Li and Yang, 1985).In the present set of material, estimates of broad sense heritability were higher for plant height (94.30%) followed by ear height (90.30%), leaf width (85.60%) and 100 Seed Weight (58.60%). This suggested the greater effectiveness of selection and improvement to be expected for these characters in future breeding programme as the genetic variance is mostly due to the additive gene action. Similar results were observed by several workers, high heritability estimates for plant height by Kumar and Kumar (1997), Umakanth and Sunil (2000) and Choudhary and Chaudary (2002), for 100-grain weight by Choudhary and Chaudary (2002) and for grain yield per plant by Kumar and Kumar (1997), Choudhary and Chaudary (2002) and Rafiq *et al.* (2010).

Genetic advance as percent of mean was also high for plant height (41.74%) followed by ear height (39.49%), leaf width (18.71%) and cob length without husk (8.27%). Similar results were observed for plant height by Reddy and Agarwal (1992), for ear height and cob length by Singh and Pradhan (2000) and Kumar *et al.* (2011). The high heritability coupled with high genetic advance noticed for these traits indicate the role of additive gene action in controlling the traits; hence pedigree method of breeding will be a rewarding one to improve the traits under investigation.

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