

# GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE STUDIES IN NEWLY DEVELOPED MAIZE GENOTYPES (*ZEA MAYS L.*)

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## ABSTRACT

The present investigation was undertaken to assess the variability, heritability and genetic advance of twenty five genotypes of maize obtained from All India Co-ordinated Maize Improvement Project for their further utilization in breeding programme(s). Analysis of variance revealed significant differences among genotypes for all the traits studied. Genotype CM-145 gave highest seed yield per plant (113.80g) followed by HUZM-478 (105.14g), HUZM-88 (101.91g), HUZM- 60 (101.82g), HKI-1105 (95.21g), V-336 (93.77g), V-388 (90.96g), HUZM-185 (90.58g), HKI-162 (86.85g) and HKI-287(86.27g). Estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits. PCV was highest for grain yield per plant (25.68%) followed by number of kernels per row (23.69%) and ear height (23.10%). GCV was highest for ear height (20.00%) followed by 100 seed weight (19.72%). Estimates of broad sense heritability were higher for all the characters except for number of kernels per row (33.80). High heritability coupled with high genetic advance was observed for grain yield per plant (54.50, 28.82) and ear height (75.00, 35.69), while, days to 50% tasseling (56.20, 7.62) and days to 50% silking (47.80, 5.19) showed higher heritability coupled with low genetic advance as percentage of mean.

## INTRODUCTION

Maize (*Zea mays L.*) is an important cereal crop belonging to family, *Poaceae*. It is cultivated over a wide range of climatic conditions; considered as a promising option for diversifying agriculture in various agro-climatic zones and ranks as third most important food crops in India. Being a major food, feed and fodder crop it contributes to food security in most of the developing countries. Maize production in India is 24.35 mt with area 8.49 mha and yield of 2408 kg/ha (Agricultural statistics at a glance-2014).

Knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative character like yield and its components is essential for effecting genetic improvement (Rakesh Kumar Dhanwani *et al.*, 2013) The success of any crop improvement programme is not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Sumathi *et al.*, 2005; Kashiani *et al.*, 2008; Hussain *et al.*, 2011; Khan *et al.*, 2011 and Wang *et al.*, 2011). Genetic variability for agronomic characters therefore, is a key component of breeding programmes for broadening gene pool of crops (Ahmad *et al.*, 2011). The knowledge of nature and magnitude of genotypic and phenotypic variability present in the crop species plays a vital role in formulating a successful

breeding programme to evolve superior cultivars. Heritability is a measure of phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences choice of selection procedures used by plant breeders to decide which selection methods would be most useful to improve the character(s), to predict gain from selection and to determine relative importance of genetic effects (Waqar-Ul-Haq *et al.*, 2008; Kashiani *et al.*, 2010 and Laghari *et al.*, 2010; Bello *et al.*, 2010). Most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay, 1996). Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance (Najeeb *et al.*, 2009).

Genetic advance shows degree of gain obtained in a character under particular selection pressure. High genetic advance coupled with high heritability estimates offers most suitable condition(s) for selection. Ramanujam and Thirumalachar (1967) reported the limitation of estimating heritability in narrow sense, as it included both additive and epistatic gene effects, and there by suggested that heritability estimates in broad

sense will be reliable if accompanied by high genetic advance. Availability of good knowledge of these genetic parameters existing in different yield contributing characters and in various quantitative traits is a pre-requisite for effective crop improvement. The present study was therefore, conducted to assess genetic variability, heritability and genetic advance for grain yield and its component characters in twenty five genotypes of maize to provide necessary information that could be utilized in maize improvement programmes directed at improving grain yield.

## MATERIALS AND METHODS

The present investigation was carried out in *Kharif-2012* on Agricultural Research Farm, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi with 25 genotypes of maize obtained from All India Co-ordinated Maize Improvement Project in a Randomized Block Design (RBD) with three replications. Genotypes viz., HUZM-185, HUZM-121, HUZM-60, HUZM-323, HUZM-47, HUZM-97.1.2, HUZM-509, HKI-1105, HKI-287, HKI-162, HUZM-478, HUZM-80.1, HKI-164-4-1-3-2, HUZM-88, V-336, V-341, V-25, V-388, V-348, V-351, V-358, V-386, V-335, CM-145, CM-141 were used for this study. Each entry was sown with three rows of 3 m length with row to row spacing of 60 cm and plant to plant spacing of 20 cm. Initially two seeds per hill were planted and later on one plant was thinned to maintain single plant per hill. Two border rows were also planted to avoid the border effect. Recommended cultural practices were carried out to raise a healthy crop. The pre and post harvest observations were recorded on five plants selected at random from each genotype in each replication for eleven characters viz., days to 50% tasseling recorded from date of sowing to date on which 50% plants of each plot exhibited flowering, days to 50% silking measured as days after sowing when 50% of plants in the entry had silks, plant height (cm) measured from ground level to the base of flag leaf at dry silk stage, ear height (cm) height from base of plant to base of main ear, tassel length (cm) measured from the lowest nodal portion to main tip of tassel, cob length (cm) measured from base to tip of ear, cob diameter (cm) measured at a point of maximum diameter after de husking of ear, number of kernel rows per cob recorded by counting number of rows per cob at middle of the ear for five randomly selected ears, number of kernels per row, 100 grain weight (g) measured as random sample of 100 kernels taken and weight was recorded with the help of electronic top pan balance, grain yield per plant (g) measured from five cobs from random plants harvested and

after shelling, grain was dried to get uniform moisture of 15% and weight was measured with pan balance.

Mean of data from the sampled plants of each plot in respect of different characters were subjected to the following statistical analysis: analysis of variance by using Panse and Sukhatme, (1961) method, the genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) was calculated by the formula given by Burton (1952). Heritability in broad sense was calculated by the formula given by Hanson *et al.* (1956). From the heritability estimates, the genetic advance was calculated by the following formula given by Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

### Analysis of variance

The analysis of variance for twenty five genotypes of maize indicated existence of significant variability among all characters under study. Presence of large amounts of variability is due to diverse source of material as well as environmental influences, which pre-dominantly governed by phenotype (Table 1). The mean performance of 25 genotypes of maize for eleven characters is presented in Table 2. The mean performance for grain yield per plant was reported highest in genotype, CM-145 followed by HUZM-478, HUZM-88, HUZM-60, HKI-1105, V-336, V-388, HUZM-185, V-351, HKI-162, HKI-287, HUZM-97.1.2, HKI-164-4.1.3.2, HUZM-121 these genotypes also possessed high mean performance for 100 grain weight, number of kernels per row, cob diameter, cob length, ear height and plant height. In addition to these genotypes, many exhibited above average performance for grain yield per plant, which could be used in breeding programme(s).

### Phenotypic and genotypic coefficients of variation

The study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimate the scope for improvement by selection. The reliability of a parameter to be selected for breeding programme among other factors is dependent on the magnitude of its coefficient of variations (CV) especially the GCV. However, the differences between genotypic and phenotypic coefficient of variability indicate the environmental influence. (Bello *et al.*, 2012) while a lower value of CV generally depicts low variability among the tested sample; a high proportion GCV to the PCV is desirable in breeding works. The results given in Table 3

**Table 1 : Analysis of variance of Randomized Block Design for eleven characters in maize**

SV	d. f.	DTT	DTS	TL	PH	EH	CL	CD	KRC <sup>-1</sup>	KR <sup>-1</sup>	100 GW	GYP <sup>-1</sup>
Replications	2	17.08	13.77	37.09	32.38	6.29	3.61	0.02	2.57	20.65	44.26	1258.26
Genotypes	24	28.47**	19.81**	61.78**	668.63**	101.35**	5.87**	0.17**	3.45**	26.94**	90.71**	896.18**
Error	48	5.87	5.29	6.82	44.27	10.13	1.7	0.02	0.43	10.64	6.18	195.18
SEm +		1.4	1.33	1.51	3.84	1.84	0.75	0.09	0.38	1.88	1.44	8.07
CV (%)		4.36	3.75	10.97	8.37	11.54	13.96	4.24	6.07	19.27	9.23	17.32
CD (5%)		3.98	3.78	4.29	10.92	5.22	2.14	0.24	1.08	5.36	4.08	22.94

\*Significant at 5% level, \*\* Significant at 1% level, SV = Source of variation, d. f. = degree of freedom

DTT = Days to 50% tassling, DTS = Days to 50% silking, TL = Tassel length, PH = Plant height, EH = Ear height, CL = Cob length, CD = Cob diameter, KRC<sup>-1</sup> = Number of kernel rows per cob, KR<sup>-1</sup> = Number of rows per cob, 100GW = 100 grain weight, GYP<sup>-1</sup> = Grain yield per plant

**Table 2 : Mean performance of twenty five genotypes with respect to eleven characters in maize**

S. No.	Genotypes	DTT	DTS	TL	PH	EH	CL	CD	KRC <sup>1</sup>	KR <sup>1</sup>	100 GW	GYP <sup>1</sup>
1	HUZM-185	56.667	61	32	90.8	30.5	10	3.622	10.8	17.5	33.023	90.58
2	HUZM-121	58	62.667	24.8	93.03	30.1	8.9	3.473	10.4	17.7	27.11	80.838
3	HUZM-60	56.333	63	26.5	85.5	29.9	10	3.835	12	21	28.573	101.824
4	HUZM-323	53.667	57.667	17.8	63.5	23.8	6.5	3.193	8.2	11.3	24.05	52.225
5	HUZM-47	51.667	58	21.7	63.7	21.8	7.1	3.162	9	11.9	27.21	59.13
6	HUZM-97.1.2	54.667	59	25.9	97.9	31.4	8.933	3.111	10.533	18.7	25.053	82.58
7	HUZM-509	54.667	59	28.6	88.8	35.5	10.3	3.206	10.2	18.9	27.083	85.121
8	HKI-1105	55	58.667	30.5	97.5	34.6	10.6	4.025	11	18	32.183	95.216
9	HKI-287	49.667	59	27.7	92.6	37.5	11.5	3.683	12.2	14.767	31.213	86.271
10	HKI-162	57	62	23.4	88.6	38.9	9.433	3.475	12.2	18.6	24.663	86.85
11	HUZM-478	58	63	28.5	106.3	26.9	9.3	3.539	10.2	19.8	37.24	105.147
12	HUZM-80.1	59.667	66	15.4	63.5	20	10.8	3.357	9.2	15.3	15.98	52.536
13	HKI-164-4.1.3.2	54	59	23.13	56.4	17.2	9.333	3.459	9.6	17	31.903	82.027
14	HUZM-88	49	58	25.4	84.1	29.4	11.433	3.903	12.6	18.9	30.16	101.916
15	V-336	57	61.667	23.7	83.2	27.5	9.233	3.496	11.633	16.6	32.97	93.777
16	V-341	59	66	24.7	81.7	24.9	8.2	3.272	10.8	15	17.13	57.747
17	V-25	49	58	20.9	67.9	25.3	9.033	3.478	11.6	17.4	17.69	65.302
18	V-388	56.667	62	24.33	57.9	20.2	7.6	3.667	12	15.3	33.313	90.96
19	V-348	55.333	62	20.3	79.9	27.5	8.6	3.622	10.6	16.9	24.19	73.48
20	V-351	55.333	60	27.8	88.2	30.333	10.9	3.799	11.6	18	26.513	87.312
21	V-358	58	64	16.6	57.8	21.7	8.833	3.248	10.6	16.1	21.15	66.089
22	CM-141	57.667	64	22.7	90.6	26.5	6.8	3.343	10.2	11	27.67	61.038
23	V-386	59.667	64.667	18.1	58.9	23.2	9.5	3.284	11	18.4	25.31	79.843
24	V-335	57.667	62	16.5	64.6	20.5	9.2	3.357	11	14.5	20.473	62.587
25	CM-145	57.667	63	28.1	84.8	34	11.533	3.486	11	24.6	31.033	113.8
	Grand Mean	55.64	61.333	23.8	79.5	27.565	9.342	3.491	10.807	16.927	26.916	80.648
	Sem +	1.399	1.508		3.842	1.837	0.753	0.085	0.378	1.884	1.435	8.066
	CV (%)	4.355	3.749	10.97	8.368	11.544	13.965	4.236	6.071	19.274	9.233	17.323
	CD (5%)	3.978	3.775	4.287	10.92	5.224	2.142	0.243	1.077	5.356	4.08	22.935

CV = Coefficient of variation, CD = Critical difference, Sem = Standard error mean, DTT = Days to 50% tassling, DTS = Days to 50% silking, TL = Tassel length, PH = Plant height, EH = Ear height, CL = Cob length, CD = Cob diameter, KRC<sup>1</sup> = Number of kernel rows per cob, KR<sup>1</sup> = Number of rows per cob, 100GW = 100 grain weight, GYP<sup>1</sup> = Grain yield per plant

**Table 3 : Estimates of variability, heritability and genetic advance as percentage of mean for 11 characters in 25 genotypes of maize**

S. No.	Characters	Mean + SEM	Range		PCV (%)	GCV (%)	h <sup>2</sup> (bs) (%)	GA as % of mean
			Minimum	Maximum				
1	DTT	55.64 + 1.399	49	59.67	6.58	4.93	56.2	7.62
2	DTS	61.333 + 1.328	57.67	66	5.19	3.59	47.8	5.19
3	TL	23.803 + 1.508	15.4	32	21.07	17.99	72.9	31.63
4	PH	79.509 + 3.842	56.4	106.3	19.98	18.14	82.5	33.94
5	EH	27.565 + 1.837	17.2	38.9	23.1	20	75	35.69
6	CL	9.343 + 0.753	6.5	11.53	18.82	12.62	45	17.43
7	CD	3.491 + 0.085	3.11	4.03	7.71	6.44	69.8	11.09
8	KRC <sup>1</sup>	10.807 + 0.379	8.2	12.6	11.09	9.28	70	15.99
9	KR <sup>1</sup>	16.927 + 1.884	11	24.6	23.69	13.77	33.8	16.49
10	100 GW	26.916 + 1.435	15.98	37.24	21.78	19.72	82	36.79
11	GYP <sup>1</sup>	80.648 + 8.066	52.23	113.8	25.68	18.95	54.5	28.82

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h<sup>2</sup>(bs) = Heritability broad sense, GA = Genetic advance as percent of mean, DTT = Days to 50% tassling, DTS = Days to 50% silking, TL = Tassel length, PH = Plant height, EH = Ear height, CL = Cob length, CD = Cob diameter, KRC<sup>1</sup> = Number of kernel rows per cob, KR<sup>1</sup> = Number of rows per cob, 100GW = 100 grain weight, GYP<sup>1</sup> = Grain yield per plant

depicted that phenotypic variances ( $\sigma_p^2$ ) and PCVs were slightly higher than genetic variances ( $\sigma_g^2$ ) and GCVs for all the characters, suggesting the least influence of environment in the expression of these characters. Similar results have also been reported by Nelson and Somers, (1992).

Present findings revealed higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) for all traits studied. PCV was higher for grain yield per plant followed by number of kernels per row, ear height, 100 grain weight, Ear height, plant height, cob length, number of kernel rows per cob, cob diameter, days to 50% tasseling and days to 50% silking. Similar finding have been reported earlier by Swati Barche *et al.* (2014) Percentage of PCV and GCV were of dissimilar magnitude for all the traits indicating least effect of environmental factors in their expression (Table 3). The highest

GCV was recorded for ear height and lowest for days to 50% silking indicating that highest variability of genotypes were found for ear height and thus selection would be more effective than days to 50% silking. High coefficient of variation provides ample scope for selection of desirable types, thus more effective in isolating superior genotypes. Similar findings have been reported by Rafiq *et al.*(2010) who revealed presence of substantial variability for all traits studied in his experiment. Grain yield per plant, Tassel length, ear height, 100 grain weight had high GCV estimates. Moderate GCV and PCV values were recorded for cob diameter. The trait days to 50% tasseling and days to 50% silking both recorded low PCV and GCV values. Similar findings have been reported by Mukti Ram Poudel *et al.* (2016).

**Heritability and genetic advance**

High heritability should be accompanied with high genetic advance to arrive more reliable conclusion. Expected genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding method. In the present set of material, estimates of broad sense heritability were higher for all characters except for number of kernels per row (Table 3). This suggested greater effectiveness of selection and improvement expected for these characters in future breeding programme(s) as the genetic variance is mostly due to additive gene action. Similar results were also observed by several workers, like high heritability estimates for plant height and number of kernels per row by Choudhary and Choudhary (2002), for cob diameter (Dawood and Mohammed, 1989), for 100 grain weight (Choudhary and Choudhary, 2002) and for grain yield per plant (Sofi and Rather, 2007; Rafiq *et al.*, 2010).

Genetic advance as percentage of mean was high for grain yield per plant, 100 grain weight, ear height, plant height and Ear height (Table 3). Similar results were observed for plant height (Reddy and Agarwal, 1992), Number of kernels per row, ear height and cob length (Singha and Prodhan, 2000; Kabdal *et al.*, 2003). Genetic advance as percentage of mean was moderate for characters like number of kernels per row, number of kernel rows per cob, cob diameter and cob length. Genetic advance was low for characters like days to 50% tasseling and days to 50% silking. The high heritability coupled with high genetic advance was noticed for above traits indicating, the role of additive gene action in controlling the traits; hence pedigree method of breeding will be rewarding for improving the traits under investigation. Other traits like days to 50% tassling and days to 50% silking recorded high heritability with low genetic advance as percentage of mean, indicating that the characters were influenced by environment and were not stable. High heritability coupled with high genetic advance was observed for many characters *viz.*, plant height, 100 grain weight, ear height, tassel length and grain yield per plant. Higher values of heritability for quantitative character(s) enables plant breeders to form basis of selection programme on the phenotypic value of a specific character for its further improvement. Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance are usually more helpful than heritability alone in predicting the resultant effect for selecting the best genotypes.

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