

Original Research Article

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## Assessment of Genetic Diversity and Variability of Maize (*Zea mays* L.) Inbreds

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### ABSTRACT

Genetic Diversity (GD) present in the germplasm is pre-requisite for crop improvement as it helps in the development of superior recombinants. Knowledge about Genetic diversity between the genotype can be utilized for the selection of diverse parents in hybridization to exploit the heterosis. Mahalanobis  $D^2$  statistics assist in grouping the genotypes into different clusters. A set of trial consisting of 20 inbred lines of maize were grown in the experimental field of IASc. BHU, Varanasi and morphological diversity and genetic variability was assessed. Based on the morphological data a cluster diagram (Through Ward's similarity coefficient) minimum distance was obtained consisting of a total of two clusters. The diversity analysis through rooted dendrogram revealed the maximum inbreds in cluster 2 and HUZM 152 found to be most diverse among the twenty experimental inbreds. Maximum intra cluster distance obtained in cluster 4 (Eucladian distance) whereas, maximum inter cluster distance found between cluster 2 and 3. Genetic variability studies indicated narrow difference in PCV and GCV for most of the traits. High heritability followed by high genetic advance under selection was found for the traits i.e., plant height and ear height. The inbreds chosen in the present study can be subjected to molecular analysis to confirm the morphological results and can be utilized in obtaining better recombinants.

#### Keywords

Breeding, Diversity,  
Inbreds,  
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### Introduction

The success of plant breeding program depends on the development of high yielding, input responsive, better quality, disease and insect resistant varieties, which in turn depends on the selection of suitable plants to be utilized in crop improvement. Mahalanobis  $D^2$  statistics assist in grouping the genotypes into different clusters based on their divergence level. This analysis takes into account the contribution of each character

towards the total divergence. So that provides the idea about the total genetic divergence among the genotypes with the estimates of Inter-cluster and Intra-cluster distance. Hybridization program involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to the complementary interaction of divergent genes in parents (Ovung *et al.*, 2012), hence, helps to pick up appropriate

genotypes for utilization in the hybridization program.

Maize (*Zea mays* L.) is the world's third most important cereal after wheat and rice and popularly known as "Queen of Cereals". It has worldwide significance as human food, animal feed and for a large number of many other industrial products like glucose, starch, oil etc. It is a major food crop and main source of dietary energy and protein for the most food insecure people in the world. Maize was domesticated in Mexico, from where it was introduced to other regions of the world with diverse agro-climatic conditions (Anjali Kumari *et al.*, 2018). Therefore, a wide diversity is found within and among the maize genotypes at both phenotypic and genotypic level. The knowledge of genetic diversity in maize is important for understanding of the genetic structure and subsequently helps the breeder in choosing desirable parents to conduct breeding program (AlBadeiry *et al.*, 2014). The more diverse genotypes can be used to produce superior hybrids/lines, segregating population with high variability and introgression of desirable traits/genes. Therefore, there is a need to evaluate the available genotypes for the extent of genetic diversity.

### **Materials and Methods**

Exploitation of natural genetic variability help to meet short-term objective as very often breeders are forced to meet immediate requirement of the farmers, consumers and end-users (Gayatonde *et al.*, 2017). The present investigation was conducted during the *kharif* season 2015-2016 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi using twenty maize inbreds *viz.*, HKI- 193-1, HKI 1105, CML 161, LM 10, CML 163, PBNI 3-1, HUZM 343, HUZM 152, HUZM 242, HKI 536,

HUZM 185, HKI 323, HUZM 56, HUZM 265, HKI 162, HUZM329, HKI586, HUZM 379, HUZM 53 and HUZM 246. The experiment was laid out in randomized block design (RBD) with three replications and crop was maintained as per the standard agronomic practices. The field observations were recorded for 18 traits which includes days to tasseling (DT), days to silking (DS), anthesis silking interval (ASI), Plant height (PH), ear height (EH), leaf area (LA), panicle length (PL) cob length (CL), cob diameter (CD), rows per cob (ROW), days to maturity (DM), test weight(TW), Per cent germination (PG)total soluble sugar (TSS), Per cent grain moisture (GM) grain yield per plant (GP), number of cobs per plot (NP) and yield per plot (YP). Genetic divergence analysis carried out as per Mahalanobis'  $D^2$ -statistics procedure.

The  $D^2$ -values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. After arranging the  $D^2$ -values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). In all the combinations of genotypes, each character was ranked on the basis of  $d_i = Y_i^j - Y_i^k$  values. Rank 1 was given to the highest mean difference and rank p to the lowest mean difference, where, p represented the total number of characters. The analysis of variance was done as suggested by Panse and Sukhatme (1967). Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability were estimated by formula suggested by Burton (1952). Genetic advance (GA) was calculated by the method suggested by Johnson *et al.*, (1955). Analysis of variance for all the characters was carried out by Windows stat and the genetic parameters such as PCV and GCV, heritability broad sense ( $h^2$ ) were

calculated (Nechifor *et al.*, 2011), genetic advance in percent of mean (genetic gain) and expected mean in next generation were work out.

## Results and Discussion

The Diversity analysis (Euclidian distance) resulted in major four clusters out of which highest intra-cluster distance can be revealed from cluster 4 (i.e. 446.66) and minimum in cluster 1 (180). Maximum intercluster distance observed between cluster 2 and 3 (1541) followed by 1 and 4 (Fig. 1). The minimum cluster distance was recorded between cluster 1 and 3 (494.61). The clusters showing maximum internal diversity can be utilized as a diverse pool to cross with the other clusters consisting maximum distance e.g. 2 and 3. Similar studies were reported by Mortier *et al.*, (2005) and Wang *et al.*, (2008).

A dendrogram constructed based on the Ward's similarity index resulted in three major groups among which HUZM 152 found as a diverse inbred. Maximum clustering pattern is recorded at 600 unit distance which divides the rooted figure into two major clusters. Cluster 2 showed maximum number of inbreds indicates, the similarity in the genetic background of those inbreds. Similar studies were reported by Nikkhoy and Shiri (2017) and Iqbal *et al.*, (2015).

Genetic variability and heritability and genetic advance parameters The results pertaining to phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance expressed as percent of mean for all the characters under study are presented in Table 1. Phenotypic and genotypic coefficient of variation The ANOVA revealed considerable variations over the traits under study exhibiting a wide range of phenotypic as well as genotypic coefficient of variation. In

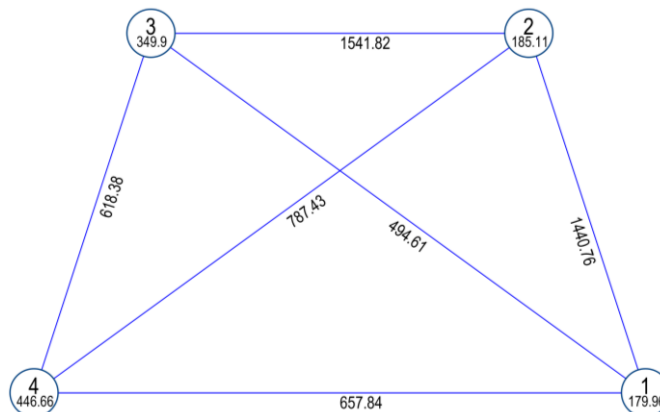
general, the values of phenotypic coefficient of variance were higher than those of genotypic coefficient of variance. The relative magnitudes of the phenotypic as well as genotypic variances between the traits were compared based on the phenotypic and genotypic coefficient of variation. PCV was recorded highest for ASI (55.93) followed by yield per plant (33.00) and cob length (25.76). Low magnitude of PCV was exhibited by days to silking (3.77) followed by days to tasseling (3.8) and days to maturity (4.11). Rest other traits exhibited medium values of PCV. Similarly, GCV was also high for ASI (36.7) followed yield per plot (31.35) and cob diameter (14.3). Whereas, low magnitude of GCV was exhibited by grain yield per plant (1.74) followed by Per cent germination (2.64) and number of cobs per plot (2.73). The differences between the values of PCV and GCV were small for almost all the traits indicating less influence of environment in expression of these traits. However, the differences were comparatively greater in case of ASI grain weight per plant and number of cobs per plot. Heritability In the present study, heritability (broad sense) ranged from 35% to 95%. The highest heritability was found in plant height and ear height (95%) followed by days to maturity (93 %) and yield per plant (89%). Lowest heritability was observed in effective tillers/plant (55%) followed by harvest index (56%). Other traits showed intermediate heritability Genetic advance Genetic advance as percent of mean (5%) was realized highest for plant height (47.12) followed by biomass (32.29) and grain yield per plant (32.10). Lowest value was observed in percent germination followed by ASI (43) and days to maturity (55). The studies of variance among 20 inbreds for 18 characters revealed that the genotypes differed significantly for all the characters which suggested that the materials selected for the studies might be of diverse origin. Several workers have reported the presence of

variability in and amongst the genotypes of maize for different traits. These findings are in accordance with the findings of Gayatonde *et al.*, (2017), Rajesh *et al.*, (2013), Mahmood *et al.*, (2004), Praveen Kumar *et al.*, (2014). The early flowering and maturity was seen in three inbreds namely HUZM 152, HKI 193-1, HKI 1105 and HUZM 343 whereas inbreds HUZM-185 HUZM 329 and LM 10 exhibited late flowering and maturity suggesting that short duration genotypes can be used for evolving early maturity or short duration maize suitable for rainfed and zaid cropping areas. Late maturity in maize is a better ideotype character and inbreds showing better grain filling can be further utilized in various breeding purpose. Several workers Praveen Kumar *et al.*, (2014) also reported positive as well as negative value for earliness in maize inbreds. The negative significant value for plant height is desirable because dwarf plant stature is essential to utilize for directed biomass accumulation in cobs, even believed to be lodging resistant.

The magnitude of genetic variability decides the effectiveness of selection. It is an established fact that greater the variability among the genotypes better is the chance for further improvement in the crop. But this variability can be utilized better if it is heritable. The heritable portion of the overall

observed variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance. In this study, the estimates of PCV were higher than their corresponding GCV for all the traits studied. These findings were similar to the findings of Kapoor and Batra (2017). The highest PCV and GCV were high recorded for ASI followed by cob length, grains yield per plot and grains yield per plant indicating that these traits were under the major influence of genetic control and less variable due to environmental factors. Therefore, such traits are important for further improvement. These findings are in close agreement with the researchers Ali *et al.*, (2007) and Nagaraju (2012). The GCV provides a measure of comparison of variability and sometimes give some indication regarding validity of traits for selection. However, it does not provide clean picture of the extent of genetic gain to be expected from selection of phenotypic traits, unless heritable fraction of variation (heritability) is known (Burton, 1952). The difference between the values of PCV and GCV were small for almost all the traits except ASI, indicating less influence of environment in expression of these traits suggesting phenotypic differences may be considered as genetic difference among genotypes for selection.

**Fig.1** Mahalanobi's Eucladian distance pattern



**Table.1** Genetic variability parameters for various characters in 20 inbreds of maize

	DT	DS	ASI	PH	EH	LA	PL	CL	CD	ROW	DM	TW	PG	TSS	MP	GP	NP	YP
GCV	3.541	3.447	36.753	8.584	14.301	12.904	14.895	25.588	14.873	9.825	3.961	14.751	2.638	10.072	6.317	1.742	2.731	31.359
PCV	3.826	3.772	55.798	8.785	14.631	13.331	15.289	25.767	15.501	12.425	4.11	15.075	11.67	11.374	6.773	6.365	11.609	33.256
$h^2$ (Broad Sense)	0.856	0.835	0.434	0.955	0.955	0.937	0.949	0.986	0.921	0.625	0.929	0.957	0.55	0.78	0.87	0.875	0.855	0.889
Genetic Advancement 5%	7.393	7.292	1.463	20.882	15.13	0.991	8.671	7.506	1.18	2.219	11.801	6.143	0.21	0.746	0.572	0.091	0.227	1.881
Gen. Adv as % of Mean 5%	6.75	6.49	49.87	17.278	28.797	25.731	29.893	52.345	29.398	16.005	7.864	29.732	1.229	18.372	12.137	0.982	1.323	60.916
Gen. Adv as % of Mean 1%	8.651	8.317	63.91	22.142	36.905	32.975	38.31	67.083	37.675	20.511	10.078	38.103	1.574	23.545	15.554	1.258	1.696	78.067
General Mean	109.525	112.358	2.933	120.863	52.541	3.853	29.007	14.339	4.015	13.867	150.067	20.661	17.1	4.06	4.717	9.228	17.15	3.088
Exp Mean next Generation	116.918	119.65	4.396	141.746	67.671	4.844	37.678	21.845	5.195	16.086	161.868	26.804	17.31	4.806	5.289	9.319	17.377	4.969

This also indicates that per-se performance of these traits should not be taken directly as the basis of selection other variability parameter for these traits such as heritability may also be taken into consideration. The relative magnitude of genotypic and phenotypic variances for the traits is the broad sense heritability and it is used as analytical role in selection procedures.

In the present investigation, high heritability was recorded for most of the characters except few traits. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone and indicates presence of additive variance or Additive x Additive type of interaction. It is not necessary that a character showing high heritability will also exhibit high genetic advance. The breeder should be cautious in making selection based on heritability as it indicates both additive and non-additive gene action. Thus, heritability values coupled with genetic advance would be more reliable and useful in formulating selection procedure as it indicates that most likely the heritability is due to additive gene effects. In the present set of materials, high heritability coupled with high genetic advance as percent was recorded for plant height, ear height and days to maturity, indicating effectiveness of selection for the improvement of these traits while high heritability coupled with low genetic advance

as cob length, leaf area, cob length which is indicative of non-additive gene action. High heritability coupled with high genetic advance may be attributed to additive gene action (Khan, 1990). The high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding. These results are in conformity with the findings of Ali *et al.*, (2007) and Krishna *et al.*, (2010).

**The major findings and implications are summarised as follows**

Analysis of variance for 20 maize inbreds with regards to yield and yield components revealed that the existence of significant differences among the genotypes studied for all the traits. There was a significant diversity found among the inbreds which was confirmed through  $D^2$  cluster analysis by obtaining two major clusters. These clusters can be further utilized for making diverse cross combinations and further heterotic pools which may help to opt best cross combination and heterotic for one or multiple traits. The Eucladian distance pattern analysis revealed favorable inter and intra-cluster distance, reveals scope for selecting diverse parents in breeding programs.

The maximum traits were recorded with close PCV and GCV values except ASI, percent germination and grain yield per plot. This shows the less influence of environment on

the traits which are desirable to improve yield per-se. Four traits exhibited high heritability plus high genetic gain under selection reveals presence of additive variance and further scope for selection. Majority of the traits are recorded with high expected mean yield in the next generation, shows prediction is the better option if at all the objective is to select the inbreds for double or three way crosses.

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