



## ASSESSING GENETIC DIVERSITY OF MAIZE (*Zea mays* L.) GENOTYPES FOR AGRONOMIC TRAITS

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Maize is one of the most important cereals globally and a promising cereal supplement in Bangladesh. The current study was undertaken to assess genetic diversity among nine maize genotypes. Data were recorded on seven morphological traits *viz.* plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernels/ear, 1000-kernel weight (g) and yield/plant (g). Statistical analysis showed significant variation among maize genotypes. Considering plant height, ear length, ear diameter, ear height, number of kernels/ear and yield/plant BHM-7 was observed as the best one. Among all the traits higher phenotypic coefficient of variation and genotypic coefficient of variation were observed for yield/plant. Genetic advance was highest for 1000-kernel weight followed by number of kernels/ear. The correlation study revealed only two positive significant associations: plant height with yield/plant and ear diameter with ear length. Nine genotypes were grouped into three clusters. These all clearly indicated the presence of ample genetic diversity among maize genotypes which can be exploited in future breeding program for better utilization of maize germplasm.

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## INTRUDUCTION

Maize is an amazing crop throughout the world which occupies a large portion of world economy. Total maize production in the world for the 2013-14 is 959 million tons which is more than that of wheat (709 million tons) and rice (473 million tons) (GMR 2014). In 2009, over 159 million hectares of maize were planted worldwide which gave a yield of 5.12 tons/ha (FAOSTAT, 2009). From nutritional view point it is better than rice and wheat (<http://ndb.nal.usda.gov/ndb/search/list>). Maize is also important in industrial and medicinal uses. In Bangladesh maize is considered as second most important cereal crop which occupies 165.5 thousand hectares land and produces 1018 thousand metric tons with an average yield of 6.1 tons/ha (BBS, 2011). The main use of maize is as poultry feed (Hossain and Shahjahan, 2007). In Bangladesh current need of maize is 1.60 million metric tons annually (Ahmed, 2013). If the traditional prolonged rice dependent food habit of Bangladesh can be diversified with maize, it would probably be possible to attain food self sufficiency to a great extent. Because, it is a high yielding and low-cost crop compared to rice and wheat. For satisfying this purpose, diversity assessment of existing genotypes would provide valuable inputs to move forwarding with the current and upcoming breeding needs.

Genetic diversity is the variation of heritable characteristics in genetic makeup present in a population of the same species. Knowledge of diversity in a germplasm is very important for the improvement of crop plants through breeding program (Hallauer et al., 1988). Different methods can be used to assess genetic diversity in plant species, such as pedigree and heterosis data, morphological marker and molecular markers (Melchinger, 1999; Xia et al., 2005; Legesse et al., 2007). Morphological traits are the earliest, convenient and effective genetic markers used for germplasm management (Statonet et al., 1994). Morphological markers is of great value in studies of maize landraces (Galarreta and Alvarez, 2001; Lucchin et al., 2003; Ortiz et al., 2008). Both qualitative and quantitative traits have been considered to study phenotypic diversity of maize (Alika et al., 1993; Taba et al., 1998; Lucchin et al., 2003). The most commonly used parameters are related to plant architecture traits, tassel traits, ear and kernel characteristics. The variables contributing to genetic diversity are grain weight and grain yield (Hoque, 2008); kernel weight and days to maturity (Ahmed, 2007); ear height, days to silking, % tryptophan content, cob length and 1000-seed weight (Kadir, 2010); ear length and diameter (Ahmed, 2013). The present investigation was conducted to analyze genetic diversity of maize genotypes using morphological traits.

## MATERIALS AND METHODS

### Experimental site, duration and materials

The experiment was conducted in the field lab of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh from March 2013 to April 2014. Nine maize genotypes were selected as experimental materials, those were: Uttaran, Duranta, BARI Hybrid Maize 5 (BHM-5), BARI Hybrid Maize 7 (BHM-7), BARI Hybrid Maize 9 (BHM-9), V-92, H-981, Pop Corn and Sweet Corn. All of them were collected from Bangladesh Agricultural Research Institute (BARI).

### Experimental design and data collection

The experiment was conducted following randomized complete block design (RCBD) with three replications. The plot size was 4.2 m x 2.7 m, row to row and plant to plant distances were 60 cm and 30 cm, respectively. Recommended production packages i.e. application of recommended doses of fertilizers, weeding, thinning, irrigation, pesticide etc. was followed as per BARI recommendation, as and when necessary to ensure the optimum plant growth and development.

At field maturity, five randomly selected plants were used for recording observations on the traits: plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernels/ear, 1000-kernel weight (g) and yield/plant (g). Analysis of variance (ANOVA) was done on the sample for all the seven character mentioned using MStat-c statistical program. The total variance of each character was partitioned into replication, genotype and error. The differences within the classes of effects were tested by F-test. The mean performance of the nine genotypes for their traits was shown through lettering by DMRT (Duncan's Multiple Range Tests) using the same software.

Genotyping and phenotypic variances were estimated according to the formula given by Johnson et al., (1995).

$$\text{Genotypic variance, } \sigma^2_g = \frac{\text{GMS} - \text{EMS}}{r}$$

Where,

GMS= Genotypic mean square, EMS= Error mean square

r = Number of replication, Phenotypic variance,  $\sigma^2_{ph} = \sigma^2_g + \text{EMS}$

Where,

$\sigma^2_g$  = Genotypic variance

EMS = Error mean square

Heritability in broad sense ( $h^2_b$ ) was estimated according to the formula suggested by Johnson et al. (1995) and Hanson et al. (1956).

Heritability,  $h^2_b = (\sigma^2_g / \sigma^2_{ph}) \times 100$

Where,

$\sigma^2_g$  = Genotypic variance,  $\sigma^2_{ph}$  = Phenotypic variance

Genotypic and phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Chaudhary (1985).

$$\text{Genotypic co-efficient of variations, GCV} = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

Where,

$\sigma^2_g$  = Genotypic variance; and  $\bar{X}$  = Population mean

$$\text{Phenotypic co-efficient of variations, PCV} = \frac{\sqrt{\sigma^2_{ph}}}{\bar{X}} \times 100$$

Where,

$\sigma^2_{ph}$  = Phenotypic variance; and

$\bar{X}$  = Population mean

Estimation of genetic advance was done following formula given by Johnson *et al.* (1955) and Allard (1960).

Genetic advance,  $GA = h^2_b \cdot K \cdot \sigma_p$

Where,  $h^2_b$  = Heritability

K = Selection differential, the value of which is 2.06 at 5% selection intensity

$\sigma_p$  = Phenotypic standard deviation

Genetic advance in percent of mean was calculated by the formula of Comstock and Robinson (1952) as follows:

$$\text{Genetic advance in percentage of mean, GA (\%)} = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance,  $\bar{X}$  = Population mean

The correlation coefficient (r) between two variables such as X and Y can be estimated using following formula:

$$r_{xy} = \frac{\sum XY - \frac{\sum X \sum Y}{N}}{\sqrt{\sum Y^2 - \frac{(\sum Y)^2}{N}} \sqrt{\sum X^2 - \frac{(\sum X)^2}{N}}}$$

Where,

$\sum XY - \frac{\sum X \sum Y}{N}$  = Sum of products of X and Y

$\sqrt{\sum Y^2 - \frac{(\sum Y)^2}{N}}$  = Sum of squares of Y

$\sqrt{\sum X^2 - \frac{(\sum X)^2}{N}}$  = Sum of squares of X

The genotypes were arranged in different clusters followed by the method suggested by Ward's Method based on Squared Euclidean distance and hierarchical cluster analysis. The initial cluster distances in Ward's minimum variance method are therefore defined to be the squared Euclidean distance between points:

$$d_{ij} = d(\{X_i\}, \{X_j\}) = \|X_i - X_j\|^2$$

## RESULT

The analyses of variance of different genotypes of maize for different agronomic traits are shown in Table 1. It indicated that the difference among genotypes for all the traits under study viz., plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernels/ear, 1000-kernel weight (g) and yield/plant (g) was highly significant.

**Table 1.** Analysis of Variances (mean squares) for different characters of nine genotypes of maize

Source of variation	Degrees of freedom (df)	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernels/ear	1000 kernel weight (g)	Yield/plant (g)
Replication	2	37.33	5.82	2.22	0.13	81.93	1.79	0.46
Genotype	8	1105.17**	82.95**	11.29**	0.74**	5459.12*	10016.53**	1510.9**
Error	16	3.67	6.57	0.62	0.04	97.01	0.96	1.53

\*\* indicate significant at 1% level of probability

### Trait-wise mean performance of the genotypes

Trait-wise mean performance of genotypes gives a clear comparison among genotypes. The mean performance of the nine genotypes for their traits with lettering by DMRT (Duncan's Multiple Range Tests) is shown in Table 2.

**Table 2.** Mean performance of nine genotypes of maize based on different agronomic traits

Genotype	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernels /ear	1000-kernel weight (g)	Yield/plant (g)
Pop corn	151.6e	53.7ab	7.50b	2.56bc	278a	137h	88.95b
BHM-9	198a	53ab	8.23b	2.80bc	245c	149g	86.86c
BHM-7	182.3b	53.7ab	8.40b	2.84b	264abc	291a	98.35a
BHM-5	182.3b	53.7ab	12.03a	3.81a	282a	214f	78.66e
V-92	145f	45.3c	6.43b	2.26c	153e	227d	75.39f
Uttaran	171.3c	55.3a	11.73a	3.48a	274ab	216e	50.47g
Duranta	164.3d	43.3c	7.97b	2.74bc	251bc	257b	37.80i
H-981	160d	47bc	8.33b	2.73bc	202d	241c	82.39d
Sweet corn	140g	41.7c	7.20b	2.43bc	270abc	122i	39.76h
<b>CV%</b>	<b>1.15</b>	<b>5.16</b>	<b>9.12</b>	<b>7.28</b>	<b>3.99</b>	<b>0.48</b>	<b>1.74</b>
<b>Maximum</b>	<b>200</b>	<b>59</b>	<b>13.7</b>	<b>4.2</b>	<b>291</b>	<b>292.5</b>	<b>99.2</b>
<b>Minimum</b>	<b>138</b>	<b>40</b>	<b>6.2</b>	<b>2</b>	<b>136</b>	<b>121.6</b>	<b>36.5</b>
<b>Mean</b>	<b>166.1</b>	<b>49.6</b>	<b>8.7</b>	<b>2.8</b>	<b>246.9</b>	<b>206.7</b>	<b>70.9</b>
<b>F-test</b>	<b>**</b>	<b>**</b>	<b>**</b>	<b>**</b>	<b>**</b>	<b>**</b>	<b>**</b>

Note: CV (%) = Coefficient of variation, \*\* indicate significant at 1% level of probability  
Similar letter indicates there is no significant difference at 5% level of probability as per DMRT  
Different letter indicates significant difference at 5% level of probability

### Estimation of correlation co-efficient

The correlation value denotes only the nature and extent of association existing among characters. In this experiment, two associations showed positive significant correlation: plant height with yield/plant and ear diameter with ear length (Table 3). In the current study, only one negative association had been observed for number of kernels/ear with 1000-kernel weight which is non-significant.

**Table 3.** Correlation co-efficient between yield and other yield related characters

Characters	Plant height(cm)	Ear height (cm)	Ear length (cm)	Ear diameter(cm)	Number of kernels/ear	1000-kernel weight(g)
Ear height (cm)	0.606					
Ear length (cm)	0.500	0.515				
Ear diameter (cm)	0.568	0.539	0.969**			
Number of kernels/ear	0.320	0.410	0.530	0.553		
1000-kernel weight (g)	0.246	0.050	0.177	0.198	-0.263	
Yield/plant (g)	0.906**	0.513	0.522	0.574	0.175	0.447

\*\* indicate significant at 1% level of probability

### Estimation of genetic parameters of maize genotypes

Genotypic variances, phenotypic variances, heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance and genetic advance (GA) as percent of mean (GA %) for all the yield contributing traits are presented in Table 4. Among the all traits yield/plant exhibited high estimates of GCV (31.61%), PCV (31.66%) and highest value of genetic advance in percentage (62.47%). On the other hand highest heritability (99.97%) and genetic advance (113.23) was observed in 1000-kernel weight.

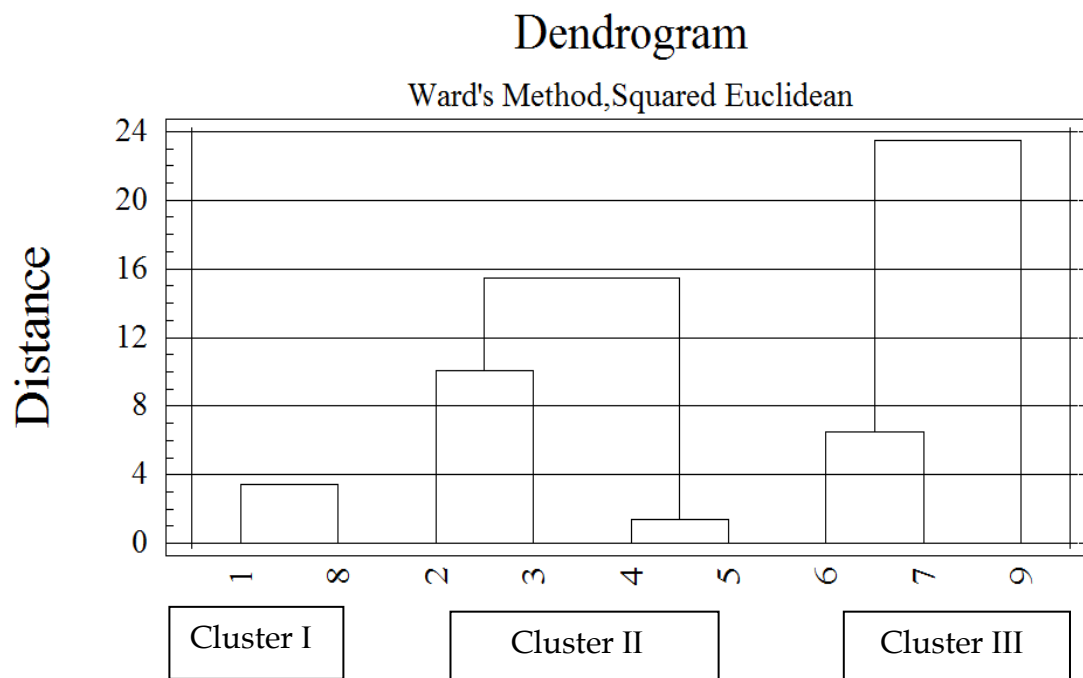
**Table 4.** Genetic parameters of seven different characters of nine maize genotypes

Traits	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
Plant Height (cm)	370.84	367.17	11.59	11.54	99.00	37.89	22.81
Ear height (cm)	32.03	25.46	11.40	10.17	79.49	8.92	17.97
Ear length (cm)	6.67	6.05	29.86	28.44	90.70	3.75	43.36
Ear diameter (cm)	0.27	0.23	18.22	16.82	83.94	0.88	30.86
No. of kernels/ear	1884.38	1787.37	17.58	17.14	94.85	81.96	33.19
1000-kernel weight (g)	3339.49	3338.52	27.98	27.97	99.97	113.23	54.82
Yield/plant(g)	504.67	503.14	31.66	31.61	99.97	44.33	62.47

GCV = Genotypic co-efficient of variation, PCV = Phenotypic co-efficient of variation, GA = Genetic advance, GA% = Genetic advance as percent

### Dendrogram

In the present experiment, dendrogram of nine maize lines had been made using mean value of different agronomic traits which results in three clusters (Fig. 1).



**Figure 1.** Dendrogram showing distribution of nine genotypes among three clusters

**Table 5.** Distribution of nine maize genotypes among three clusters

Cluster	No. of Genotypes	Genotypes
I	2	Popcorn, H-981
II	4	BHM-9, BHM-7, BHM-5, V-92
III	3	Uttaran, Duranta, Sweet corn

## DISCUSSION

Analysis of genetic diversity is an important step for better understanding and utilization of germplasm. Maize is a diverse and highly cross pollinated crops. There exists a good number of work on genetic diversity of maize but the genotypes experimented in this study were not studied yet. We found wide array of diversity among these genotypes. The ANOVA table suggested presence of ample genetic variability among the genotypes. Shahrokhi and Khorasani (2013) also observed significant variation among genotypes for days to silking, days to anthesis, plant height, ear height, kernel number, rows number, 1000-kernel weight and yield. Ahmed (2013) also observed significant variation among maize genotypes for yield, ear length, ear diameter, number of kernels/ear, 1000-kernel weight, days to maturity, days to silking, plant height and ear height. Prasanna et al. (2001) noted that genetic variability for most of the yield and yield contributing traits in maize were very high and amenable to genetic enhancements.

The presence of a wide range between minimum and maximum values for each trait assures the existence of sustainable variation among the genotypes studied (Table 2). Such variation in the germplasm collection of maize is an opportunity for breeders to improve traits of interest through parent selection, hybridization and recombination of desirable genotypes (Ahmed, 2013). In this experiment, each trait indicated separate genotype as best one, such as BHM-9 considering plant height; BHM-5 considering ear length, ear diameter and number of kernel/ear; and BHM-7 considering 1000-kernel weight and yield/plant.

Correlation is also an important measurement indicating that traits which should be given importance to increase yield. In this experiment, two associations showed positive significant correlation: plant height with yield/plant and ear diameter with ear length (Table 3). Positive significant correlation between plant height and yield/plant had also been recorded by Salami et al. (2007) and Rafiq et al. (2010). This positive and significant association between the traits suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, most of the associations were recorded as positive but non-significant. This type of association referred information of inherent relation among the pairs of combination. Positive and non-significant association between plant height with ear height and ear height with grain yield had also been observed by Olakojo and Olaoye (2011). Munawar et al. (2013) also studied positive, non-significant association between plant height with ear height and ear length. Positive and non-significant association for ear height with ear length and yield/plant was recorded by Rafiq et al. (2010). The negative insignificant association for number of kernels/ear with 1000-kernel weight referred a complex linked of relation among pair of combinations.

Table 4 indicated that variability within the maize genotypes is sufficiently divergent and constitutes potential candidate genotypes on which improvement program can be initiated. Phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits. Similar findings were observed by Salami et al. (2007), Bello et al. (2012) and Anshuman et al. (2013). The estimates of genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability. Since most of the economic characters (grain yield) are complex in inheritance and are greatly influenced by several genes interacting with various environmental conditions, 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. Table 4 indicated that for all traits PCV were higher than GCV. However, the differences between genotypic and phenotypic coefficient of variation indicated the environmental influence. In the present experiment, low value of GCV and PCV for plant height and ear height were recorded which was also observed by Anshuman et al. (2013).

Heritability estimates is of tremendous significance to the breeder, as its magnitude indicates the accuracy with which a genotype can be recognized by its phenotypic expression. Almost all traits studied here showed high heritability (Table 4). High heritability for ear length and 1000-kernel weight was also recorded by Noor et al. (2010). Aminu and Izge (2012) studied high heritability for plant height and yield/plant. Very high heritability (above 90%) was observed for plant height, ear height, number of kernels/ear, 1000-kernel weight and yield/plant by Bello et al. (2012) and Anshuman et al. (2013).

Character exhibiting high heritability may not necessarily give high genetic advance. Johnson et al., (1955) showed high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. Bello et al. (2012) recorded higher genetic advance for plant height, number of kernels/ear and yield/plant. In the present study high heritability with high genetic advance was found for the trait number of kernels/ear and 1000-kernel weight which indicated the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generations. The author suggested that these parameters were under the control of additive genetic effects. Sumathi et al. (2005) also suggested that these parameters could be manipulated according to requirements, and worthwhile improvement could be achieved through selection. However, high heritability and low genetic advance were observed for ear height, ear length and ear diameter which may be attributed to non-additive gene action governing these traits, and these characters could be improved through the use of hybridization and hybrid vigour.

Maize plant height, yield/plant, number of kernels/ear, 1000-kernel weight can be improved by selection, as these characters exhibited high genotypic and phenotypic coefficient of variations along with high heritability and genetic advance. Ear length, ear height and ear diameter had high heritability but the genetic coefficient of variations was low. This indicated that though, the character was highly heritable, its improvement through early generation selection may not give the desired results. Effective selection for superior genotypes is possible considering yield/plant, number of kernels/ear, 1000-kernel weight, plant and ear heights and can be used as target traits to improve maize grain yield.

Dendrogram grouped nine genotypes into three clusters (Fig 1). Maximum genotypes (four: BHM-9, BHM-7, BHM-5 and V-92) were distributed under cluster II, followed by cluster III and cluster I containing three (Duranta, Uttaran and Sweet corn) and two (Popcorn and H-981) genotypes, respectively (Table 5).

Subramanian and Subbaraman (2010) made dendrogram on 38 genotypes which results in four clusters: 14 genotypes under cluster 1, 13 under cluster 3, 9 under cluster 3 and remainder under cluster 4. 30 maize inbred lines were distributed by Azad et al. (2012) among six clusters. Another study was carried out by Chen et al. (2007) who reported that 186 maize genotypes could be classified into ten clusters.

## CONCLUSIONS

Assessing of genetic diversity is the basic need for the utilization of any germplasm. The research findings suggested adequate genetic diversity exists among studied nine genotypes. Though BHM-7 performed well other genotypes were good enough considering different traits. All these genotypes can be utilized for further improvement of maize germplasm for the desired characters.

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