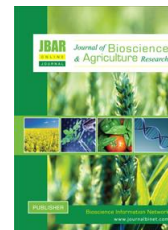


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## Morphological characterization and genetic diversity analyses of plant traits contributed to grain yield in maize (*Zea mays* L.)

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### ABSTRACT

Genetic variability and divergence among landraces and cultivars are invaluable resources that lead the breeder to understand the performance of an attribute or genotype, which possess paramount importance in selecting suitable genotypes or traits for hybridization programme. Thirteen maize genotypes were used to estimate the genetic parameters, variability, correlation and path coefficient, principal component analysis (PCA) and cluster analysis. The analysis of variance showed the presence of highly significant morphological variation among the thirteen genotypes. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the traits studied indicating their interaction with the environment to some extent. Most of the plant traits under study showed high heritability estimates, >60%. The high heritability (91.35%, 86.73%, 61.79% and 96.41%) coupled with high genetic advance (34.45, 107.98, 90.93 and 55.92) and genetic advance in percentage of mean (87.64%, 305.77%, 34.08% and 59.01%) were observed in plant height, kernel numbers row<sup>-1</sup>, thousand kernel weight and yield per plant; respectively, that designate the role of additive gene expression for these traits which would facilitate better scope for improvement of these traits through direct selection. The correlation analysis exhibited significant positive associations between yield per plant and plant height (0.603), ear girth (0.518), kernel numbers row<sup>-1</sup> (0.509), thousand kernel weight (0.806) and kernel width (0.715). Besides it showed a significant positive correlation of thousand kernel weight with plant height (0.583), ear girth (0.590) and kernel width (0.794). Furthermore, the positive direct effects of ear girth (0.749), kernel number row<sup>-1</sup> (0.771), thousand kernel weight (0.356) and kernel width (0.291) on yield per plant were observed through path analysis. While plant height, ear length, kernel rows ear<sup>-1</sup> and kernel length showed negative direct effect on yield per plant. The PCA showed that the first four principal components (PCs) accounted for more than 80% of total variation where PC1 explained 38.9% of total variability which was dominated by thousands kernel weight (0.448), yield per plant (0.444), kernel width (0.381), plant height (0.38), ear girth (0.378) and kernel rows ear<sup>-1</sup> (0.318). Cluster analysis exhibited three distinct clusters with five genotypes in cluster I and cluster II, and three genotypes in cluster III. The cluster I having the genotypes BHM-15, BHM-13, BHM-12, BHM-9 and BHM-7 was loaded with the highest mean values of thousand kernel weight (339.67), yield per plant (121.33) and kernel width (9.20). Moreover, these genotypes showed close proximate with kernel width, thousand kernel weight, ear girth, plant height and yield per plant in PCA biplot. Therefore, the analysis of variance, principal component and cluster analyses revealed the presence of wider diversity in the studied maize genotypes. The findings of this study would be useful to select the potential traits and genotypes for further breeding programs to increase the grain yield in maize.

**Key Words:** Genetic variability, Diversity, Correlation, Path coefficient, PCA and Clustering

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## I. Introduction

Besides rice and wheat, maize (*Zea mays* L.) is one of the most cultivated cereal crops for its high genetic diversity and adaptability over extended environmental conditions (Rocha et al., 2019). Maize being nutritionally an important crop is rich respiratory of carbohydrate, protein, starch, fat, vitamins and minerals along with fiber (Roy et al. 2018; Singh et al., 2020). Furthermore, it possesses multiple functions in the conventional farming system. Besides used as staple food and fuel for humans, maize is also used as feed for livestock and poultry (Kandel et al., 2018). The world's total maize production was estimated as 1050 million metric tons in 2019. The USA is the top maize producing country that accounted for 33.23% of the world's maize production in 2019. Other top maize producing countries include China, Brazil, Argentina, and Ukraine (World Data Atlas, 2020). Bangladesh is the 23<sup>rd</sup> country in terms of maize production in world and maize is the second most cereal crop in Bangladesh after rice in terms of its value of production and value of byproducts (World Data Atlas, 2020; BBS, 2019). Maize production of Bangladesh increased from 15.52 lakh metric tons in 2010 to 40.00 lakh metric tons in 2019 showed an average annual growth rate of 11.40% (World Data Atlas, 2020).

In spite of its increased production and wider adaptability, maize production in Bangladesh is still very low as compared to other maize producing countries as well as the country's current demand. Bangladesh is still facing challenges to attain long-term food security despite the success in rice production (Saha et al., 2019). Therefore, it is mandatory to develop high yielding varieties of other cereals like maize to break the existing yield plateau. Existing genetic diversity, variability and heritability within the existing germplasm or varieties are the key driving forces that lead enhanced success in breeding programs for crop improvement (Roy et al., 2018) that allow the plant breeders to produce advanced varieties or to develop new varieties (Yared and Misteru, 2016). The knowledge on genetic parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability estimates provide the better understanding of genetic advance and also offer precise information on selection on which the breeding methods are formulated for high yielding crops (Singh et al., 2017; Saha et al., 2019). The study of morphological traits has obtained supreme importance in plant breeding due to the probability of identifying existing variability among germplasm and additionally to select the superior germplasm of interest (Roy et al. 2018). In this regard, correlation studies that can be of phenotypic, genotypic or environmental nature, combined with the study of genetic parameters involved, between morphological traits allow the breeder to reveal the significant correlations among traits and also help to designate strategies that ensure a higher probability of obtaining superior materials (Roy et al. 2018; Rocha et al., 2019).

Correlation coefficient determines the reciprocal relationship between various plant traits but does not allow any conclusion about cause and effect relationships between them (Kinfe and Tsehaye, 2015; Rocha et al., 2019). However, path analysis splits the correlation coefficients into direct and indirect effects of the traits on a basic variable (Singh et al., 2017). Therefore, correlation combined with path coefficient analyses could help in identifying the appropriate traits of interest for improvement of the multifaceted character like yield (Rocha et al., 2019). The quantification of genetic diversity using biometrical procedure such as cluster analysis and principal component analysis is useful for quantifying the degree of divergence between biological populations. Moreover, it determines the relative contribution of different variables to the total divergence both in intra and inter cluster levels (Singh et al., 2020; Kumari et al., 2017). Therefore, the present investigation was aimed to estimate genetic variability, heritability and the extent of genetic diversity of plant traits among maize genotypes contributing to grain yield.

## II. Materials and Methods

This experiment was conducted at the Experimental Field Laboratory of the Department of Genetics and Plant Breeding in Bangladesh Agricultural University, Mymensingh, Bangladesh from January 2018 to August 2018. Geographically the experimental plots were located at 24°43'19.4" N latitude and 90°25'23.8" E longitudes at the elevation of 18 m above the sea level. A total of thirteen maize genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh (Table 01). The field experiment was carried out in a Randomized Complete Block Design (RCBD) with three replications. Plot size was 1.75 meters x 1.5 meters comprised of two rows. Seed was sown in January 2018 in a row. Row to Row distance was 75 cm and plant to plant distance was 25 cm. The experimental plots were prepared by ploughing, cross ploughing along with recommended doses of manures and fertilizers (Rahman et al., 2016) and all necessary intercultural operations such as irrigation, weeding, thinning, staking etc. were performed regularly.

**Table 01. List of thirteen maize genotypes used in the experiment**

Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
G1	BHM-15	G6	BHM-5	G11	BM-5
G2	BHM-13	G7	Mohor	G12	BM-6
G3	BHM-12	G8	Bornali	G13	BM-7
G4	BHM-9	G9	Khoibhutta		
G5	BHM-7	G10	BARI Sweet corn		

### Data recording

Harvesting was done manually when the plants of each plot reached to maturity in May, 2018. Data were recorded on five randomly selected plants of each genotype for each replication for ten plant traits related to yield. Height of plant was measured after anthesis and silking from the ground to the tip (cm), data on ear length (cm); ear girth (cm); number of kernel rows ear<sup>-1</sup>, kernel numbers row<sup>-1</sup>; kernel length (mm); kernel width (mm); kernel thickness (mm); thousands kernel weight (g) and yield plant<sup>-1</sup> (g) were recorded.

### Statistical analysis

Analysis of variance (ANOVA) was performed using the statistical software Statistical Analysis System version 9.3 (SAS). Correlation and path co-efficient was performed using the BASICA software. Minitab 17 Statistical Software was used for Principal Component Analysis (PCA) and cluster analysis. The genetic parameters i.e. genotypic and phenotypic variances, heritability, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), genetic advances were estimated by using the formula.

### Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated by the formula given by Johnson et al. (1955).

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

Where, GMS = Genotypic mean square; EMS = Error mean square; r = Number of replication

$$\text{Phenotypic variance, } \sigma_p^2 = \sigma_g^2 + \text{EMS}$$

Where,  $\sigma_g^2$  = Genotypic variance; EMS = Error mean square

### Estimation of heritability

Heritability in broad sense ( $h^2_b$ ) was estimated following the formula suggested by Johnson et al. (1955) and Hanson et al. (1956).

$$\text{Heritability, } h^2_b = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,  $h^2_b$  = Heritability in broad sense,  $\sigma_g^2$  = Genotypic variance;  $\sigma_p^2$  = Phenotypic variance

### Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic and phenotypic coefficient of variations were estimated according to [Burton \(1952\)](#) and [Singh and Chaudhary \(1985\)](#).

$$\text{Genotypic coefficient of variations, GCV} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,  $\sigma_g^2$  = Genotypic variance and  $\bar{X}$  = Population mean

$$\text{Phenotypic coefficient of variations, PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,  $\sigma_p^2$  = Phenotypic variance; and  $\bar{X}$  = Population mean

### Estimation of genetic advance

Estimation of genetic advance was estimated by the formula given by [Johnson et al. \(1955\)](#) and [Allard \(1960\)](#).

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

Where,  $h^2_b$  = Heritability in broad sense;

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

$\sigma_p$  = Phenotypic standard deviation

### Estimation of genetic advance in percentage of mean, GA (%)

Genetic advance in percent of mean was calculated by the formula of [Comstock and Robinson \(1952\)](#).

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

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

## III. Results and Discussion

The analysis of variance (ANOVA) of different morphological parameters of maize is shown in [Table 02](#). The ANOVA showed that the difference among genotypes for all the traits under study viz., plant height (cm), ear length (cm), ear girth (cm), kernel rows ear<sup>-1</sup>, kernel numbers row<sup>-1</sup>, kernel length (mm), thousand kernel weight (g), kernel width (mm), kernel thickness (mm), yield plant<sup>-1</sup> (g) were significant which indicates ample genetic differences among the genotypes ([Ferdoush et al., 2017](#)). However, the difference among replication was significant for kernel rows ear<sup>-1</sup> ([Table 02](#)). High variability for plant traits such as plant height, ear length, 50% tasselling, 50% silking, ear length, ear diameter, number of ears, number of rows ear<sup>-1</sup>, number of grains row<sup>-1</sup>, yield per plant, thousand grain weight and 100 grain weight were also reported in previous studies ([Rahman et al. 2015](#); [Ferdoush et al., 2017](#); [Singh et al., 2017](#)).

**Table 02. Analysis of variance for different plant traits of thirteen maize genotypes**

Items	df	PH (cm)	EL (cm)	EG (cm)	KRE (no.)	KNR (no.)
Replication	2	7.27	1.05	0.03	0.90*	22.56
Genotypes	12	173.73***	7.48***	4.83***	3.68***	109.58***
Error	24	5.32	1.89	0.25	0.76	5.32
Items	df	KL (mm)	TKW (g)	KW (mm)	KT (mm)	YP (g)
Replication	2	1.02	3334.90	0.51	0.07	42.33
Genotypes	12	2.76***	15184.69***	4.00***	0.90***	2378.83***
Error	24	0.44	2594.90	0.39	0.23	29.18

df= Degrees of freedom, PH= Plant height (cm), EL= Ear length (cm), EG= Ear girth (cm), KRE= Kernel rows ear<sup>-1</sup>, KNR= Kernel numbers row<sup>-1</sup>, KL= Kernel length (mm), TKW= Thousand kernel weight (g), KW= Kernel width (mm), KT= Kernel thickness (mm), YP= Yield plant<sup>-1</sup> (g). \*indicates significant at 0.05 and \*\*\* indicates significant at 0.001 probability level.

### Estimation of genetic parameters

Phenotypic and genotypic variances and coefficients of variation, heritability (broad sense) and genetic advances for all plant traits under study were estimated and presented in [Table 03](#). It was observed that the phenotypic variances ( $6^2p$ ) and phenotypic coefficients of variation (PCV) were higher than the genotypic variances ( $6^2g$ ) and genotypic coefficients of variation (GCV) for all traits. Nevertheless, the differences were very minimal for most of the traits, which indicates low environmental influence on the expression of the traits. The influence of environment on the expressions of similar traits was reported earlier in maize genotypes ([Ferdoush et al., 2017](#)). Only exception of high difference between phenotypic (6791.49) and genotypic (4196.60) variances was observed in thousand kernel weight ([Table 03](#)) indicating high environmental effect on this trait which was also reported in previous studies ([Roy et al. 2018](#); [Rocha et al., 2019](#)).

The highest plant height (204.67 cm) was observed in BM-6 while the lowest (180.67 cm) was in BARI sweet corn with a mean of 197.46 cm indicating high genetic variability for plant height in the studied maize genotypes. Plant height exhibited high heritability estimates (91.35%) along with high genetic advance (34.45) and high genetic advance in percentage of mean (87.64%). Similar observations of high heritability and high genetic advance for plant height in maize genotypes were reported earlier ([Maruthi and Rani, 2015](#); [Singh et al., 2017](#)).

The genetic variability for ear length (cm) ranges from 14.60 (BM-6) to 18.63 (BHM-7) with a mean of 15.99 and for kernel thickness (mm) 3.58 (BHM-5) to 5.32 (BHM-13) with a mean value 4.88, which indicate low variability for these traits among the studied genotypes. Ear length and kernel thickness showed moderate heritability of 49.64% and 49.51%; respectively coupled with low genetic advance (16.14 and 5.59; respectively) and genetic advance in percentage of mean (25.90% and 15.20%; respectively) which would make these traits difficult for improvement through selection. Similar findings of low genetic advance and genetic advance in percentage of mean were observed in case of ear length and kernel thickness by [Roy et al. \(2018\)](#). Moreover, moderate heritability of 27% was also observed in previous study for ear length that showed some level of environmental effect in maize genotypes ([Qureshi and Khalil, 2019](#)). The range of genetic variability for ear girth (cm) was 11.67 (Khoibhutta) to 17.33 (BHM-7) with a mean of 14.53. The observed heritability was high (85.90%) with the high genetic advance in percentage of mean (154.47%) and moderate genetic advance (22.44).

The genetic variability ranges from 12.33 (Khoibhutta) to 16.00 (BHM-7) for kernel rows ear<sup>-1</sup> with a mean of 13.96 and kernel numbers row<sup>-1</sup> exhibited a mean of 35.31, ranging from 24.00 (BARI sweet corn) to 42.33 (BM-6). The heritability estimates showed high heritability for kernel numbers row<sup>-1</sup> (86.75%) along with high genetic advance (107.98) while lower heritability (56.08%) combined with low genetic advance (12.80) was observed in kernel rows ear<sup>-1</sup>. Furthermore, both traits exhibited high genetic advance in percentage of mean of 305.77% and 91.72%; respectively. These findings were in accordance with [Singh et al. \(2017\)](#) and [Roy et al. \(2018\)](#).

**Table 03. Estimates of genetic parameters for various plant traits of thirteen maize genotypes**

Plant traits	Mean ± S.E	Range		$6^2p$	$6^2g$	$h^2_b$ (%)	PCV (%)	GCV (%)	GA	GA (%)
		Min	Max							
PH	197.46 ± 1.85	180.67	204.67	61.45	56.14	91.35	3.97	3.79	34.45	87.64
EL	15.99 ± 0.38	14.60	18.63	3.76	1.86	49.64	12.12	8.54	16.14	25.90
EG	14.53 ± 0.31	11.67	17.33	1.78	1.53	85.90	9.18	8.51	22.44	154.47
KRE	13.96 ± 0.27	12.33	16.00	1.74	0.97	56.08	9.44	7.07	12.80	91.72
KNR	35.31 ± 1.47	24.00	42.33	40.07	34.75	86.73	17.93	16.69	107.98	305.77
KL	10.17 ± 0.23	9.67	11.67	1.21	0.77	63.50	10.84	8.64	12.53	23.28
TKW	266.77 ± 17.3	143.33	361.67	6791.49	4196.60	61.79	30.89	24.28	90.93	34.08
KW	8.21 ± 0.28	5.76	10.10	1.59	1.20	75.68	15.36	13.36	17.99	219.15
KT	4.88 ± 0.13	3.58	5.32	0.45	0.22	49.51	13.86	9.75	5.59	15.20
YP	94.77 ± 6.83	42.67	151.00	812.40	783.22	96.41	30.08	29.53	55.92	59.01

PH= Plant height (cm), EL= Ear length (cm), EG= Ear girth (cm), KRE= Kernel rows ear<sup>-1</sup>, KNR= Kernel numbers row<sup>-1</sup>, KL= Kernel length (mm), TKW= Thousand kernel weight (g), KW= Kernel width (mm), KT= Kernel thickness (mm), YP= Yield plant<sup>-1</sup> (g),  $6^2p$  = Phenotypic variance,  $6^2g$  = Genotypic variance,  $h^2_b$  = Heritability in broad sense, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation and GA= Genetic advance, GA (%) = genetic advance in percentage of mean.

The ranges of genetic variability observed for kernel length (KL) and kernel width (KW) were low. It varied from 9.67 mm to 11.67 mm with a mean of 10.17 mm for kernel length and in case of kernel width, 5.76 mm to 10.10 mm with a mean of 8.21 mm. The heritability estimates were 63.50% (KL) and 75.86% (KW) with a low genetic advance of 12.53 (KL) and 17.99 (KW). Low genetic advance for these traits was found by [Ferdoush et al. \(2017\)](#). High heritability does not always indicate a high genetic gain; heritability should be combined with genetic advances in predicting the ultimate effect for selecting a promising trait ([Muchie and Fentie, 2016](#)). On the other hand, KL showed moderate genetic advance in percentage of mean (23.28%), while a high genetic advance in percentage of mean (219.15%) was found for KW. The range of genetic variability for thousand kernel weight (TKW) was 143.33 g (Khoibhutta) to 361.67 g (BHM-12) with a mean of 266.77 g. The heritability was 69.79% with high genetic advance (90.03) and high genetic advance in percentage of mean (34.08%). Similar findings for TKW in maize with high heritability, high genetic advance and genetic advance in percentage of mean were reported in several studies ([Rahman et al. 2015](#); [Ferdoush et al., 2017](#); [Roy et al. 2018](#)).

Grain yield per plant (YP) showed a range from 42.67g (BARI sweet corn) to 151.00g (BHM-12) with a mean of 94.77 g indicating a high range of genetic variability among the maize genotypes. The heritability estimates for this trait was the highest (96.41%) with high genetic advance (55.92) and high genetic advance in percentage of mean (59.01%). Similar observations were reported in earlier studies ([Aman et al., 2016](#); [Singh et al., 2017](#)).

The observed heritability estimates for most of the traits under present experiment were high (60% to 94%) with high genetic advance (22 to 107) and high genetic gain over the percent of mean (25% to 305%) indicating the presence of additive gene effects and selection for these traits could be effective for possible improvement of maize grain yield. Similar observations were recorded in several previous studies ([Maruthi and Rani, 2015](#); [Singh et al., 2017](#); [Roy et al., 2018](#); [Rocha et al., 2019](#)). High heritability combined with low genetic advance and high genetic advance in percentage, and high to moderate heritability with moderate to low genetic advance for several yield traits has been reported in maize genotypes ([Anshuman et al., 2013](#); [Singh et al., 2017](#); [Rocha et al., 2019](#)), which is in accordance with our findings. High heritability values indicate that the characters under study are less influenced by environment for their phenotypic expression; therefore, the plant breeder may select a genotype based on phenotypic expression for the desired characters ([Gana et al., 2013](#))

### Estimation of correlation coefficients

The correlation coefficient analysis revealed 12 significant associations in the phenotypic level among the traits under study ([Table 04](#)). Grain yield per plant exhibited positive and significant correlations with plant height (0.603), ear girth (0.518), kernel numbers row<sup>-1</sup> (0.509), thousand kernel weight (0.806) and kernel width (0.715). Several previous researchers reported the similar findings of positive and significant correlations of grain yield in maize with plant height, 1000-grain weight, 100-grain weight, cob diameter, kernel numbers row<sup>-1</sup>, ear length, ear girth, husk girth etc. ([Khodarahmpour and Choukan, 2011](#); [Ghimire and Timsina, 2015](#); [Hussain and Mohamad, 2017](#); [Singh et al., 2017](#); [Kandel et al., 2018](#)) which suggest the lower environmental influence on additive genetic model ([Afrin et al., 2017](#)). This finding suggested that the improvement of maize grain yield could be directly linked with the above associations. Furthermore, the positive and significant correlations were observed between plant height and ear girth (0.586), plant height and thousand kernel weight (0.583), ear length and kernel length (0.727), ear girth and kernel rows ear<sup>-1</sup> (0.705), ear girth and thousand kernel weight (0.590) and thousand kernel weight and kernel width (0.794). Similar significant positive correlations among agronomic traits in maize were also reported in earlier studies ([Kumari et al., 2017](#); [Roy et al. 2018](#)). However, a significant negative correlation was observed between kernel length and kernel thickness (-0.586) along with a number of non-significant positive and negative associations ([Table 04](#)). The presence of non-significant and negative correlations among or between traits could suggest the inherent relationships among the studied genotypes ([Afrin et al., 2017](#)).

**Table 04. Phenotypic correlation coefficients of different plant traits among thirteen maize genotypes**

Traits	PH	EL	EG	KRE	KNR	KL	TKW	KW	KT	YP
PH	1.00									
EL	-0.171	1.00								
EG	<b>0.586*</b>	0.112	1.00							
KRE	0.327	0.420	<b>0.705**</b>	1.00						
KNR	0.441	0.399	-0.105	0.008	1.00					
KL	0.121	<b>0.727**</b>	0.153	0.355	0.394	1.00				
TKW	<b>0.583*</b>	-0.086	<b>0.590*</b>	0.453	0.168	0.037	1.00			
KW	0.429	0.011	0.340	0.269	0.180	-0.039	<b>0.794***</b>	1.00		
KT	-0.054	-0.429	0.186	0.047	-0.478	<b>-0.586*</b>	0.303	0.351	1.00	
YP	<b>0.603*</b>	0.132	<b>0.518*</b>	0.294	<b>0.509*</b>	0.114	<b>0.806***</b>	<b>0.715**</b>	0.114	1.00

PH= Plant height (cm), EL= Ear length (cm), EG= Ear girth (cm), KRE= Kernel rows ear<sup>-1</sup>, KNR= Kernel numbers row<sup>-1</sup>, KL= Kernel length (mm), TKW= Thousand kernel weight (g), KW= Kernel width (mm), KT= Kernel thickness (mm), YP= Yield plant<sup>-1</sup> (g); \* =Significant at 5% level of probability, \*\* =Significant at 1% level of probability and \*\*\* =Significant at 1% level of probability.

### Estimation of path coefficient

Path analysis allows partitioning the direct effect and the indirect effects of correlations for better interpretation of cause and effect relationship among the traits. The satisfactory use of path coefficients is directly linked to causal effects, which allows finding the most important variables in the expression of the main variable (Rocha et al., 2019). The path coefficient analysis (Table 05) showed that plant height, ear length, kernel rows ear<sup>-1</sup> and kernel length had negative direct effect on yield per plant. Whereas, ear girth, kernel numbers row<sup>-1</sup>, thousand kernel weight, kernel thickness showed highly positive direct effect on yield per plant. Therefore, the breeding program based on the selection for these traits would provide a direct contribution towards the high grain yield in maize. Previous studies showed the same findings of high positive direct effect of thousand or 100-kernel weight, kernel numbers row<sup>-1</sup>, kernel width, ear girth along with negative direct effect of plant height on grain yield as found in the present study (Singh et al., 2017; Roy et al., 2018). These findings also showed that ear length and kernel rows ear<sup>-1</sup> exhibited positive direct effect while in our study these traits possessed negative direct effect on yield per plant which could be due to the difference in maize genotypes used. The residual effect was 0.3059 at phenotypic level which indicates the ten studied plant traits explained nearly 70% of the total variability existed in yield. The similar findings of having phenotypic residual effects (0.5547) in maize was reported by Raghu et al. (2011). The residual effect determined how best the causal factors such as PH, EG, KNR, TGW etc. accounted for the variability of the dependent factor i.e. grain yield (Eti et al., 2018).

**Table 05. Partitioning of phenotypic correlation coefficients into direct and indirect effects of ten component characters on grain yield per plant in maize by path coefficient analysis**

Traits	PH	EL	EG	KRE	KNR	KL	TKW	KW	KT	YP
PH	<b>-0.454</b>	0.031	0.438	-0.083	0.340	-0.0008	0.207	0.124	-0.002	<b>0.603*</b>
EL	0.078	<b>-0.183</b>	0.084	-0.107	0.308	-0.005	-0.031	0.003	-0.016	0.132
EG	-0.266	-0.020	<b>0.749</b>	-0.179	-0.081	-0.001	0.210	0.099	0.007	<b>0.518*</b>
KRE	-0.148	-0.077	0.528	<b>-0.254</b>	0.006	-0.002	0.161	0.078	0.002	0.294
KNR	-0.200	-0.073	-0.079	-0.002	<b>0.771</b>	-0.003	0.059	0.052	-0.018	<b>0.509*</b>
KL	-0.055	-0.133	0.115	-0.090	0.304	<b>-0.007</b>	0.013	-0.011	-0.022	0.114
TKW	-0.265	0.016	0.442	-0.115	0.129	-0.0002	<b>0.356</b>	0.231	0.011	<b>0.806***</b>
KW	-0.195	-0.002	0.255	-0.068	0.139	0.0003	0.283	<b>0.291</b>	0.013	<b>0.715**</b>
KT	0.025	0.078	0.139	-0.012	-0.368	0.004	0.108	0.102	<b>0.037</b>	0.114

Residual effect =0.3059

PH= Plant height (cm), EL= Ear length (cm), EG= Ear girth (cm), KRE= Kernel rows ear<sup>-1</sup>, KNR= Kernel numbers row<sup>-1</sup>, KL= Kernel length (mm), TKW= Thousand kernel weight (g), KW= Kernel width (mm), KT= Kernel thickness (mm), YP= Yield plant<sup>-1</sup> (g); \* =Significant at 5% level of probability, \*\* =Significant at 1% level of probability and \*\*\* =Significant at 1% level of probability. Direct effects are marked as bold.

### Principal component analysis (PCA)

The PCA analysis determined the Eigenvalues of ten variables (plant traits) of thirteen maize genotypes along with their variability % and cumulative (%) explained variances (Table 07). Eigenvalues measure the importance and impact of each component to total variance (Nuruzzaman et al., 2019). It was observed that first four principal components (PCs) accounted for more than 80% of the total variance. It was also observed that first three principal components (PCs) explained more than one Eigenvalues contributing 79.2% of variation (Table 06). Similar findings of PCs contribution to the total variability were also observed in maize genotypes (Kumari et al., 2017).

**Table 06. Cumulative variances and Eigenvalues for first four principal components (PCs)**

	PC1	PC2	PC3	PC4
Eigenvalue	3.8928	2.5945	1.4357	0.8883
Variance (%)	38.9	25.9	14.4	8.9
Cumulative (%)	38.9	64.9	79.2	88.1

PCs= principal components

The PC1 explained the highest variance (38.9%) with the highest eigenvalue (3.8928) which was dominated by thousands kernel weight (0.448), yield plant<sup>-1</sup> (0.444), plant height (0.38), kernel width (0.381) ear girth (0.378) and Kernel rows ear<sup>-1</sup> (0.318) (Table 07). Kumari et al. (2017) also reported important contribution of the first PC in total variability while studying different traits of maize. In PC2, kernel thickness, kernel width and thousands kernel weight exhibited more variability and PC2 contributed 25.9% to the total variation. The third principal component explained 14.4% of total variation, was governed by kernel numbers row<sup>-1</sup>, yield plant<sup>-1</sup>, plant height and ear girth. PC4 was dominated by plant height and ear girth contributing 8.9% of total variability (Table 07).

**Table 07. Contribution of variables in total variability (PC1 to PC4) of maize genotypes**

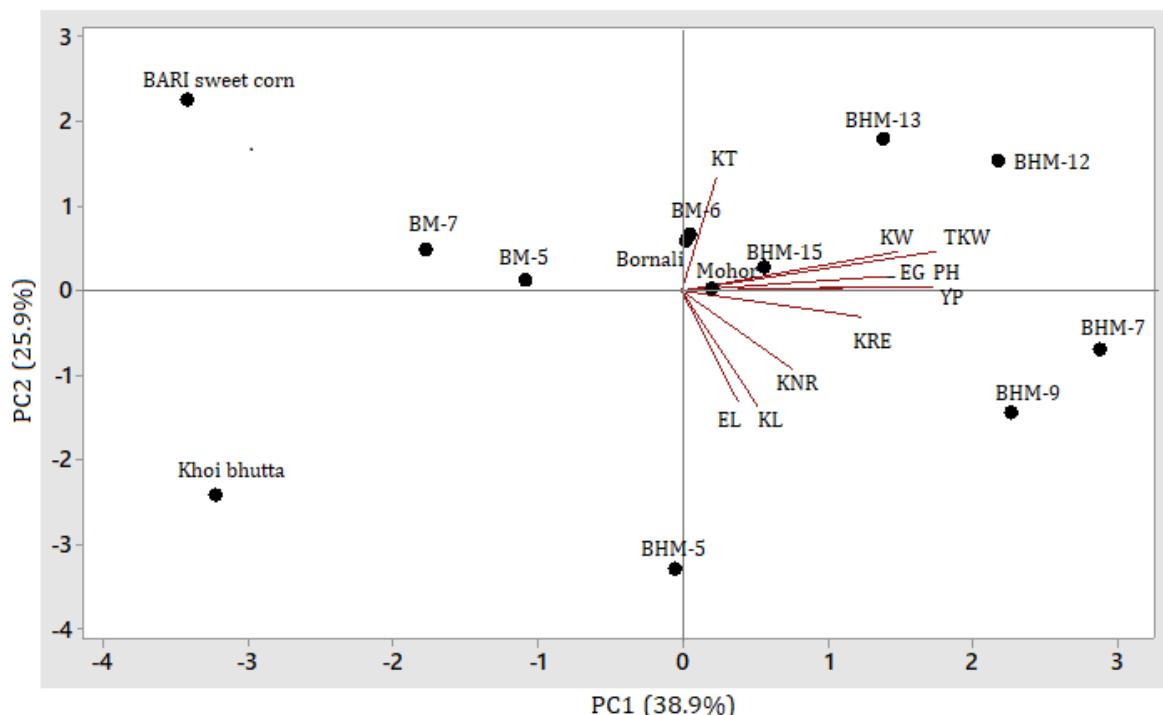
Variables	PC1	PC2	PC3	PC4
Plant height (cm)	0.38	0.022	0.222	0.586
Ear length (cm)	0.098	-0.5	-0.241	-0.434
Ear girth (cm)	0.378	0.068	-0.41	0.338
Kernel rows ear <sup>-1</sup>	0.318	-0.115	-0.545	0.06
Kernel numbers row <sup>-1</sup>	0.195	-0.36	0.531	-0.014
Kernel length (mm)	0.132	-0.522	-0.152	-0.04
Thousand kernel weight (g)	0.448	0.178	0.048	-0.122
Kernel width (mm)	0.381	0.182	0.155	-0.453
Kernel thickness (mm)	0.06	0.514	-0.176	-0.319
Yield plant <sup>-1</sup> (g)	0.444	0.024	0.256	-0.163

The variables that were super imposed as vectors are represented in the principal component biplot (Figure 01) where the relative length of variables represented the relative proportion of the variability in each variable, as well as the biplot, provided the visual comparison among genotypes based on the studied traits (Alvi et al., 2003; Yan et al., 2005). The biplot showed large variability among the genotypes and plant traits. Figure 01 depicts that the genotypes which were similar in their performance with respect to the ten plant traits (variables), showed close proximity with those traits such as BHM-15, BHM-13, BHM-12, BHM-7, BHM-9, BM-6, Bornali and Mohor. Whereas, BARI sweet corn, Khoibhutta, BM-7, BM-5 and BHM-5 were further apart from the traits under study.

The biplot also revealed the correlation among the traits such as kernel width, thousand kernel weight, ear girth, plant height and kernel rows ear<sup>-1</sup> were strongly correlated with yield per plant as those traits showed close lied position (lower angel) with yield per plant which supports our correlation coefficient analysis. The yield contributing traits such as kernel weight, plant height, ear girth etc. in maize genotypes showed similar findings of correlation using PCA analysis (Kumari et al., 2017). The loadings for kernel rows ear<sup>-1</sup>, kernel numbers row<sup>-1</sup>, kernel length and ear length showed positive correlation to PC1 (38.9%) variance but were loaded in the negative region of PC2 (25.9%). This finding suggested that these traits contributed to the highest variability of the dataset accounted for PC1 (38.9%). On the other hand, plant height, ear girth, thousand kernel weight, kernel width and kernel thickness showed correlation to the positive loadings of PC1 and PC2 variances indicating their



contribution to the highest variability for both PC1 and PC2. Therefore, the results indicate that plant height, ear girth, thousand kernel weight, kernel width and kernel thickness were responsible for maximum variation in the maize grain yield (Ferdousi et al., 2020). Similar PCA biplot loadings of maize genotypes regarding their yield performance were reported by (Oyekunle et al., 2015). Therefore, the PCA analysis revealed the differential contribution of different traits in total variation. Moreover, it explicated the interrelationship among the traits and genotypes contributing plant yield showing high diversity among the studied genotypes. This diversity and variability are sources of germplasm improvement in the respective trait leading to better yield performance.



PH= Plant height (cm), EL= Ear length (cm), EG= Ear girth (cm), KRE= Kernel rows ear<sup>-1</sup>, KNR= Kernel numbers row<sup>-1</sup>, KL= Kernel length (mm), TKW= Thousand kernel weight (g), KW= Kernel width (mm), KT= Kernel thickness (mm), YP= Yield plant<sup>-1</sup> (g). The [•] indicates thirteen maize genotypes.

**Figure 01. Principal component biplot: two dimensional orientations of maize genotypes for different plant traits for first two components, PC1 and PC2.**

### Cluster analysis

Cluster analysis has significant aptitude to recognize the homogenous variables at different degrees of similarities in the form of dendrogram (Oyekunle et al., 2015). Thirteen maize genotypes used in the present study were grouped into three clusters based on their performance for ten plant traits (Figure 02). Significant differences among the genotypes for all the traits suggested the presence of variation among the genotypes for all the traits under study contributed to grain yield (Singh et al., 2020).

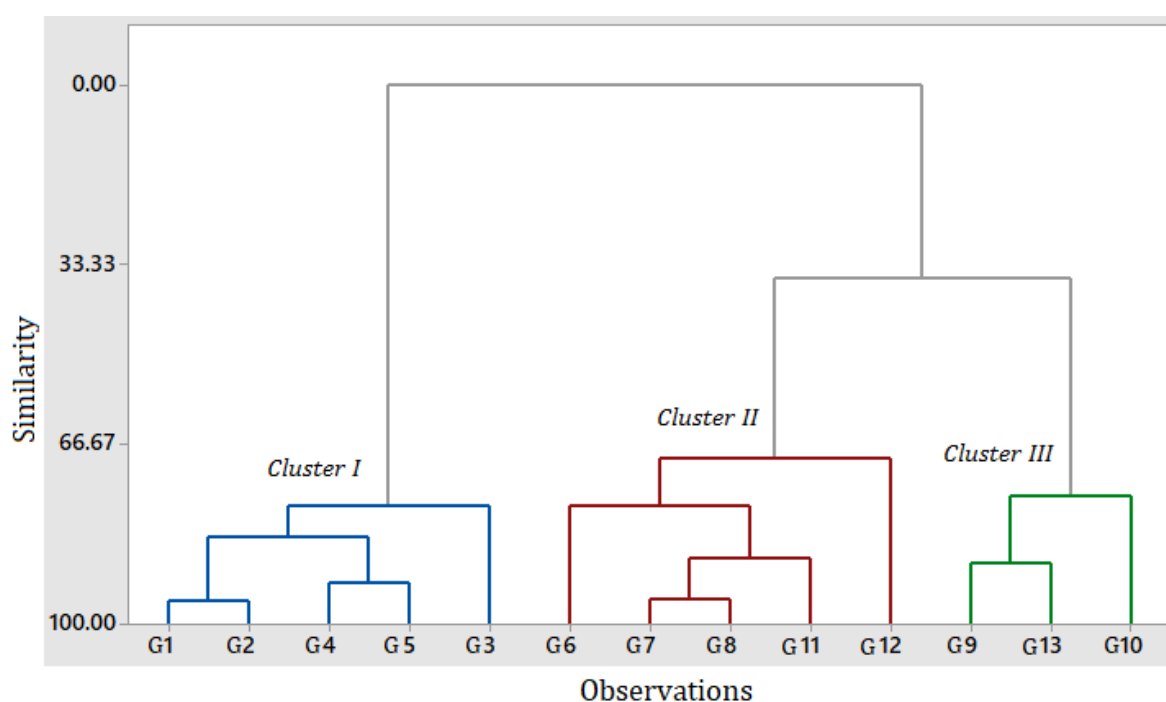
The distribution pattern revealed that five genotypes were in cluster I (Figure 02) which was characterized by the highest mean values of thousands kernel weight (339.67), yield plant<sup>-1</sup> (121.33) and kernel width (9.20) than clusters II and III along with the high mean of plant height (200.47) and kernel numbers row<sup>-1</sup> (37.40) (Table 08). Five genotypes were also assigned in cluster II (Figure 02), dominated by the highest value of plant height (202.33) and kernel numbers row<sup>-1</sup> (38.20) with high mean of thousands kernel weight (254.00) and yield plant<sup>-1</sup> (83.20). Similar observations were reported in maize where the clusters having the highest number of genotypes were characterized by having similar performances of plant traits i.e. plant height, 100-grain weight and grain yield per plant (Kumari et al., 2017; Singh et al., 2017). Cluster III showed the lowest mean values for most of the plant traits except for ear length (16.46) and kernel thickness (4.81) (Table 08) which was comprised of three genotypes (Figure 02). The dendrogram (Figure 02) represents the similarities among the genotypes, clustered in three clusters based on their performance for the studied plant traits. Figure 02 explained more than 75% similarities among the genotypes lied in cluster I (G1, G2, G3, G4 and G5)

and cluster III (G9, G10 and G13), while more than 68% similarities were observed among the genotypes of cluster II (G6, G7, G8, G11 and G12).

**Table 08. Cluster mean for different plant traits among thirteen maize genotypes**

Clusters	PH	EL	EG	KRE	KNR	KL	TKW	KW	KT	YP
I	200.47	16.84	15.57	14.47	37.40	10.47	339.67	9.20	4.92	121.33
II	202.33	15.85	14.59	13.73	38.20	10.53	254.00	7.73	4.51	83.20
III	187.11	16.46	13.22	12.89	33.78	10.00	158.89	7.00	4.81	63.33

PH= Plant height (cm), EL= Ear length (cm), EG= Ear girth (cm), KRE= Kernel rows ear<sup>-1</sup>, KNR= Kernel numbers row<sup>-1</sup>, KL= Kernel length (mm), TKW= Thousand kernel weight (g), KW= Kernel width (mm), KT= Kernel thickness (mm), YP= Yield plant<sup>-1</sup> (g)



G1=BHM-15, G2= BHM-13, G3= BHM-12, G4= BHM-9, G5= BHM-7, G6= BHM-5, G7=Mohor, G8= Bornali, G9= KhoiBhutta, G10= BARI sweet corn, G11= BM-5, G12= BM-6, G13= BM-7

**Figure 02. Dendrogram (Complete Linkage and Euclidean Distance) showing clusters of thirteen maize genotypes.**

#### IV. Conclusion

High heritability along with high genetic advances was observed for plant height, kernel numbers row<sup>-1</sup>, thousand kernel weight and grain yield per plant in maize genotypes under study. Correlation and path analyses showed that plant height, thousand kernel weight, ear girth, kernel numbers row<sup>-1</sup>, kernel width had strong association and possessed positive direct effects on grain yield per plant. These findings of the present study justified the presence of significant relationships between the corresponding plant traits and grain yield, thereby direct selection for these traits would result in reasonable effect on grain yield in maize. The PCA biplot also revealed positive correlations between plant traits i.e. plant height, thousand kernel weight, ear girth, kernel width and yield per plant, as these vectors were aligned at a lower angle. Moreover, PCA and cluster analysis exhibited the interrelationship between the genotypes and their performance regarding the plant traits under study, thus revealed the high level of genetic variation existing in the genotypes and explained the traits contributing to this diversity. PCA analysis also explained that the genotypes BHM-12, BHM-13 and BHM-15 were closely tied with the plant traits leading significant impact on maize yield and would be potential materials for further maize breeding program. Assessment of genetic diversity also provides the breeder an opportunity to identify the gaps in the collection, finding the traits and genotypes for which useful variability is limited and also allow maximizing variation in the collection. Therefore, the present findings of identifying potential yield contributing plant traits along with high level of genetic

diversity among the genotypes would be beneficial for maize genotype characterization, conservation and planning for further maize breeding program for enhanced yield potential.

**Author's contribution:** AH and Aleya Ferdausi (AF) conceptualized and designed the experiment. SI performed the field experiment. SI, AYS and Ashrafi Ferdoush collected and recorded the data. AF and AD performed the data analysis and interpreted the data. SI and AF drafted the manuscript which was critically reviewed by AH and AD.

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