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Variability and traits association in maize (*Zea mays* L.) for yield and yield associated characters

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Abstract

Maize (*Zea mays* L.) is world's third most important cereal crop that has a remarkable productive potential in Bangladesh. In Bangladesh, maize is the second most important cereal crop in terms of production. The selection for high yield with desirable traits depends on the genetic variability in the existing germplasm. Successful breeding programs need adequate genetic variation for selection and improvement based on necessity. The research was conducted in the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh during November 2015 to April 2016. The aim of this study was to evaluate the performance of 20 maize genotypes based on their yield and yield contributing characters to determine existing genetic variability. The extrapolated ANOVA for different yield contributing parameters showed a high degree of variation among the genotypes used. Correlation co-efficient analysis revealed that yield plant^{-1} (g) had positive and significant association with ear girth (cm), 1000-kernel weight (g), yield plot^{-1} (g), grain yield (tha^{-1}) with dry weight. The genotypes differed significantly for most of the phenotypic traits. The phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) in all traits studied indicating that those traits were interacted with the environment. The traits under study expressed wide heritability estimates (26.81% to 99.95%). Among the characters, highest heritability was recorded for 1000-kernel weight (g). High heritability along with high genetic advance was noticed for 1000-kernel weight (g), yield plot^{-1} (g) and grain yield (tha^{-1}). Considering different desirable traits P-12, Popcorn, V$_{90-1}$, 988 were observed as superior genotypes. The data would be useful for proper identification and selection of appropriate parents in breeding programs to develop new maize varieties.

Introduction

Maize (*Zea mays* L.) is a major cereal holding second position after rice in terms of production, in Bangladesh. It is mostly used and traded as a leading feed crop but is also an important staple food in different parts of the world. It is a good source of carbohydrates (18.7g g^{-1} grain) and energy (360 KJ g^{-1}) and rich in other nutritive values. So it can be a supplementary food along with rice and wheat. Maize is a versatile crop due to its multiple roles and uses of maize as feeds, food and industrial raw material (Ahmed, 2013). Maize is the highest produced crop of the world and in Bangladesh the crop is gaining popularity as food and feed with the increasing poultry, dairy and fisheries sector. The crop is holding second position after rice in terms of production. In 2015, maize was produced in 3.5 lac hectare with the production of 23 lac mton with average yield of Maize is 6.6 t ha^{-1} in Bangladesh (FAO, 2016). Maize production for last ten years has been increased by more than 12 times due to its high demand in the local markets. Still the country annually needs more maize kernels to meet up the demand. Improving maize production is considered as one of the most important strategies for food security and livelihoods improvement in developing countries, including Bangladesh (Iqbal *et al.*, 2001; Ababulgu, 2014). However, the changing environmental conditions affect the performance of maize genotypes which requires a rigorous breeding program that needs to take into account the consequences of environment and exploring and developing more competitive maize genotypes. A comparative study of various traits specially those associated with the yield, is useful for the plant breeder to select breeding materials through secondary traits to initiate efficient breeding program. Sujiprihati *et al.*, (2003) suggested different agronomic parameters like estimated means, genotypic-phenotypic variances, heritability and the correlation coefficients are important to select the superior genotypes and to determine the efficiency of a breeding. Genetic improvement in traits of economic importance along with maintaining sufficient amount of variability is always the desired objective in maize breeding programs (Hallauer and Scobs, 1973).

Genetic diversity is the existed variability in the genotypes of the individuals of a population belongs to same species. The variation could prevail in the entire genome, chromosomes, gene or in the nucleotide levels. Maize is both phenotypically and genetically diverse. Genetic variability among individuals in population offers effective selection (Rather *et al.*, 2003). Genetic diversity among maize lines can be examined based on morphological traits (Xia *et al.*, 2005). Grain weight and grain yield; kernel weight and days to maturity, ear height, days to silking, % tryptophan content, cob length and 1000-seed weight (Kadir, 2010); ear length and diameter (Hoque *et al.,* 2008); days to 50% anthesis, days to 50% silk emergence, days to maturity, ear aspects, grain yield, plant height, ear height and number of diseased cobs (Muchie and Fentie, 2016) are variables that can contribute to genetic diversity assessment. Characterization of available maize genotypes based on phenotypes is critical to utilize the resources. Hence, the specific objectives of current research program were to assess the genetic variability of locally available 20 maize genotypes for economically important agronomic traits and to select superior genotypes for applied breeding.

Materials and Methods

Experimental site, materials and design

An experiment was carried out at the field laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh. The duration of the experiment was from November 2015 to April 2016. Twenty locally available maize genotypes were used as experimental materials. Those were: BARI Hybrid Maize 7 (BHM-7), BARI Hybrid Maize 9 (BHM-9), H-981, Popcorn, Elite-1, E-2, E-121, E-155, P-4, P-8, P-12, P-23, P-27, V90-1, V90-2, V90-3, V91, V90-1-1, 891 and 988. The material consisted two BARI released hybrids and 18 advanced lines. The experiment was laid out in a randomized complete block design (RCBD) with three replicates. The maize genotypes were planted. The recommended fertilizer rates used for maize were 200 kg N, 50 kg P, 100 kg K and 40 kg S ha^{-1} (Rahman *et al.,* 2016) and weeding, thinning, irrigation, pesticide etc. were done as and when necessary to ensure the normal plant growth and development.

Data collection and analysis

At field, five randomly selected plants were used for data recording from each plot on the following parameters : emergence percentage (%), days to anthesis (days), plant height (cm), ear height (cm), ear length (cm), ear girth (cm), root lodging (%). After harvesting no. of kernels ear^{-1}, 1000-kernel weight (g), yield plant^{-1} (g), yield plot^{-1} (g) and grain yield (t ha^{-1}) were recorded.

Analysis of variance (ANOVA) and correlation analysis were conducted using SAS software version 9.3 (SAS Institute, 2010).

We extrapolated genotyping and phenotypic variances by utilizing the formula narrated by Johnson *et a*l., (1955). The formula described by Johnson *et al*., (1955) and Hanson *et al*., (1956) were used to calculate heritability in broad sense (h^2_b). Genotypic and phenotypic co-efficient of variations were estimated according to the formula given by Singh and Chaudhary (1985). Estimation of genetic advance was estimated following formula given by Johnson *et al.,* (1955) and Allard (1960). Genetic advance in percent of mean was calculated by the following formula of Comstock and Robinson (1952):

$$\text{GA (\%)} = \frac{\text{GA}}{\text{X}} \times 100$$

Where, GA = Genetic advance, $\bar{X}$ = Population mean, was used to calculate genetic advance in percent of mean.

Results and Discussion

Analysis of Variance:

The results of analysis of variance (ANOVA) of the quantitative traits of the tested genotypes are presented in (Table 1). The analyses of variance revealed that the differences among genotypes for all the traits under study viz., emergence percentage (0.0255), days to anthesis (0.0001), plant height (cm) (<0.0001), ear height (cm) (<0.0001), ear length (cm) (0.0034), ear girth (cm) (0.0066), root lodging (%) (0.004), number of kernels ear^{-1} (0.0148), 1000-kernel weight (g) (<0.0001), yield plant^{-1} (g) (0.004), yield plot^{-1} (g) (<0.0001) and grain yield (t ha^{-1}) (<0.0001) were significant (p-value = 0.05, 0.01, 0.001). The analysis of variance result showed that there were considerable amount of variation between the tested genotypes.

Muchie and Fentie, (2016) also found highly significant variation for days to 50% anthesis, plant height, cob length, ear height, number of cobs per plant, number of grains per row and grain yield. This result is in agreement with the findings of Ahmed, (2013) incase of ear length and diameter. Maximum grain yield (5.19 t/ha) was observed for P-12, whereas the minimum grain yield (1.89 t/ha) was recorded for V90-1-1 (Table 2).

Table 1. Analysis of variance (mean squares) for different characters of twenty maize genotypes

SV	Df	EP	DA	PH	EH	EL	EG	RL	KE	TKW	YP	YPlot	GY
Rep	2	301.67	4.32	1.24	14.54	1.09	0.86	798.77*	2280.32	1.87	238.97	94717.62	0.67
TRT	19	406.67*	19.37***	572.49***	208.23***	4.6**	2.16**	582.92**	4768.09*	16354.51***	2539.59**	250231.29***	1.78***
Error	38	193.77	4.71	10.33	19.61	1.68	0.84	212.78	2085.41	2.92	921.29	21421.53	0.15

Legend, SV=Source of variance; Df=Degrees of freedom; EP=Emergence percentage; DA=Days to anthesis; PH=Plant height (cm); EH=Ear height (cm); EL=Ear length (cm); EG=Ear girth (cm); RL=Root lodging (%); KE=No. of kernel ear^{-1}; TKW=1000-kernel weight (g); YP=Yield plant^{-1} (g); YPlot=Yield plot^{-1} (g); GY=Grain yield (t ha^{-1})
*, **, *** = Significant at 5%, 1%, 0.1% level of probability, respectively

Table 2. Mean performance of maize genotypes for different agronomic traits

GE	EP (%)	DA (days)	PH (cm)	EH (cm)	EL (cm)	ED (cm)	RL (%)	KE	TKW (g)	YP (g)	GY (tha^{-1})
BHM-7	68.33	90	215.33	84.22	15.06	14.18	5.34	361.33	403.08	1578.2	4.21
BHM-9	70	89.67	218.89	61	13.88	13.45	3.03	324	345.73	1547.9	4.13
H-981	71.67	90.5	216.99	74.11	15.03	14.13	3.7	388.67	313.34	1596.8	4.25
Popcorn	66.67	87.17	218.44	76.67	14.79	15.18	17.38	393	416.38	1907.4	5.08
Elite-1	61.67	84.17	217.67	85.78	15.85	14.67	3.03	371.33	277.48	1372.8	3.66
E-2	50	84.17	190.45	73.67	14.41	14.08	22.62	356.33	306.54	1318.4	3.52
E-121	78.33	86.33	187.33	71.78	12.98	13.29	43.52	310	393.56	1734.1	4.62
E-155	51.67	85.17	198.22	81.67	14.43	14.83	13.33	379	373.92	1677.1	4.47
P-4	78.33	85.33	224.33	93.34	17.19	15.92	29.29	439.33	226.16	1296.6	3.46
P-8	86.67	84.67	211.44	85	14.57	13.66	11.11	347.67	360.52	1762.5	4.7
P-12	80	85.5	214	74.67	16.88	15.17	10.25	448.67	345.58	1946.1	5.19
P-23	78.33	86.33	211.89	84.78	15.8	13.97	21.21	422.67	193.30	1405.1	3.75
P-27	63.33	86.33	219.33	88.89	14.25	14.32	50.53	361	397.3	1820.4	4.85
V90-1	78.33	84.83	182.22	72.33	14.38	14.02	18.41	353	347.33	1910.3	5.09
V90-2	86.67	84	217.67	87	13.49	13.53	15.56	306.33	386.34	1628.3	4.34
V90-3	53.33	86.17	203.33	76.78	14.09	13.78	0	342	344.69	1455.8	3.88
V91	88.33	80.33	190.67	74.44	13.56	14.39	21.05	333.67	403.08	1809.6	4.82
V90-1-1	71.67	90.67	183.33	71	11.71	12.1	39.46	319.33	147.77	712.3	1.89
891	58.33	87.33	207.67	80.1	14.46	15.15	27.59	381	326.66	1636.5	4.36
988	65	85.17	222	63.78	14.79	14.89	18.52	380.33	393.74	1837.5	4.9
CV%	19.79	2.52	1.55	5.67	8.88	6.44	77.79	12.47	0.51	9.16	9.09
LSD(0.05)	23.009	3.58	5.31	7.32	2.14	1.52	24.11	75.48	2.83	241.92	0.62
min	50	80.33	182.22	61	11.71	12.1	0	306.33	147.77	712.3	1.89
max	83.33	90.67	224.33	93.34	17.19	15.92	50.53	448.67	416.38	1946.1	5.19
mean	70.33	86.22	207.56	78.05	14.58	14.23	18.75	365.93	335.13	1597.68	4.26

Legend, EP=Emergence percentage; DA=Days to anthesis; PH=Plant height (cm); EH=Ear height (cm); EL=Ear length (cm); EG=Ear girth (cm); RL=Root lodging (%); KE=No. of kernel ear^{-1}; TKW=1000-kernel weight (g); YP=Yield plant^{-1} (g); GY=Grain yield (t ha^{-1})

Correlation co-efficient

The correlation value denotes the nature and extent of association existing between pairs of characters. Correlation is also a measure that indicates traits to be considered to increase yield. In this experiment, some association showed positive significant correlation: yield plant^{-1} (g) with ear girth (cm), 1000-kernel weight (g), yield plot^{-1} (g), grain yield (t ha^{-1}) with dry weight; plant height (cm) with ear length (cm), ear girth (cm), no. of kernel ear^{-1}; ear height (cm) with ear length (cm); ear length (cm) with ear girth (cm), no. of kernel ear^{-1}; ear girth (cm) with no. of kernel ear^{-1}, yield plot^{-1} (g), grain yield (t ha^{-1}) with dry weight; 1000-kernel weight (g) with yield plot^{-1} (g), grain yield (t ha^{-1}) with dry weight; yield plot^{-1} (g) with grain yield (t ha^{-1}) with dry weight (Table 3).

Khodarahmpour (2012) also reported that grain yield (0.68), grains per row (0.74), grains per ear (0.80), ear height (0.46), ear-down leaves (0.40), total leaves (0.58), grain depth (0.81), grain dry matter weight (0.87) and 1000-grain weight (0.56) had significant and positive correlation. This correlation can be used as basis for character selection if similar research is conducted in future using additional morphological traits.

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

	YPlant	EP	DA	PH	EH	EL	EG	RL	KE	TKW	YPlot	GY
YPlant	1	–0.65**	–0.17	0.11	–0.06	0.16	0.49*	–0.16	0.17	0.62**	0.57**	0.57**
EP		1	–0.21	0.02	0.09	0.01	–0.17	0.08	–0.06	–0.002	0.21	0.21
DA			1	0.14	–0.23	–0.16	–0.34	–0.02	–0.02	–0.26	–0.36	–0.36
PH				1	0.34	0.61**	0.49*	–0.31	0.46*	0.13	0.21	0.21
EH					1	0.42*	0.33	0.14	0.31	–0.13	–0.07	–0.07
EL						1	0.79***	–0.34	0.88***	–0.09	0.24	0.24
EG							1	–0.13	0.76***	0.23	0.45*	0.45*
RL								1	–0.12	–0.14	–0.13	–0.13
KE									1	–0.25	0.15	0.15
TKW										1	0.83***	0.83***
YPlot											1	1***
GY												1

Legend, EP=Emergence percentage; DA=Days to anthesis; PH=Plant height (cm); EH=Ear height (cm); EL=Ear length (cm); EG=Ear girth (cm); RL=Root lodging (%); KE=No. of kernel ear^{-1}; TKW=1000-kernel weight (g); YPlot=Yield plot^{-1} (g); GY=Grain yield (t ha^{-1}); YP=Yield plant^{-1} (g)
*, **, *** indicate significant at 5%, 1%, 0.1% level of probability, respectively

Phenotypic and Genotypic variation

The phenotypic variance was separated into genotypic and environmental variances to estimate the contribution of each to the total variation. However, phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits (Table 3). Similar findings were also observed by Bello *et al.*, (2012). The PCV values for root lodging were higher than the rest traits. It indicates on this trait the phenotypic difference among the tasted genotypes is high (Muchie and Fentie, 2016). PCV values for emergence percentage, ear height (cm), ear length (cm), no. of kernel ear^{-1}, 1000 kernel weight (g), yield plant^{-1} (g), yield plot^{-1} (g), grain yield (t ha^{-1}) were medium. It indicates the phenotypic difference among the tested maize genotypes with the above traits is moderate. This result is in agreement with the result of Bello *et al.*, (2012); Golam *et al.*, (2014); Muchie and Fentie (2016). Days to anthesis, plant height (cm), ear girth (cm) had low PCV values. This result is in conformity with the finding of Reddy *et al.*, (2012)**;** Muchie and Fentie (2016) observed low PCV for days to maturity, plant height and days to anthesis. Genotypic coefficient of variation measures the genetic variability with in a character. Genotypic coefficients of variability (GCV) values were low for days to anthesis, plant height (cm), ear girth (cm), no. of kernel ear^{-1}. Medium GCV was observed for emergence percentage, ear height (cm), 1000 kernel weight (g), yield plant^{-1} (g), yield plot^{-1} (g), grain yield (t ha^{-1}). Higher genotypic coefficient of variation (GCV) was recorded for root lodging. Similar results have been reported for days to anthesis and days to silking by Golam *et al.*, (2014), Muchie and Fentie, (2016).

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. Traits such as plant height, ear height, 1000-kernel weight (g), grain yield (t ha^{-1}), yield plot^{-1} (g) were showed exhibited high heritability accompanied with high to moderate genotypic and phenotypic coefficient of variation and genetic advance which indicates that most likely the heritability is due to additive gene effects and for these traits, selection may be effective in early generations. High heritability of those traits indicated that influence of environment on these characters is negligible or low. Therefore, selection can be effective on the basis of phenotypic expression of these traits in the individual plant by implementing simple selection methods. High heritability was observed for plant height, ear height and yield plot^{-1} by Bello *et al.*, (2012). Whereas moderate heritability for no. of kernel ear^{-1}, ear girth, yield plant^{-1} (g), root lodging, ear length, days to anthesis (Table 3). The result is in line with the findings of Lorenzana and Bernardo (2008). The moderate levels of heritability indicated that this trait was moderately influenced by environmental factors.

High heritability does not always indicate a high genetic gain; heritability should be used together with genetic advance in predicting the ultimate effect for selecting superior varieties (Muchie and Fentie, 2016). Bello *et al.*, (2012) recorded higher genetic advance for plant height, number of kernels ear^{-1} and yield plot^{-1}. In the present study high heritability with high genetic advance was found for the trait 1000-kernel weight, yield plot^{-1} and grain yield (t ha^{-1}) which indicated the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generations. This research 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 meanwhile improvement could be achieved through selection of genotypes. However, high heritability was observed for plant height and ear height; the traits could be improved through appropriate breeding techniques, may be by planned hybridization. Effective selection for superior genotypes is possible considering grain yield (t ha^{-1}), yield plot^{-1} (g), 1000-kernel weight (g), plant and ear heights (cm) and can be used as target traits to improve maize grain yield. Variability within the maize genotypes is sufficiently divergent and constitutes potential candidate genotypes on which improvement program can be initiated (Table 4).

Table 4. Genetic parameters of different characters of twenty maize genotypes

Traits	Phenotypic variance (δ^2p)	Genotypic variance (δ^2g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
Emergence (%)	264.74	70.97	23.13	11.98	26.81	8.98	12.77
Days to anthesis	9.59	4.89	3.59	2.56	50.92	3.25	3.77
Plant height (cm)	197.72	187.38	6.77	6.59	94.77	27.45	13.23
Ear height (cm)	82.48	62.87	11.64	10.16	76.23	14.26	18.27
Ear length (cm)	2.68	1.01	11.23	6.87	37.39	1.26	8.65
Ear girth (cm)	1.28	0.44	7.94	4.66	34.37	0.81	5.63
Root lodging (%)	336.16	123.38	97.78	59.24	36.71	13.86	73.93
No. of kernel ear^{-1}	2979.64	894.23	14.92	8.17	30.01	33.75	9.22
1000-kernel weight (g)	5453.45	5450.53	22.04	22.03	99.95	152.04	45.37
Yield plant^{-1} (g)	1460.77	539.43	31.96	19.42	36.93	29.07	24.31
Yield plot^{-1} (g)	97691.45	76269.92	19.56	17.28	78.07	502.68	31.46
Grain yield (t ha^{-1})	0.69	0.54	19.55	17.31	78.36	1.34	31.55

GCV=Genotypic Co-efficient of Variation, PCV=Phenotypic Co-efficient of Variation, GA=Genetic Advance, GA%= Genetic Advance as Percentage of mean

The above findings approved that the studied twenty maize genotypes exhibited adequate genetic diversity. Without diversity further improvement is unattainable. This would ensure the enough chance for better utilization of these maize germplasm for respective desired characters in maize breeding programs.

Conclusion

Without having genetic diversity further varietal improvement is unexpected. The findings suggested that there is ample opportunity for better utilization of the studied maize genotypes for selective desired characters in maize breeding programs as diversity existed in the studied twenty maize genotypes. Considering, all the traits P-12, Popcorn, V90-1 and 988 performed well among the studied genotypes.

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