



Plant Breeding
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Genetic variability, correlation and path co-efficients analyses of selected maize (*Zea mays* L.) genotypes

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ABSTRACT

Twenty-five maize genotypes were evaluated to study the genetic variability, correlations and path co-efficient analyses for yield and yield contributing characters. Analysis of variance for sixteen yield contributing traits showed highly significant variations among the genotypes. The estimates of genetic components for the yield contributing traits showed higher phenotypic coefficient of variation than genotypic co-efficient of variation indicating more environmental influence on the studied traits. Traits under study showed moderate to high heritability. The highest heritability was observed in 1000 kernel weight (79.79), seed numbers ear⁻¹ exhibited the highest genetic advance (55.45) and shoot lodging (223.07) showed the highest genetic advance in percentage of mean. Thousands kernel weight exhibited the highest significant positive correlation (0.746) with yield per plant followed by husk girth (0.620) and ear length (0.432). The negative correlation with yield per plant was observed for days to anthesis, days to maturity and seed numbers per row. Path co-efficient analysis exhibited that the thousands kernel weight had a maximum positive direct effect on grain yield followed by husk girth and ear length. This experiment revealed that the selection based on thousands kernel weight, husk girth and ear length would increase grain yield for yield improvement in maize. Therefore, the research findings would be useful for the identification and selection of traits for future breeding programs of maize.

Keywords: Variability assessment, heritability, genetic advance, traits association, path analysis

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1 Introduction

Maize (*Zea mays* L.) is one of the broadly cultivated cereal crops around the world over extended environmental conditions (Muraya et al., 2017). The crop secures second position in terms of production with total production of 22,72,000 metric tons in 2014-2015 after rice in Bangladesh (BBS, 2016). and is third most

important cereal crop of the world after wheat and rice (Singh, 2017). Besides used as staple food for human consumption, it is used as a basic element of animal feed, starch, oils, flour, sugar, alcoholic beverages and bio-fuel (Kumar et al., 2006). Moreover, it is an important source of carbohydrates and rich in other nutritive values containing vitamin A, vitamin C and other trace elements like magnesium,

potassium, phosphorus and sodium along with fiber (Ranum et al., 2014).

Maize has high productivity and vast genetic potentiality compared to any other cereal crops (Muraya et al., 2017). The improvement of a crop is mainly dependent on the nature and enormity of available genetic variability and heritability. High variability within the existing germplasm is the key driving force for enhanced success of breeding programs. It allows the plant breeder to produce advanced varieties from the existing ones or to develop new varieties (Yared and Misteru, 2016; Meena and Bahadur, 2014). Therefore, knowledge on genetic components of variation along with heritability estimates would provide the better understanding of genetic advance, which provides precise information on selection, is crucial for any breeding programs (Singh, 2017). Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are functional biometric tools for measuring genetic variability Hussain and Mohamad (2017).

Like other crops, a complex chain of interrelating effects of different characters attributes the final yield of maize (Kumar et al., 2017). Therefore, considerable attention should be executed on selection of yield and yield contributing traits. The degree of association between characters as indicated by the correlation coefficients has always been an obliging tool for the selection of desirable characters. Correlation coefficient quantifies the reciprocal relationship between various plant characters on which selection can be performed for yield improvement (Kinfe and Tsehaye, 2015). Path analysis splits the correlation coefficients into direct and indirect effects, a set of dependent variables on the independent variable, which helps in selecting elite genotypes (Singh, 2017). Therefore, the current research objectives were to assess the genetic variability of yield and yield associated traits, to estimate genetic parameters with heritability and genetic advance, and to measure the extent and direction of relationship among the studied variables.

2 Methodology

The field experiment was conducted at the experimental farm (24°43'19.4"N, 90°25'23.8"E) of the Department of Genetics and Plant Breeding (GPB), Bangladesh Agricultural University (BAU), Mymensingh, Bangladesh. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Seeds were sown in 3.5 m long row considered as a plot. Block to block distance was 1 meter and row to row distance was 0.60 meter. Plot size was 1.75 m² containing 10 to 15 plants. Twenty Maize genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur; and five hybrids generated at the Depart-

ment Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh were also used in this study (Table 1).

At the time of final land preparation, fertilizers and manures were applied following doses described as Rahman et al. (2016). All necessary intercultural operations such as irrigation, weeding, staking were performed.

Harvesting was performed based on variable maturity time of different genotypes. Data were collected on sixteen yield contributing traits *i.e.* days to anthesis (days), plant height (cm), ear height (cm), root lodging (%), shoot lodging (%), days to maturity (days), ear length (cm), ear girth (cm), husk girth (cm), grain moisture (%), kernel rows ear⁻¹, kernel numbers row⁻¹, seed numbers ear⁻¹, 1000 kernels weight (g), yield plant⁻¹ (g), yield ha⁻¹ (ton). Data were collected for this study on individual plant basis from five randomly selected plants. Days to anthesis (days) was counted as the number of days from planting to 50% of plants shedding pollen on half of the tassel of the plot. Plant height was measured as the distance from soil surface to the top of the plants and ear height was the distance from soil surface to the base of the top ear attachment and measured in centimeters. Root lodging was the percentage of plants in a plot leaning at an angle greater than 30 °C from vertical while stalk lodging was measured as the percentage of plants in a plot with stalks broken at or below the top ear. Lodging was counted before harvest and analyzed as percentages to total stands per plot. Days to maturity (days) was considered as the number of days from planting to when plants of the plots attained maturity. Ear girth was measured in three different places of the ear and averaged in cm while husk girth was measured in cm in three different areas top, middle and base of the husk after removing the kernels and averaged. Grain moisture refers percent moisture at harvest. Grain yield (ton ha⁻¹) was converted from yield plot⁻¹.

Analysis of variance was performed using the statistical software Statistical Analysis System version 9.3 (SAS). Genotypic and phenotypic variances were estimated according to the formula given by Johnson et al. (1955). Heritability in broad sense (h^2_b) was estimated according to the formula [Equation (1)] suggested by Johnson et al. (1955) and Hanson (1961).

$$h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100 \quad (1)$$

where, σ^2_g and σ^2_p are genotypic and phenotypic variances, respectively.

Phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Morris (1997).

Table 1. List of maize genotypes and their sources used in the experiment

Sources	Genotypes
BARI, Gazipur	Elite-1, E-2, E121, E-155, H981, P4, P8, P12, P23, P27, Popcorn, V90-1, V90-2, V90-3, V90-1-1, 891, 988, 991, BHM-7, BHM-9
BAU, GPB Field Laboratory	H981 x E121, P27 x V90-2, 991 x V90-2, Popcorn x E155, E121 x V90-3

Table 2. Analysis of variance (mean square) for different characters of 25 genotypes of maize

SV	df	DA	PH	EH	RL	SL	DM	EL	EG	HG	%M	KR	KN	SN	TKW	YPP	YTH
Rep.	2	0.04	411.76	1.71	0.037	0.128	1.96	0.53	0.66	0.12	0.08	0.43	0.03	105.62	673.37	76.72	0.36
Geno.	24	10.73**	307.69**	104.77**	147.94**	44.29**	10.75**	1.39**	1.01**	1.32**	21.61**	3.12**	3.67**	3268.72**	4810.51**	152.89**	1.59**
Error	48	2.66	137.36	3.18	0.1	0.18	2.37	0.6	0.4	0.15	0.29	0.33	0.73	339.34	2005.81	32.1	0.144

** Indicate significance at 0.01% level of probability. SV = source of variation, Rep. = replication, Geno. = genotype, DA = days to anthesis (days), PH = plant height (cm), EH = ear height (cm), RL = root lodging (%), SL = shoot lodging (%), DM = days to maturity (days), EL = ear length (cm), EG = ear girth (cm), HG = husk girth (cm), %M = moisture %, KR = kernel rows ear⁻¹, KN = kernel numbers row⁻¹, SN = seed numbers ear⁻¹, TKW = 1000 kernels weight (g), YPP = yield plant⁻¹ (g), YTH = yield ha⁻¹ (ton)

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \quad (2)$$

where, GCV , σ_g^2 and \bar{X} are genotypic coefficient of variation, genotypic variance, and population mean, respectively.

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100 \quad (3)$$

where, PCV , σ_p^2 and \bar{X} are phenotypic coefficient of variation, phenotypic variance, and population mean, respectively.

$$GA = h^2_b \cdot K \cdot \sigma_p \quad (4)$$

where, GA = genetic advance, h^2_b = heritability, K = selection differential, the value of which is 2.06 at 5% selection intensity, and σ_p = phenotypic standard deviation as given by Johnson et al. (1955) and Allard (1960).

The phenotypic correlations were estimated by the formula suggested by Miller et al. (1958).

$$r_{p(x1.x2)} = \frac{CoV_{p(x1.x2)}}{\sqrt{\sigma_{p x1}^2 \cdot \sigma_{p x2}^2}} \quad (5)$$

where, $r_{p(x1.x2)}$ = phenotypic correlation, $CoV_{p(x1.x2)}$ = phenotypic covariance between the trait $x1$ and $x2$, $\sigma_{p x1}^2$ = phenotypic variance of the trait $x1$, $\sigma_{p x2}^2$ = phenotypic variance of the trait $x2$.

Correlation co-efficient were further portioned into components of direct and indirect effects by path co-efficient analysis, developed by Wright (1921) and later described by Dewey and Lu (1959). The equation is as follows:

$$r_{yi} = P_{yi} + \sum_{i'=1, i' \neq i}^k r_{ii'} P_{yi'} \quad \text{for } i \neq 1 \quad (6)$$

where, r_{yi} = correlation coefficient between the i -th causal variable (X_i) and effect variable (y), $r_{ii'}$ = correlation coefficient between the i -th and i' -th causal variables, P_{yi} = path coefficient (direct effect) of the i -th causal variable (X_i), and $r_{ii'} P_{yi'}$ = indirect effect of the i -th causal variable via the i' -th causal variable.

3 Results and Discussion

The analysis of variance (ANOVA) showed the significant variation among maize genotypes for all yield contributing characters under study (Table 2). Therefore, data were considered for correlation coefficient (Table 4) and path coefficient (Table 5) analyses.

Previous study showed that the analysis of variance of different genotypes of maize for different agronomic traits were significant for treatment whereas it was non-significant for replication (Rahman et al., 2015), which supports our findings. Significant variation among maize genotypes for plant height, ear length, ear height, ear girth, kernel numbers, rows number, 1000 kernels weight, days to maturity, days to silking and yield was also reported Shahrokhi et al. (2013); Ahmed (2013). A wide range of variations was present among the studied genotypes (Table 3). Variation in the germplasm collection of maize is an opportunity for breeders to improve traits of interest through selection, hybridization and recombination of desired genotypes (Ahmed, 2013).

The genetic parameters viz. genotypic variances, phenotypic variances, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability estimates, genetic advance and predicted genetic advance as percent of mean for characters studied are presented in Table 3. It was observed that the phenotypic variances (σ_p^2) in general were higher than genotypic variances (σ_g^2) for all the traits. However, the differences were very low for most of the traits, indicating low environmental

Table 3. Estimates of genetic parameters of sixteen different characters of 25 maize genotypes

Characters	σ^2_g	σ^2_p	GCV (%)	PCV (%)	Heritability (%)	GA	GA (% of mean)
DA	42.69	63.35	1.8	2.54	50.22	2.39	2.63
PH	256.78	394.14	4.67	8.63	49.24	8.39	5.2
EH	33.86	37.05	15.65	16.37	77.41	11.46	30.83
RL	49.28	49.28	25.4	25.5	59.79	14.45	196.33
SL	14.7	14.88	28.96	29.63	48.78	7.85	223.07
DM	2.79	5.17	1.05	1.43	54.01	2.53	1.59
EL	15.26	19.17	23.24	19.86	70.5	0.59	3.68
EG	2.6	3.7	20.06	16.26	73.87	0.54	3.67
HG	0.39	0.54	6	7.04	72.64	1.1	10.53
M	7.11	7.4	16.91	17.25	66.09	5.38	34.14
KR	0.93	1.26	7.4	8.6	74.07	1.71	13.12
KN	0.98	1.71	5.17	6.82	57.54	1.55	8.08
SN	1976.46	2315.8	13.26	15.39	74.21	55.45	23.52
TKW	2934.9	3140.71	28.02	31.23	79.79	35.51	9.32
YPP	40.26	72.36	8.09	10.85	76.82	9.75	12.43
YTH	0.48	0.63	14.38	16.39	77	1.25	25.99

DA = days to anthesis % (days), PH = plant height (cm), EH = ear height (cm), RL = root lodging (%), SL = shoot lodging (%), DM = days to maturity (days), EL = ear length (cm), EG = ear girth (cm), HG = husk girth (cm), %M = moisture %, KR = kernel rows ear⁻¹, KN = kernel numbers row⁻¹, SN = seed numbers ear⁻¹, TKW = 1000 kernels weight (g), YPP = yield plant⁻¹, (g), YTH = yield ha⁻¹ (ton) σ^2_g = genotypic variance, σ^2_p = phenotypic variance, GCV = genotypic coefficient of variance, PCV = phenotypic coefficient of variance, GA = genetic advance, GA (%) = genetic advance in percentage of mean

Table 4. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for 25 maize genotype

	DA	PH	EH	RL	SL	DM	EL	EG	HG	M	KR	KN	SN	TKW
YPP	-0.168	0.241	0.249	0.052	0.069	-0.209	0.432*	0.235	0.620***	0.058	-0.065	0.311	-0.308	0.746***
DA		-0.440*	-0.332	-0.264	-0.27	0.989***	0.158	-0.22	-0.068	-0.061	0.085	-0.333	-0.049	-0.326
PH			0.719***	0.369	0.354	-0.459*	0.068	0.094	0.311	0.217	0.219	0.061	0.002	0.292
EH				0.286	0.294	-0.357	0.095	-0.21	0.271	0.067	-0.196	0.321	-0.152	0.291
RL					0.986***	-0.294	-0.325	0.015	0.032	0.031	0.013	-0.072	-0.116	0.046
SL						-0.296	-0.274	0.047	0.04	0.023	0.033	-0.003	-0.113	0.059
DM							0.149	-0.24	-0.053	-0.041	0.086	-0.347	-0.023	-0.361
EL								0.531**	0.139	0.11	0.309	0.326	0.278	0.442*
EG									0.118	0.187	0.447*	0.294	0.5312**	0.33
HG										0.036	-0.048	0.195	-0.152	0.351
M											-0.132	-0.034	0.084	0.087
KR												-0.109	0.582**	0.007
KN													0.207	0.242
SN														-0.079

* Indicates significant at 0.05 probability, ** Indicates significant at 0.01 probability, *** Indicates significant at 0.001 probability, DA= days to anthesis % (days), PH= plant height (cm), EH= ear height (cm), RL= Root lodging (%), SL= Shoot lodging (%), DM= Days to maturity (days), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), M= (%) Moisture, KR= Kernel rows ear⁻¹, KN=Kernel numbers row⁻¹, SN=Seed number ear⁻¹, TKW= 1000 kernels weight (g) and YPP = yield plant⁻¹ (g)

Table 5. Phenotypic path coefficient analysis showing direct and indirect effects of different characters on yield of maize

	DA	PH	EH	RL	SL	DM	EL	EG	HG	M	KR	KN	SN	TKW	YPP
DA	2.125	0.131	0.079	-0.509	0.481	-2.484	0.094	0.089	-0.042	-0.011	0.024	-0.07	0.016	-0.093	-0.168
PH	-0.935	-0.297	-0.172	0.724	-0.624	1.154	0.041	-0.036	0.186	0.039	0.065	0.013	0	0.082	0.241
EH	-0.701	-0.214	-0.239	0.568	-0.517	0.903	0.053	0.085	0.162	0.013	-0.059	0.067	0.048	0.082	0.249
RL	-0.552	-0.11	-0.069	1.957	-1.765	0.728	-0.194	-0.008	0.018	0.005	0.003	-0.015	0.038	0.014	0.052
SL	-0.574	-0.104	-0.069	1.938	-1.783	0.753	-0.159	-0.02	0.024	0.004	0.009	0	0.035	0.017	0.069
DM	2.104	0.136	0.086	-0.568	0.535	-2.509	0.088	0.097	-0.03	-0.007	0.027	-0.074	0.006	-0.102	-0.209
EL	0.34	-0.021	-0.021	-0.646	0.481	-0.376	0.587	-0.214	0.084	0.02	0.092	0.07	-0.089	0.124	0.432*
EG	-0.467	-0.027	0.05	0.039	-0.089	0.602	0.311	-0.403	0.072	0.034	0.133	0.061	-0.169	0.093	0.235
HG	-0.149	-0.092	-0.064	0.059	-0.071	0.125	0.082	-0.048	0.599	0.007	-0.015	0.04	0.048	0.099	0.620***
% M	-0.127	-0.065	-0.017	0.059	-0.036	0.1	0.065	-0.077	0.024	0.179	-0.038	-0.006	-0.026	0.025	0.058
K R	0.17	-0.065	0.048	0.02	-0.053	-0.226	0.182	-0.181	-0.03	-0.023	0.295	-0.023	-0.185	0.003	-0.065
KN	-0.701	-0.018	-0.076	-0.137	0	0.878	0.194	-0.117	0.114	-0.005	-0.032	0.211	-0.067	0.068	0.311
SN	-0.106	0	0.036	-0.235	0.196	0.05	0.164	-0.214	-0.09	0.014	0.171	0.044	-0.319	-0.023	-0.308
TKW	-0.701	-0.086	-0.069	0.098	-0.107	0.903	0.258	-0.133	0.21	0.016	0.003	0.051	0.026	0.282	0.746***

Residual effect = 0.099, Bold diagonal values are direct effects and off diagonal values are indirect effects

* Indicates significant at 0.05 probability, ** Indicates significant at 0.01 probability, DA= days to anthesis % (days), PH= plant height (cm), EH= ear height (cm), RL= Root lodging (%), SL= Shoot lodging (%), DM= Days to maturity (days), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), M= (%) Moisture, KR= Kernel rows ear⁻¹, KN=Kernel numbers row⁻¹, SN=Seed number ear⁻¹, TKW= 1000 kernels weight (g) and YPP = yield plant⁻¹ (g)

effect on the expression of those traits except high differences indicating high environmental influence on plant height, seed numbers ear⁻¹, 1000 kernels weight (g), and yield plant⁻¹ (g). The estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) also showed similar results of higher PCV (%) than GCV (%) for all traits under study (Table 3).

Most of the traits showed high heritability (above 70%) such as ear height, root lodging, shoot lodging, husk girth, moisture (%), kernel rows ear⁻¹, seed numbers ear⁻¹, yield plant⁻¹, yield ha⁻¹. The highest heritability was observed in 1000 kernel weight (79.79) followed by yield ha⁻¹ (77.00) and yield plant⁻¹ (76.82). And the highest genetic advance (55.45) was observed in seed numbers ear⁻¹ and high genetic advance in percentage of mean was observed in root lodging (196.33) and shoot lodging (223.07) (Table 3).

The 1000 kernels weight and seed numbers ear⁻¹ showed high phenotypic variance with low genotypic variance. Heritability for these traits was high with high genetic advance. Similar findings for these traits in maize genotypes were observed in several studies (Rahman et al., 2015; Singh, 2017). Heritability was higher with low genetic advance and high genetic advance in percentage. High to moderate heritability with moderate genetic advance for several yield traits has been reported in maize genotypes (Anshuman et al., 2013), which is in accordance with our findings. Yield ha⁻¹ showed slightly higher phenotypic variance than genotypic variance, high heritability with low genetic advance but high genetic advance in mean percentage (Olakojo and Olaoye, 2005). Days to maturity and kernel rows ear⁻¹ showed low PCV and GCV and high heritability with low genetic advance. Similar findings were observed earlier in maize geno-

types (Kinfe and Tsehaye, 2015; Azad et al., 2012).

Phenotypic variance for ear length was slightly higher than the genotypic variance. In the present study, heritability was higher than most of the traits with low genetic advance, which made the traits difficult for improvement through selection. Rahman et al. (2015), also observed high heritability combined with low genetic advance for the yield contributing traits in maize. High to moderate heritability with moderate estimates of genetic advance for grain yield plant⁻¹ and plant height was also observed in maize (Kumar et al., 2017; Anshuman et al., 2013). Genetic advance as percentage along with heritability for plant height were higher showing that these parameters were under the control additive genes reported by (Rafique et al., 2004).

Relationship between morphological and qualitative traits of maize has been studied through correlation coefficient analysis and results are represented in Table 4. Correlation analysis was performed among fourteen characters in all possible combinations to know the nature of relationship among them. In the phenotypic correlation assessment, nine associations showed significant positive correlations viz. plant height and ear height (0.719), root lodging (%) and shoot lodging (%) (0.986), days to anthesis and days to maturity (0.989), ear length and ear girth (0.531), ear girth and kernel rows ear⁻¹ (0.447), ear girth and seed number ear⁻¹ (0.531), kernel rows ear⁻¹ and seed number ear⁻¹ (0.582), ear length and 1000 kernels weight (0.442). In addition, ear length (0.432), husk girth (0.620) and 1000 kernels weight (0.746) showed significant positive association with yield plant⁻¹ (Table 4) which suggest the lower environmental influence on additive genetic model (Afrin et al., 2017). Positive correlation of these traits with yield plant⁻¹ suggesting the need of more emphasis on these traits

for increasing the grain yield in maize. Similar findings were reported in several studies (Singh, 2017; Rahman et al., 2015). In addition, two associations, days to anthesis and plant height (0.440), and plant height and days to maturity (0.459) showed significant negative correlations. Most of the traits showed positive correlations with yield plant⁻¹ except days to anthesis, days to maturity, kernel rows ear⁻¹ and seed number ear⁻¹ (Table 4). The presence of those negative and non significant correlations among the traits could suggest the inherent relationships among the genotypes under study (Afrin et al., 2017).

Similar correlations have been reported in yield contributing traits of maize. As for example, it was revealed that ear girth had significant correlation with yield (Beiragi et al., 2011). Grain yield showed positive correlation with plant height, ear height, ear length, ear girth, kernel numbers row⁻¹, 100 kernels weight (Hussain and Mohamad, 2017; Ghimire and Timsina, 2015). Positive significant correlation has been reported between plant height and yield plant⁻¹ (Salami et al., 2007). Plant height showed significant positive correlation with ear height (Bello et al., 2010).

Ear height showed a positive significant association with, ear length and number of kernels row⁻¹ (Najeeb et al., 2009). Ear height also showed significant negative correlation with number of kernels row⁻¹, and 100 kernels weight (Sadek et al., 2006). Ear length had a positive significant association with ear girth, number of kernels row⁻¹, kernel rows ear⁻¹, 100 Kernels weight and grain yield (Abou-Deif, 2007). Kinfe and Tsehaye (2015) revealed that grain yield was positively correlated with ear length and diameter, ear height and plant height. Plant height, ear height, ear length, ear girth, number of kernel rows ear⁻¹, kernel numbers row⁻¹, ear weight and 1000 seeds weight showed positive correlation with grain yield in maize (Ghimire and Timsina, 2015).

The path co-efficient analysis involves a method of partitioning correlation co-efficient into direct and indirect effects through different pathways. Yield per plant was considered as a response variable and plant height, days to anthesis, ear height, ear length, root lodging, shoot lodging, ear girth, days to maturity, grain moisture, kernel rows ear⁻¹, kernel numbers row⁻¹, seed numbers ear⁻¹, 1000 kernel weight were considered as causal variables (Table 5). The results revealed that plant height, ear height, ear length, root lodging, shoot lodging, ear girth, grain moisture, kernel numbers row⁻¹ and 1000 kernel weight were positively associated with yield per plant (Table 5). Similar findings of positive association of plant height, ear height, ear length, ear girth, 100 seed weight, days to anthesis and number of seeds row⁻¹ with grain yield were observed in maize (Singh, 2017; Kumar et al., 2006; Rafique et al., 2004). Kernel numbers row⁻¹ and kernel rows ear⁻¹ also showed positive correlation with grain yield reported by Kashiani and Saleh

(2010). The phenotypic residual effect of 0.099 indicates the fourteen parameters of this study explain nearly 90% of the total variabilities existed in yield. The similar findings of having genotypic (0.3302) and phenotypic (0.5547) residual effects in maize was reported by Raghu et al. (2011).

4 Conclusion

Genetic parameters estimated in this study indicated scope for improvement of maize yield through selection using genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) that are of great importance for developing efficient breeding programs for maize. Results exhibited the highest GCV and PCV values for shoot lodging, root lodging, (%) moisture, and yield ha⁻¹ (ton) and the lowest for plant height, days to maturity, ear length and ear girth. The experiment showed low to high heritability ranges from 48.78 to 79.79%. The highest genetic advance was estimated in shoot lodging while the lowest value recorded in days to maturity. Therefore, the estimated genetic variation of yield contributing characters obtained in this study reveals that the materials could be a good source for breeders to exploit desirable allelic effects, transgressive segregants, and heterosis to improve yield in maize. The present study also exhibited several yield contributing traits and their correlation as well as their direct and indirect partitioning to the seed yield per plant such as ear height, shoot lodging, days to maturity, ear girth, husk girth, kernel rows ear⁻¹, seed number ear⁻¹, 1000 kernels weight and yield plant⁻¹. These yield influencing traits can also be considered for predicting yield thus, helpful for selecting better genotypes to accelerate breeding programs to improve the grain yield of maize.

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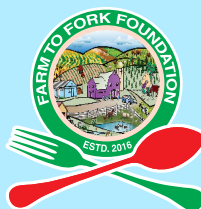
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