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Studies of Heritability, Genetic Parameters, Correlation and Path Coefficient in Elite Maize Hybrids

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A total of forty eight maize hybrids produced through a line by tester mating design with two checks of BH-546 and BH-547 were evaluated at Bako National Maize Research Center on station under rain fed condition in 2013 using alpha lattice design with two replications to determine the heritability, genetic advance, correlation and genetic parameters governing the inheritance of grain yield and related agronomical traits. Knowledge of the magnitude of genetic variability, heritability and genetic gains in selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes. The characters days to anthesis and silking, plant height, ear height, number of seeds per row, number of kernel rows per ear, ear length and diameter, 100 seed weight, and grain yield revealed higher values of heritability. High genetic advance coupled with heritability was observed for plant height, grain yield and number of kernel rows per ear. Thus selection based on these traits will be effective in maize breeding program. Genotypic and phenotypic correlation study among days to anthesis and silking showed highest positive significant association. Grain yield was positively and strongly correlated with ear length and diameter, ear height and plant height. The positive relationships observed in this study imply that the desirable traits in these hybrids could be exploited in further breeding activities for the development of composites and synthetics for the resource constrained maize farmers who cannot access hybrid seeds every year. The highest direct positive effect was obtained for ear diameter, days to 50% anthesis, anthesis silking interval, ear length and plant height, these traits were the most important yield contributing factors and an attempt should, therefore, be made for an effective selection of these traits.

Keywords: Correlation, Genetic Advance, Heritability, Maize Path coefficient Analysis

INTRODUCTION

Maize (Zea mays L.) is a sturdy, annual plant of North American origin belonging to Poaceae sub-family Maydeae. It is a very versatile crop growing in all sorts of altitudinal and fertility conditions. Maize also plays an important role in the world economy and is valuable ingredient in manufactured items that affect a large proportion of the world population (Alvi *et al*., 2003). Hybrid varieties of maize have been commercially exploited in different cereal leading countries of the world because it has a greater genetic potentiality compared to synthetic and composite varieties. The area and production of maize is increasing day by day in Ethiopia and it continues to expand rapidly in a good average rate of per year increment (CSA, 2012). Despite of staple food of maize in Ethiopia, its average yield is incomparable with world average yield and less than to meet the food requirements of increasing population growth in Ethiopia.

Correlation coefficient analyses help researchers to distinguish significant relationship between traits. Correlation and path coefficient analyses can assist to determine certain characters to be used in the improvement of the complex character such as yield (Kusaksiz, 2010). The genetic improvement of yield and its component depends up on the nature and the magnitude of variability present in genotypes. Most of the characters of breeders' interest are complex and polygenically controlled. A successful selection program depends not only on heritability of desirable characters but also on the information on association among various yield component characters and their association with grain yield (Abdurakhmonov, 2008). High heritability is associated with additive gene effect where as low heritability is due to dominance and epistasis. Consideration of genetic relationships between important attributes in exploiting genetic populations through breeding and directed selection is essential, primarily to understand how changes made by selecting one character may cause changes in others (Tyagi and Khan, 2010). Breeding program depends mainly on the direction and magnitude of the association between yield and its components that provide basic information which was useful as indicators of more important ones under consideration and separate correlation relationships as a result selection will be more affective (Agarma, 2006).

Path coefficient which is a standardized partial regression coefficient (Wright, 1921) specifies the causes and effects and measures the relative importance of each variable. So, correlations in combination with path coefficient analysis are an important tool to find out the association and quantify the direct and indirect influences of yield contributing characters on grain yield. The estimates of path coefficient analysis are important for better understanding of the crop. It gives specific measures of direct and indirect effect of each component character under seed yield (Singh and Singh, 1974).

Accordingly, the present study on genetic analysis for grain yield and yield related traits improvement in selected maize hybrids was carried out with the objective of generating information on heritability, correlation and to investigate extent of character association as well as path coefficient analysis between yield and its attribute in order to select superior genotypes among the material. Hence, the goal of present study were proposed to determine the usefulness of heritability, genetic advance as well as to analyze the associations between grain yield and related characters to help as indicators in predicting yield and setting selection criteria in maize breeding.

MATERIAL AND METHODS

The Genotypes, Study Area and Experimental Design

The experiment material for the present investigation comprised of forty eight F1 hybrids that were developed line x tester mating schemes along with two standard check varieties namely: L1, L2, L3, L4, L5, L6, L7 and L8 and six testers namely T1, T2, T3, T4, T5 and T6 including two checks BH-546 and BH-547 (Table 1) were studied in alpha lattice design with two replications at the field of Bako National Maize Research Center, under rain fed condition in 2013 main season. Each plot consisted of one row with 5.1 m length a spacing of 75 cm x 30 cm was adopted.

Data Collection

Observation was recorded on plot basis and on selected five plants in each genotype for twelve important characters. These characters were days to 50 percent anthesis and silking, days to >75 percent maturity, plant height, ear height, ear length, ear diameter, ear per plant, number of seeds per row, number of seeds row per cob, 100 seed weight and grain yield. The mean of plot observed and five plants of each genotype in each replication were used for statistical analysis. The analysis of variance, correlations, estimates of heritability and genetic advance were calculated for all pairs of characters.

Statistical Analysis

Phenotypic and Genotypic Correlation

Phenotypic and genotypic correlations were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae (Robinson and Comstock, 1952):

Genotypic coefficient variation (GCV) = $\frac{\sqrt{\sigma 2\text{g}}}{G.mean} * 100$

Genotypic variance (σ^2_g) = $\frac{msg - mse}{r}$

MSg and MSe = genotype and error mean sum of square and r = Number of replication

Phenotypic variance (σ^2_{ph}) = $\sigma^2_g + \sigma^2_e$

Environmental variance (σ^2_e) = MS_e

Phenotypic Coefficient of Variation (PCV) = $\frac{\sqrt{\sigma 2\text{ph}}}{G.mean}$*100

Table 1. Pedigree history and mean of morphological characters of maize inbred lines

Parents	Pedigree	AD	SD	MD	AS	PH	EH	El	EPP	Ewt	NRE	NKR	100kwt	GY_tha
L1	SZsyyna 99F2-7-2-1-1	72.5	74.4	158.8	1.9	260.6	129.0	18.9	1.2	0.17	13.8	38.2	25.6	9.2
L2	ILO' 003E-47-2-3-1-1	71.9	72.8	158.5	0.9	273.6	129.1	18.2	1.1	0.19	14.2	38.2	31.3	10.3
L3	30H83-7-1-3-1-1-1-1	73.5	74.3	155.8	0.8	283.2	139.6	18.0	1.4	0.17	16.9	39.8	20.3	10.2
L4	Gibe-1-20-2-2-1-1-1	71.8	72.4	156.8	0.7	283.7	136.8	19.0	1.2	0.22	14.7	39.0	33.7	10.9
L5	POOL 9A -128-5-1-1-1-1	71.3	72.3	156.4	1.0	263.3	121.7	17.1	1.0	0.18	15.4	37.8	26.2	7.2
L6	Gibe-1-91-1-1-1-1	73.8	74.7	157.8	0.9	277.9	149.3	18.2	1.2	0.20	15.2	38.0	28.3	11.3
L7	POOL 9A-4-4-1-1-1	70.4	73.2	156.9	2.8	272.4	133.1	17.7	1.1	0.18	15.1	39.5	27.4	9.3
L8	Kuleni320-2-3-1-1-2-1-1	72.2	72.5	156.4	0.3	293.8	155.9	18.4	1.1	0.19	15.2	37.6	30.5	10.6
T1	30H83-5-1-1-1-1-1	72.1	73.8	159.8	1.7	277.3	132.7	18.1	1.2	0.19	15.3	38.5	26.2	9.9
T2	ILO'00E-1-9-1-1-1-1-1	73.9	74.9	157.6	0.9	279.8	141.8	18.0	1.3	0.17	15.5	36.7	26.0	11.0
T3	DE-78-Z-126-3-2-2-1-1-1(g)	69.8	70.4	155.3	0.6	259.6	133.8	17.9	1.0	0.19	15.2	39.0	26.8	9.6
T4	DE-78-Z-126-3-2-2-1-1-1(P)	70.2	70.9	155.1	0.8	266.7	132.2	18.4	1.2	0.18	14.3	39.9	27.2	9.5
T5	30H83-5-1-2-1-1-1-1-1	73.6	75.1	158.7	1.4	280.6	137.8	18.4	1.1	0.18	14.9	39.7	28.6	9.4
T6	GIBE-1-178-2-1-2-1	73.3	74.8	156.5	1.5	292.4	142.4	18.4	1.2	0.20	15.1	37.3	32.7	9.8
G.mean		72.2	73.3	157.2		276.1	136.8	18.2	1.2	0.19	15.1	38.5	27.9	9.9
L.mean		72.2	73.3	157.2	1.2	276.1	136.8	18.2	1.2	0.19	15.1	38.5	27.9	9.9
T.mean		72.2	73.3	157.2	1.2	276.1	136.8	18.2	1.2	0.19	15.1	38.5	27.9	9.9
F-test		**	**	*	*	**	**	**	*	*	**	ns	*	*
CV%		2.2	2.1	1.8	95	3.7	5.5	5.1	18	3.3	12.60	6.5	15.1	9.7
Max.		73.9	75.1	159.8	2.8	293.8	155.9	19.0	1.4	5.0	0.22	39.9	33.7	11.3
Min.		69.8	70.4	155.1	0.3	259.6	121.7	17.1	1.0	4.5	0.17	36.7	20.3	7.2

Note: AD=50% anthesis date, SD=50% silking date, DM = days to > physiological maturity, PH = plant height, EH= ear height, EL = ear length, EPP = ears per plot, Ewt = ear weight, NRE = Number of Kernel rows per ear, NKR = number of kernels per row, 100KWt= hundred kernels weight, GY_tha = grain yield (ton per hectar),*,**= significant at 5% and 1% level of probability, ns= no significant, G.mean = grand mean, L.mean = line (female parent) mean, T.mean = tester(male parent) mean.

Where, σ_g and σ_{ph} are genotypic and phenotypic standard deviations (variance), respectivelyTo test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients Fisher and Yates (1917) at 5% of significance with (n-2) degree of freedom where 'n' is the number of genotypes used in the experiment.

Heritability

Heritability in broad sense (h^2_b) = = $\frac{\sigma 2g}{\sigma 2p}$ x 100

$GA = K^* \sigma^2 p^* H^2 b$

$GAM\% = \frac{GA}{G.mean} {}^*100$

Where, K= the standardized selection differential at 5% selection intensity (2.063)

GA = genetic advance, GAM % = Genetic advance as percent of means Where σg, σp, σe and GA are genotypic, phenotypic and environmental components of variance and genetic advance respectively under selection. K is the selection differential, $\sigma^2 p$ is the phenotypic standard deviation of base population and H is the heritability of the character under selection.

RESULTS AND DISCUSSION

Analysis of variance indicated significant differences (P<0.01) for all the traits among genotypes that showed diverse variability among the yield traits of different maize hybrids, indicated the presence of genetic variability in the material used and provide a good opportunity for yield improvement. Heritability and genetic advance estimates (Table 2) described the genetic attributes of the traits. Heritability estimates along with genetic advance is more helpful in predicting the genetic gain under selection than heritability estimates alone (Singh, 2000). In present study the character days to 50% anthesis and silking plant and ear height, number of seed row per cob, ear length and grain yield per plot revealed higher values of heritability. The characters, plant and ear height, number of seed row per cob, and grain yield recorded high genetic advance, indicating those traits controlled in both additive and non additive of gene inheritance. High genetic advance coupled with heritability was observed for plant height, grain yield and number of kernel rows per ear. Therefore selection based on these last three mentioned traits will be effective (Table 2). The high heritability estimates and variances suggested that these traits were simply inherited. This also implied that the plant and ear height traits could easily be passed from one generation to the next, selection for improvement of these characters would be effective through phenotypic selection and hence enhancing the efficiency of plant breeding programmes indicated the presence of greater additive gene action for this trait (Shukla *et al.*, 2006). Similarly, it was reported that high to moderate heritability with moderate estimates of genetic advance for grain yield per plant and plant height (Anshuman, 2013)

From the breeder's view point, the type of association of grain yield and its component traits is of supreme importance. Positive significant associations were obtained between grain yield and plant height, indicating selection for tall plants tends to increase grain yield per plant. Higher genotypic correlations than their corresponding phenotypic correlations showed the higher genetic association among traits with the yield and the lower differences among both GCV and PCV for most of the traits attributed to lower modifying effect of environment on the association of characters (Hossain and Joarder, 2006).

The results related to correlation studies (Table 3) revealed that grain yield had significant genotypic and phenotypic relationship with days to anthesis and maturity, plant and ear height, cob length and number of kernel rows per cob. These findings suggested that improvement of grain yield in maize is linked with the development of these traits that might have good impact on grain yield (Parkish, 2006). Among the pair of characters, the days to 50% tasseling was the significantly positive correlated with days to 50% silking (0.91), number of kernel rows per cob (0.27), days to maturity (0.41) but negatively correlated with 100-grain weight (-0.04) and anthesis silking interval (-0.14). In traits like ear diameter and length, ears per plant, ear and plant height showed higher genotypic correlations than their corresponding phenotypic correlations with grain yield.

In plant breeding, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield (Hossain A. and Joarder, 1987). Genotypic correlation coefficient is the heritable association between two variables. The strong correlation between ear height and plant height with grain yield suggested that tall plants with high ear placement gave better yields compared to the shorter plants with lower ear placement. This could be attributed to the high dry matter accumulation function carried out by the high number of leaves possessed in the case of tall plants. It also implied that the tall lines excelled in capacity to support kernel growth through stem reserve mobilization (Al-Tabbal *et al*., 2012). Kumar *et al.* (2014) also indicated the highest heritability values indicate that heritability may be due to the higher contribution of the genotypic component and the character is least influenced by environmental effects. However phenotypic correlation includes both phenotypic and environmental effect. Hence significant phenotypic correlation without significant genotypic correlation has no value. The magnitude of difference between PCV and GCV were relatively low for most of the traits revealing little influence of the environment in the expression of these traits. The higher magnitude of PCV and GCV was recorded for anthesis-silking interval, ear weight, grain yield. It was observed that days to anthesis, days to silking and ear length showed almost equal phenotypic and genotypic coefficient of variation. On the other hand, days to maturity showed low PCV and GCV values as compared to other studied traits.

The small difference between PCV and GCV of these traits indicated the existence of genetic variability's. As in plant crop the small differences between GCV% and PCV% indicated the possibility of genetic improvement in all the traits. The results of the present investigation supported the findings of Shoran and Tandon (1995) who reported days to flowering and days to maturity exhibited low PCV and GCV values but they were close in magnitude. Hossain and Joarder (2006) also reported comparatively low PCV and GCV for days to anthesis and days to maturity, which is in agreement with the present results. Since genotypic coefficient of variation (GCV) alone would not provide reliable measure of the heritable variation, heritability estimates were considered along with it.

The results related to correlation studies (Table 3)

Table 2. Estimations of heritability and genetic variance components for 14 traits in 2014 at Bako

Traits	σ^2_g	σ^2_e	σ^2_{ph}	H^2_b	G.mean	GCV %	PCV%	ECV %	GA,K=5%	GAM%
AD	4.84	1.66	6.50	74.46	72.17	3.05	3.53	1.79	5.43	7.52
SD	5.20	1.91	7.11	73.13	73.32	3.11	3.64	1.88	5.48	7.48
ASI	0.25	1.22	1.47	16.79	1.16	42.84	104.56	95.37	36.22	3122.29
MD	4.46	6.68	11.13	40.03	157.17	1.34	2.12	1.64	1.75	1.12
PH	253.24	67.09	320.33	79.06	276.10	5.76	6.48	2.97	10.57	3.83
EH	137.64	31.39	169.03	81.43	136.79	8.58	9.50	4.10	15.97	11.67
EPP	0.01	0.04	0.05	25.36	1.16	10.15	20.15	17.41	10.54	906.54
ED	0.06	0.02	0.08	73.85	4.71	5.13	5.97	3.05	9.09	192.90
EL	0.89	0.82	1.71	51.96	18.19	5.18	7.19	4.98	7.71	42.36
Ewt	0.00	0.00	0.00	44.60	0.19	10.57	15.83	11.78	14.56	7836.77
NRE	1.12	0.63	1.74	64.10	15.06	7.02	8.77	5.25	11.59	77.00
NKR	3.47	3.51	6.98	49.68	38.51	4.84	6.86	4.87	7.03	18.26
GY	1.72	1.21	2.93	58.82	9.87	13.29	17.33	11.12	21.03	213.11
HKW	17.45	18.47	35.92	48.58	27.89	14.98	21.49	15.41	21.54	77.22

Key : AD = anthesis date, SD = silking date, ASI = anthesis silking interval, MD = maturity date ,PH = plant height, EH = ear height, EPP = ear per plant, EWt = ear weight, NKR = number of kernels per row, HKW = hundred kernel weight, GY=grain yield, EL=ear length, ED=ear diameter, NRE=number of rows per ear, σ^2_g *= genetic variance, G.mean = grand mean* σ^2_p *= phenotypic variance, GCV% = genotypic coefficient of variance, PCV% = phenotypic coefficient of variance, ECV % = enviromental coefficient of variance, GA = genetic advance at 5% selection intensity, GAM% = genetic advance as percentage of mean.*

revealed that grain yield had significant positive genotypic and phenotypic relationship with cob length, rows per cob and grains per row. In line with this other researchers reported, grain yield of maize positively and highly significant affected by ear length, ear weight and ears per plant (Agarma, 2006), number of kernel rows per ear (Hefny, 2011). These findings suggested that improvement of grain yield in maize is linked with the development of these traits that might have good impact on grain yield (Falconer 1989). Generally for the positive correlation of grain yield with other yield related traits indicates that plant breeders can use these traits as indicators in predicting yield. This is because when two traits are correlated, selecting for one would ensure selection for the other trait, thus selecting for the best of the above traits would result in improved yields. Selection based on days anthesis, plant height, ear length, ear diameter, ears per plant can be effective.

Path Coefficient analysis enables a plant breeder to separate direct and indirect effects attributable by partitioning the correlations. Thus Correlation and Path coefficient analysis form a basis for selection and helps in understanding yield contributing characters affecting yield in maize. The phenotypic direct and indirect effects of yield-related traits on grain yield are presented in Table 4. This means that a slight increase in one of the above traits may directly contribute to seed yield. These traits are there fore, very important components of grain yield and should be given high weightage in any selection process aimed at improving grain yield in maize. Similar results were reported by Selvaraj and Nagarajan (2011).

The path coefficient analysis (Table 4) revealed that most of the traits had positive direct effect on grain yield. The highest direct effect on grain yield was exhibited by days to 50% anthesis followed by ear diameter and anthesis silking interval. 50% silking had highest indirect effect on grain yield through anthesis silking interval followed by plant height through rows/cob ear diameter. Similar results in maize have earlier been reported by Rafiq *et al.* (2010).

Direct contribution of ear diameter to the grain yield of maize was 0.628, while the highest indirect contributions via plant height, days to 50% anthesis and days to 90% maturity were 0.075, 0.071 and 0.014 respectively; giving a total contributions of 0.548. Direct contribution of days to 50% anthesis to the grain was 0.859 whereas major contributor indirect contributions through plant height, ears per plant, ear diameter and ear length were 0.197, 0.073, 0.052 and 0.019 respectively.

CONCLUSION

Heritability estimates along with genetic advance is more helpful in anticipate the genetic gain under selection than heritability estimates alone. High genetic advance joined with heritability was observed for plant height, grain yield and protein percent. High broad sense heritability and

Table 3. Genotypic (below diagonal) and Phenotypic (above diagonal) Correlation Coefficients of Grain Yield and Related Traits in Maize

Variable	AD	SD	ASI	MD	PH	EH	EL	EP	ED	Ewt	NRE	NKR	HKW	GY_t ha
AD	**1**1	0.88**	-0.14	0.41**	0.43**	0.31**	0.011	0.23	0.12	-0.06	0.27**	-0.03	-0.04	0.25*
SD	0.91**	**1**	0.35	0.5**	0.38**	0.21*	-0.03	0.17	-0.07	-0.12	0.19	-0.10	-0.06	0.13
ASI	-0.04	0.38**	**1**	0.22*	-0.07	-0.18	-0.08	-0.11	-0.37*	-0.12	-0.13	-0.14	-0.05	-0.212*
MD	0.4**	0.51**	0.32	**1**	0.06	-0.12	0.06	0.06	-0.10	-0.05	-0.19	0.11	-0.01	0.01
PH	0.49**	0.42**	-0.08	-0.01	**1**	0.72*	0.16	0.22*	0.09	0.16	0.29*	0.05	0.27*	0.44*
EH	0.37**	0.26	-0.20	-0.15	0.73**	**1**	0.16	0.17	0.38**	0.20*	0.27*	-0.03	0.20*	0.51**
EL	0.01	-0.03	-0.09	-0.01	0.23	0.25	**1**	0.14	0.07	0.46**	*0.25	0.55**	0.20*	0.38**
EP	0.31*	0.25	-0.09	0.02	0.35*	0.27	0.12	**1**	-0.06	-0.05	0.17	0.18	-0.15	0.32**
ED	0.09	-0.09	*-0.4	-0.14	0.14	0.46**	-0.02	-0.04	**1**	0.44**	0.36**	0.00	0.17	0.47***
Ewt	-0.05	-0.14	-0.22	-0.10	0.31*	0.32*	0.47**	-0.12	0.44**	**1**	-0.04	0.21	0.56**	0.35**
NRE	0.28	0.20	-0.13	-0.27	0.33*	0.31*	-0.30*	0.18	0.41**	-0.03	**1**	-0.03	-0.26	0.16
NKR	-0.27	0.29*	-0.09	-0.13	-0.08	-0.04	0.54**	0.04	-0.11	0.25	-0.05	**1**	-0.08	0.05
HKW	-0.05	-0.09	-0.10	0.01	0.34*	0.24	0.32*	-0.14	0.20	0.71**	*-0.32	-0.06	**1**	0.19
GY_tha	0.31*	0.17	-0.27	-0.01	0.52**	0.62**	0.44*	0.38**	0.56**	0.43**	0.21	0.04	0.26	**1**

KEY: **=Significant at 0.05 probability level; **=Significantat0.01probabilitylevel; GY=grain yield, EPP= number of ears per plant, AD=days to anthesis, SD=days to silking, ASI=Anthesis –silking interval, MD= days to maturity, PH=plant height, EH=ear height, EL=ear length, ED=ear diameter, EWt= ear weight, NRE=number of kernels row per ear, NKR=number of kernels per row, HKW=hundred kernel weight.*

Table 4. The Direct (diagonal) and Indirect (out of Diagonal) Contribution of Maize Yield Attributes on Grain Yield of Maize Hybrids

	Effects Through													
Traits	AD	SD	ASI	MD	PH	EH	EPP	ED	EL	Ewt	NRE	NKR	HKW	Correlation with GY
AD	**0.859**	-0.691	-0.047	-0.050	0.197	-0.014	0.073	0.052	0.019	0.000	-0.050	-0.005	0.002	0.344
SD	0.789	**-0.752**	0.129	-0.064	0.168	-0.010	0.067	-0.047	0.004	-0.001	-0.027	-0.006	0.004	0.255
ASI	-0.091	-0.217	**0.445**	-0.042	-0.068	0.010	-0.011	-0.231	-0.044	-0.001	0.048	-0.002	0.009	-0.197
MD	0.388	-0.440	0.171	**-0.110**	0.064	-0.001	-0.015	-0.078	0.011	0.000	0.041	-0.005	0.002	0.030
PH	0.459	-0.343	-0.082	-0.019	**0.368**	-0.024	0.075	0.128	0.053	0.001	-0.054	-0.001	-0.029	0.532
EH	0.370	-0.224	-0.130	-0.002	0.270	**-0.033**	0.051	0.311	0.044	0.001	-0.057	-0.002	-0.018	0.582
EPP	0.316	-0.256	-0.026	0.009	0.139	-0.008	**0.198**	-0.082	0.054	0.000	-0.028	0.001	0.005	0.322
ED	0.071	0.056	-0.164	0.014	0.075	-0.016	-0.026	**0.628**	-0.002	0.001	-0.075	-0.002	-0.010	0.548
EL	0.051	-0.009	-0.062	-0.004	0.062	-0.005	0.034	-0.005	**0.315**	0.001	0.045	0.018	-0.021	0.420

Table 4. Continuation

Ewt	-0.086	0.140	-0.114	0.013	0.133	-0.009	-0.024	0.240	0.129	**0.003**	0.003	0.009	-0.050	0.386
NRE	0.252	-0.122	-0.126	0.027	0.117	-0.011	0.033	0.279	-0.084	0.000	**-0.169**	0.000	0.021	0.218
NKR	-0.145	0.143	-0.038	0.018	-0.015	0.002	0.009	-0.050	0.191	0.001	-0.001	**0.029**	0.004	0.147
HKW	-0.018	0.044	-0.054	0.003	0.146	-0.008	-0.013	0.091	0.093	0.002	0.049	-0.002	**-0.072**	0.259

Key: AD=days to anthesis, SD=days to silking, ASI=Anthesis –silking interval, MD= days to maturity, PH=plant height, EH=ear height, EPP= ears per plant, EL=ear length, ED=ear diameter, EWt= ear weight, FWt= field weight, NRE=number of rows per ear, NKR=number of kernels per row, HKW=hundred kernel weight.

Genetic advance were found for ear length and diameter, number of kernel rows per ear and grain yield. Therefore selection of genotypes based on these indicated traits will be effective. Traits like anthesis silking interval, grain yield and hundred kernel weight showed higher PCV than GCV, indicates a slight effect of environment on the expression of the characters studied, while the small difference between PCV and GCV were existed for days to 50% silking, ear diameter, ear and plant height traits.

Effective selection for superior genotypes is possible considering grain yield, number of kernel rows per ear, ear length, plant and ear heights and could be used as target traits to improve maize grain yield. Knowledge of interaction among the characters is very essential in plant breeding to determine the extent and nature of relationship between yield, yield components and physiological characters. This genetic diversity and the strong genetic association between grain yield and the agronomic traits would aid in indirect selection thus helping the breeders in the development of composites and synthetics for the resource constraint farmers with limited access to hybrid seeds. Generally, in the context of plant breeding traits that exhibited a high GCV, H^2b and GA would be useful as a base for selection.

Correlation and path coefficient analysis showed that cob diameter, anthesis silking interval, plant height, ear length and ears per plant were the important yield components in maize. Plant height, anthesis silking interval and ears per plant also showed high GCV, heritability coupled with high genetic advance. Therefore, these traits are therefore, very important components of grain yield and should be given high weightage in any selection process aimed at improving grain yield in maize.

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