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GENETIC VARIABILITY AND CORRELATION STUDIES IN YIELD AND YIELD RELATED CHARACTERS OF TROPICAL MAIZE (*Zea mays* L.)

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ABSTRACT

Ten genotypes of maize (*Zea mays* L.) were evaluated for two years in the field in a randomized complete block design and replicated four times. The results showed year effect to be significant for days to tasselling, days to silking, kernel weight and grain yield, and genotype effect was significant for all the characters. Also ,genotype x year interaction were significant for all the characters except kernel weight and grain yield. Genotypes AK-94-DMR-ESR and ACR-94-TZE COMP 5 had highest grain yield per hectare (7301.6kg and 7183.4kg respectively). Close resemblance between Genotypic correlation coefficient (GCV) and Phenotypic correlation coefficient (PCV) was observed for all traits indicating that selection for these characters would be effective. Heritability estimates in general were high for all the eight characters studied except for days to 50% tasselling. Characters studied showed significant positive correlation with grain yield except for days to tasselling and silking which showed significant negative genotypic correlation with grain yield. For the rest of the characters only days to 50% tasselling showed significant negative phenotypic correlation with grain yield. The PCA identified seedling emergence (63%), kernel weight (50%), grain yield (45%), kernels per row 44%, kernel row per ear (40%) and days to tasselling (40%) as the characters that contributed significantly to variations found in the maize genotypes examined. Highest heritability (h_b) couple with high genetic advance was observed for kernel row per ear, grain yield per plant, ear length and kernels per row. Thus, these traits could be used as selection criteria for yield in maize.

Keywords: Heritability estimate, Coefficient of variation, Correlation Coefficient, Principal component analysis.

INTRODUCTION

Maize (*Zea mays* L.) also known as corn is the world third most important cereal after wheat and rice (CIMMYT, 2000). In Nigeria, it is the second most important cereal, ranking behind only sorghum in the number of people it feeds (Ologunde, 1987). It is an important crop in developing countries, where rapid increase in population has already outstripped the available food supplies. Increased production per unit area is the primary objective in many maize breeding programmes. Of these, grain yield is the most important and complex characters with which maize breeders work. Maize displays an orderly sequence of development of yield components namely number of cob per plant, number of kernels per row, number of kernel rows and kernel weight (Viola *et al.*, 2003). Thus, indirect selection can be used through searching for improved yield components (Weish, 1981).

Grain yield in maize is the product of several interrelated traits; hence, a successful breeding programme depends largely upon the information on the genetic variability and association of desired quantitative traits with yield. Hence, consideration of quantitative approaches for exploitation of the extensive genetic variability available in maize cultivars is of paramount importance. Estimates of genetic parameters serve as a base for selection and hybridization since degree of variability for a given character is a basic prerequisite for its improvement. The study of genotypic correlations of yield and yield related components is important to enhance selections of genotypes for improvement. Multivariate analysis such as principal components analysis (PCA) has been used to measure the relative contribution of various traits to the total variability in crop collections (Baatout, 1995).

Although, several research efforts have been devoted to maize breeding to enhance its improvement, Ihsan *et al*. (2005) reported significant genetic differences for morphological parameters for maize genotypes, Naushad *et al*. (2007) observed considerable genotypic variability among various maize genotypes for cob length, number of kernel row per cob, 300 grain weight and grain yield. Although, progress has been made in terms of increased grain yields, the problem of identifying appropriate indicators of grain yield during selection still remains unresolved.

The present study was conducted to (i) evaluate the performance of different maize genotypes under field conditions (ii) estimate the nature and magnitude of variability for grain yield and yield related characters among local and improved cultivars of maize (iii) to ascertain the genetic relationship among grain yield and its related components. Information on the above objectives will definitely lead to further improvement in the development of adaptable cultivars to Ekiti state.

MATERIALS AND METHODS

The study was carried out at the experimental field of the Department of Plant Science, University of Ado-Ekiti, Ado-Ekiti (7^{o}40^{1}N, 5^{o}15^{1}E) Nigeria during 2002 and 2003 late cropping seasons under rain fed conditions. The average annual rainfall was 1450mm with mean air temperature of about 26.6^{o}C and a relative humidity of about 82.3%. The soil around Ado-Ekiti is overlaying metamorphic rock of basement complex, which shows greater variation in particle size and mineral deposition (Smith and Montgomery, 1962).

Ten maize cultivars were used for the experiment. Six of the cultivars, ACR-9931-DMR-SR, ACR 94-TZE-COMP 5, TZE COMP 3C2, AK-DMR-ESR, TZE-COMP 4E and ACR-89-DMR-SR were improved open-pollinated varieties collected from the maize improvement programme of International institute of Tropical Agriculture (IITA), Ibadan, Nigeria. The remaining four cultivars (Osoleke, Agberin, Oreolowo and Gbenuro) were from Ekiti, Ondo and Oyo states respectively, all in Nigeria.

The experimental field was manually cleared, tilled to loosen the soil adequately and then laid out in a randomized complete block design with four replications. Each cultivar was planted in two rows of 5m in length and plant to plant spacing of 25cm and between row spacing of 60cm. Weeding was done as when necessary. Foliar and ear insects were controlled by spraying with Diazinon chemical at a concentration of 2ml per litre of water just before tasseling. Harvesting was carried out 110 days after planting.

For each character studied, data were collected from ten randomly selected plants from the two middle rows of each plot and expressed on per plant basis. The data collected on the maize grains were adjusted to 14% moisture content. Data were collected on growth, developmental and grain yield characteristics of maize plant as follows:
Seedling Emergence %: The proportion of seeds that emerged expressed as emergence percentage of total number of seed sown.

Days to Tasseling: A plant was said to have tasseled when the leaf protecting the inflorescence split to expose the spikelets and this was taken as days from seed sowing date to when 50% of the plant produced tassels.

Days to Silking: This was taken as the number of days from planting to when 50% of the maize plant showed silk.

Cob length: This was taken to be the distance between first set of grains on the base of the cob and the last set of grain on the tip of the cob.

Kernel rows per cob: This was done by counting the number of rows of kernels in a cob.

Number of kernels per row: This was done by counting the number of kernels per row.

250-kernel weight: Weight of 250 kernels was determined in gramme. The grain moisture at harvest was estimated by taking 250-kernel sample from shelled grain, weighed (Fwt), and dried to a constant weight before final weight (Kwt) was determined. The moisture content was then calculated following the methods by Fakorede and Mock (1978), thus:

$$\frac{\text{Fwt} \;-\; \text{Kwt} \;\;\text{x}\;\; 100}{\text{Fwt}}$$

where

fwt = shelled weight
Kwt =final dried weight

Seed weight at harvest: The seed weight at harvest of the known moisture content were then corrected to a standard moisture content of 14% using methods of Faluyi and Smith (1995), thus:

$$\text{Weight (14\% moisture)} \;=\; \frac{\text{Measured weight x (100-measured weight)}}{100 \;-\; 14\%\text{ moisture}}$$

Grain yield per hectare: This was estimated based on the mean grain yield obtained from the maize plant. The weight of the seeds were taken in grammes using triple beam balance in five replicates and the average weight was recorded at 14% moisture content.

Data Analysis: The mean values of the scores were subjected to analysis of variance. Significant means were separated using new Duncan Multiple Range Test (DMRT) at 5% probability level. The phenotypic and genotypic correlations were calculated from the mean value of characters according to the formula by Miller, *et al.* (1958). Phenotypic ($\delta^2 p$) and genotypic ($\delta^2 g$) variances were calculated by methods suggested by Burton and Devane (1953), thus:

$$\delta^2 p = \delta^2 g + \delta^2 e$$
$$\delta^2 g = MSg - Mse/r$$

where,

$\delta^2 p$ = phenotypic variance
$\delta^2 g$ = genotypic variance
$\delta^2 e$ = Environmental variance (error mean square)

The genotypic (GCV) and phenotypic (PCV) coefficient of variation were estimated according to the procedure outlined by Joh~~n~~son, *et al.* (1955) thus:

$$PCV = \frac{\sqrt{\delta^2 p}}{\bar{X}} \times 100 \qquad \sqrt{\delta^2 p} = \delta p$$

where X = grand mean

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{X}} \times 100 \qquad \sqrt{\delta^2 g} = \delta g$$

Broad-sense heritability and genetic advance expected under selection, assuming a selection intensity of 5% were calculated as suggested by Allard (1960) for each character thus:

$$H^2 = \frac{\delta^2 g}{\delta^2 p} \times 100$$

where:

H^2 = Heritability in broad sense (in percentage)

$$GA = (K)\, \sigma_A\, (H^2)$$

where:

GA = Expected genetic advance
K = Selection differential (2.06 at 5% selection intensity)
σ_A = Phenotypic standard deviation

Genetic adva~~nc~~e as percent of mean (GAM) was calculated using the formular

$$GAM = \frac{G}{\bar{X}} \times 100$$

where,

$\underline{G}$ = genetic advance
$\bar{X}$ = grand mean

Genotypic and phenotypic coefficients of correlation were also calculated from the genotypic and phenotypic variances and covariances of the characters.

The principal component analysis (PCA) produced a score for each principal component for the first four extracted components.

RESULTS

Table 1 gives the results of combined analysis of variance over two seasons for the eight traits. Significant to highly significant differences were observed between the cultivars for all traits. There were significant differences between the years for days to 50% tasselling, days to 50% silking, 250 -kernel weight and grain yield per hectare. Significant to highly significant interactions between genotypes and years were observed for all traits except for kernel weight and grain yield per hectare. Although the magnitude of the interactions mean squares were relatively small in comparison to main effect.

Table 2 shows the mean grain yield and yield related characters of the ten genotypes in two seasons. Genotypes (Oreolowo and TZL-COMP $4E_1$) were among genotypes with the highest seedling emergence. Osoleke had highest number of days to tasseling, while Gbenuro had higher number of days to silking compared to other cultivars. Genotypes AK-94-DMR-ESR and ACR-94-TZE-COMP 5 were among genotypes with highest number of kernel rows per ear, kernels per row and ear length. Similarly, genotype TZL-COMP 4E had the highest 250-kernel weight (73.41). Agberin genotype had higher seed weight (64.36g) compared to the three improved varieties AK-94-DMR-ESR (63.49g), TZE-COMP $3C_2$ (64.15g) and ACR-94-TZE-COMP 5 (62.46g) whereas. AK-94-DMR-ESR (7301.6kg) and ACR-94-TZE-COMP 5 (7183.4kg) recorded higher grain yield per hectare compared to other genotypes.

The estimates of phenotypic, genotypic and environmental variances as well as heritability and genetic advance for the eight characters in maize are presented in Table 3. This result revealed considerable phenotypic, genotypic and environmental variations among the genotypes for all traits under consideration. In all the traits, a large portion of the phenotypic variance was accounted for by genetic components except for days to 50% tasselling in which the contribution of genetic variance to phenotypic variance was 11%. Genotypic variance for the characters ranged from 0.14 for number of days to 50% tasseling to 1045403.31 for grain yield per hectare. Phenotypic variance ranged from 1.29 for number of days to 50% tasseling to 1132779.11 for grain yield per hectare. Environmental variance ranged from 0.20 for number of days to 50% tasselling to 119449.58 for grain yield per hectare. Days to tasselling showed low heritability estimates of 10.53 whereas, moderate to high heritability values of 46.28, 47.20, 59.11, 63.45 and 67.61 were recorded for kernels per row, days to silking, ear length, seedling emergence and 250-kernel weight.

Very high heritability estimates of 83.86 and 92.29% were obtained for kernel row per ear and grain yield per hectare respectively. Also in Table 4, the expected genetic advance values for eight characters of maize genotypes were presented. These values are expressed as percentage of the genotype mean for each character so that comparison could be made among various characters, which had different units of measurement. Progress that could be expected from selecting the top 5% of the genotypes ranged from 0.46% for number of days to 50% tasseling to 39.49% for kernel row per ear. For all characters except for number of days to 50% tasseling, and seedling emergence, the genetic advances were considered moderate. Comparatively, the highest genetic advance as percent of mean was recorded for kernel row per ear (39.49) followed by grain yield per hectare (33.98) and ear length (16.54).

Table 4 presents phenotypic and genotypic coefficients of variation for the eight characters. Phenotypic coefficients of variation were highest for kernel rows per ear 22.86 and this was followed by grain yield per hectare 17.87. These two characters also exhibited highest genotypic coefficients of variation of 20.93 and 17.17. In addition to these two traits, ear length had phenotypic and genotypic coefficients of 13.59 and 10.45, respectively. The PCV and GCV were relatively moderate for kernel weight (6.38 and 5.24) and kernels per row (9.19 and 6.25) respectively. Low PCV and GCV estimates of between 0.69 and 1.68 were recorded for number of days to 50% tasseling and seed emergence.

Table 5 shows genotypic and phenotypic coefficients of correlation (r) among the eight characters. Grain yield showed significant positive genotypic correlations with kernels row per ear (0.98**), kernels per row (0.94**), ear length (0.89**) and kernel weight (0.59**). Also, strong negative genotypic correlation occurred between grain yield and days to 50% tasselling (-0.88**) and days to 50% silking (-0.96**).However, seedling emergence had positive but non significant genotypic correlation with grain yield (r = 0.16).Significant negative phenotypic association was observed between grain yield and days to 50% tasselling (-0.31**) and non significant negative phenotypic correlation were observed between grain yield and days to 50% silking (-0.21) and kernel row per ear (-0.02).However, grain yield showed weak positive phenotypic correlation with seedling emergence (0.16), kernel row per ear (0.16), ear length (0.20) and kernel weight (0.04).Generally, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients for most of the characters.

The results of the principal components analysis are presented in Table 6. From the result, it can be seen that the eight characters contributed 51.06% to the total variance as PC1 and a further 15.06% and 12.50% as PC2 and PC3 respectively. These first three principal components contributed 79.42% to the total variation. The remaining components contributed only relatively small amount to the total variance. PC1 was dominated by grain yield (0.45) and kernel row per ear (0.40) while PC2 was dominated by seedling emergence (-0.63) kernels per row (0.44) and days to 50% tasselling (0.40).Seedling emergence (0.52) and 250-kernel weight (-0.50) accounted for significant contribution to the discrimination among the genotypes in PC3.

DISCUSSION

Crop yield improvement is determined to a large extent by the effective functioning of the crop yield characters. Expression of these characters depends on the overall genetic and environmental factors (Berdahl and Barker, 1997).The variations observed for the eight characters may be attributed to diverse genetic background of the genotypes studied, which suggests that in a population of maize genotypes, there is an opportunity to select desirable genotypes with increased yield components characters which may be able to perform well and give increased yield. This result is in agreement with the results obtained by Naushad *et al.* (2007) who reported significant variability among maize cultivars for cob length, kernel rows per cob, kernel weight and grain yield.

The significant difference in genotype x year interaction for all the traits except kernel weight and grain yield indicated that the wide range of variability existing in the tested genotypes and year effects. This reveals the achievable result obtainable in any improvement programme especially in enhancing higher yield and genotype specific agro-ecology adaptation. The fact that year and genotypic variance was significant for most of the characters is an indication that variable factors associated with years such as amount of rainfall and solar radiation were important. However, the performance of the genotypes with respect to kernel weight and grain yield is stable and will be easy to select for improvement.

Phenotypic variance includes the genotypic and environmental variances. The fact that seedling emergence, ear length, kernel weight, kernel row per ear and grain yield had high heritability estimates revealed that variation in these characters is largely controlled by heritable factors. Conversely, low heritability values exhibited by days to 50% tssselling showed that it was influenced mostly by environment rather than genetic constitution. Moderately high heritability values for days to silking and kernels per row showed that both genetics and environment played equal roles in the expression of these traits. Similar results for high heritability for number of days to 50% silking, number of kernel row per cob, number of kernels per row, seed weight and grain yield was reported by Sumathi *et al.* (2005). High heritability estimate for grain yield in maize has also been reported by Satyanarayanan and Sai (1996). This suggests that greater effectiveness of selection and improvement could be expected for those traits in future breeding.

For all characters studied, the genotypic coefficient of variation was less than its corresponding estimate of phenotypic coefficient of variation (PCV), indicating significant role of the environment in the expression of these traits. The moderate to high values of genotypic correlation of variation for kernel row per ear and grain yield indicated that these traits might be further improved through selection. Although, heritability estimates provide the basis for selection on phenotypic performance, the estimate of heritability and genetic advance should always be considered simultaneously as high heritability will not always be associated with high genetic advance (Johnson, *et al*., 1995). Estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Marayanan, 1993). Thus, the heritability estimates will be reliable if accompanied by high genetic advance. The expected genetic advance of maize characters was highest for kernel row per ear followed by grain yield, while the remaining characters exhibited moderate to very low genetic advance as percent of mean. This indicates selecting the top 5% of the genotypes can makes an advance of 39.49% in kernel row per ear and 33.98% for grain yield.

Although the genotypic variance revealed the extent of genetic variability present among the cultivars for various traits, it does not provide a means of assign heritability. High heritability in addition to high genetic advance is therefore an important tool for predicting the resultant effect of selecting the best individual. In this study, high heritability and genetic advances obtained for kernel rows per ear and grain

yield will go a long way in predicting heritable trait for further improvement. Hence, selection for kernel row per ear, and grain yield would prove quite effective since these characters seemed to be governed by additive gene action.
On the other hands, characters such as ear length, kernel weight and kernels per row showed relatively moderate genetic advance however, their heritability estimates were high. The presence of high heritability and moderate genetic advance has been reported to suggest the effect of equal contribution of additive and non-additive gene action (Shelby, 2000). Seedling emergence and days to silking which showed high percentage of heritability and very low genetic advance is an indication that non-additive gene action controls these traits. An earlier work by Sumathi *et al.* (2005) reported non-additive gene action for silking in maize.

High GCV along with high heritability and genetic advance will provide better information than a single parameter alone (Sahao *et al.*1990). Hence in this study, grain yield and kernel row per ear exhibited high GCV, heritability and relatively high genetic advance indicating additive genetic effects.

Genotypic relationship among traits affecting grain yield elucidate true association as they exclude the environmental influences. Grain yield showed significant positive genotypic correlation with number of kernels per row, kernel rows per ear, ear length and kernel weight. The genes controlling these characters may be linked that is, positioned closely together on the same chromosome or being controlled by pleiotropic gene. Therefore, selection for thee traits could be used to indirectly select for grain yield. This result corroborate earlier results obtained by Venugopal *et al.* (2003), Sumathi *et al.* (2005) who reported significant genotypic correlation between grain yield and kernel weight and between grain yield as well as number of kernels per row and number of kernel rows per cob respectively. The significant negative genotypic correlations between grain yield and number of days to 50% silking and number of days to 50% tasseling indicate that earliness in maturity could lead to reduction in grain yield of the maize genotypes. Unexpectedly, seedling emergence had a positive but weak genotypic correlation with maize grain yield but it is a trait of considerably importance.

The phenotypic correlation coefficients were generally lower than genotypic correlation coefficients. The low phenotypic correlation could arise due to the modifying effect of environment on the association character at genetic level. Seedling emergence, kernel row per ear, ear length and kernel weight showed positive but weak phenotypic correlations with grain yield, while days to 50% tasselling showed significant negative correlation coefficient with grain yield. Thus suggest that those characters that showed positive phenotypic correlation with grain yield would be of major use in direct selection for grain yield, since selection is usually based on phenotypic expression of traits.

The principal components analysis help in the interpretation of results as the latent root associated with each component measures the contribution of each principal component to the total variance, while the coefficient of latent vector associated with a given principal components indicates the degree of contribution (loading) of each original variable to the principal component in question. The component correlation matrix estimated grain yield (45%) kernel row per ear (45%) in PC1. Seedling emergence (63%), kernels per row (44%), and days to tasselling (40%) in PC2, in PC3, seedling emergence 52% and kernel weight 50% were estimated and mostly responsible for variation in the maize genotypes examined. Hence these characters can be worked upon in subsequent future breeding.

CONCLUSION

This study concluded that AK-94-DMR-ESR and ACR-94-TZE-COMP 5 were the highest grain yielders among the ten genotypes evaluated. Traits with high broad sense heritability and genotypic coefficient of variation such as grain yield; kernel row per ear and kernel weight indicates the importance of additive gene action. Selection for grain yield improvement should therefore include an indirect selection for kernels row per ear, kernels per row, ear length and kernel weight since they had significant role in enhancing the yield.

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Table 1: Combined of analysis of variance (ANOVA) for grain yield and yield related characters of maize genotypes evaluated in Ado-Ekiti.

Source of variation	Df	Seed emergence	Days to 50% tasselling	Days to 50% silking	Mean Kernel rows per ear	Squares Kernels per row	Ear length	250 kernel weight	Grain yield per hectare
Replication	3	40.37	0.69	0.58	0.95	28.57	1.55	132.41	2673204.88
Year (Y)	1	1.10	310.87**	21.32**	2.53^{ns}	0.26	0.26	186.87*	4668876.54*
Genotype (G)	9	34.71*	10.29**	46.28**	49.16**	62.97**	29.00**	138.43**	9062232.87**
G x Y	9	89.45**	9.21**	24.44**	7.93*	33.83**	11.86**	44.84	699005.93
Error	57	12.95	1.57	2.92	3.28	8.55	1.89	28.43	955596.60
Total	79								

*, ** significant at $P \leq 0.05$ and 0.01 respectively

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*, ** significant at $P \leq 0.05$ and 0.01 respectively

Table 2: Mean values of grain yield and yield related characters in maize genotypes over two seasons

Cultivars	Seedling emergence	Days to 50% tasseling	Days to 50% silking	Kernel row per ear	Kernel per row	Ear length	250 kernel weight	Grain yield kg per hectare
ACR 9931-DMR-SR	93.33^{ab}	52.28^{c}	$55.63d^{e}$	12.45^{b}	32.81^{b}	12.89^{cd}	67.32^{bc}	6115.7^{b}
TZE-COMP 3C2	94.95^{ab}	52.90^{bc}	$57.25b^{cd}$	11.66^{bc}	31.83^{bc}	14.14^{bc}	64.15^{cd}	6262.50^{ab}
ACR-94-TZE-COMP 5	94.25^{ab}	52.25^{c}	54.78^{e}	15.74^{a}	30.64^{cd}	16.55^{a}	62.46^{cd}	7183.40^{ab}
TZL-COMP 4E	95.54^{ab}	52.38^{c}	55.00^{e}	11.24^{bc}	29.56^{cd}	15.04^{b}	73.41^{a}	6766.10^{ab}
AK-94-DMC-ESR	92.35^{bc}	54.25^{ab}	$56.11d^{e}$	13.21^{b}	36.19^{a}	18.60^{a}	63.49^{cd}	7301.61^{a}
ACR-89-DMR-ESR	92.68^{bc}	52.25^{c}	54.79^{e}	10.08^{cd}	31.81^{bc}	15.02^{b}	71.24^{ab}	6762.30^{ab}
Osoleke	89.19^{c}	55.45^{a}	58.38^{b}	8.68^{d}	28.65^{cde}	11.76^{de}	63.55^{cd}	4760^{c}
Agberin	93.78^{ab}	54.25^{ab}	58.04^{bc}	8.69^{d}	26.15^{e}	14.19^{bc}	64.36^{cd}	4728.90^{c}
Oreolowo	96.90^{a}	54.13^{ab}	56.51^{cde}	8.39^{d}	28.30^{de}	11.24^{e}	60.55^{d}	4894.91^{c}
Gbenuro	93.18^{ab}	53.84^{b}	$62/69^{a}$	8.29^{d}	29.30^{cde}	12.51^{de}	61.87^{cd}	4777.0^{c}

Values within a column with a letter superscript in common are not significantly different at $P < 0.05$

Table 3: Estimates of variance components, heritability and genetic advance as percent of mean for grain yield and yield related characters of ten maize genotypes over two seasons

Variance components	Seedling emergence %	Days to 50% tasseling	Days to 50% silking	Kernel row per ear	Kernel per row	Ear length	250-kernel weight	Grain yield kg/ha
Phenotypic variance δ^2p	6.84	1.29	5.79	6.15	7.87	3.63	17.30	113277.11
Genotypic variance δ^2g	4.34	0.14	2.73	5.15	3.64	2.14	11.70	1045403.31
Environmental variance δ^2e	1.62	0.20	0.36	0.41	1.07	0.24	3.55	119449.58
Heritability (H_B)	63.45	10.53	47.20	83.86	46.28	59.11	67.61	92.29
Genetic advance as percent of means	2.14	0.46	4.11	39.49	8.76	16.54	8.88	33.98

Table 4: Estimates of phenotypic and genotypic coefficient of variation of yield and yield related characters of ten maize genotypes over two seasons

Components of coefficient of variations	Seedling emergence %	Days to 50% tasseling	Days to 50% silking	Kernel row per ear	Kernel per row	Ear length	250-kernel weight	Grain yield kg per hectare
PCV	2.23	2.12	4.23	22.86	9.19	13.59	6.38	17.87
GCV	1.68	0.69	2.90	20.93	6.25	10.45	5.24	17.17

PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation

Table 5: Genotypic and phenotypic correlation coefficients among grain yield and yield related characters of ten maize genotypes over two seasons (n = 80) upper diagonal genotypic and lower diagonal phenotypic correlation coefficients values

Traits	Seedling emergence %	Days to 50% tasseling	Days to 50% silking	Kernel row per ear	Kernel per row	Ear length	250-kernel weight	Grain yield kg/ha
Seedling emergence	1.000	0.61**	0.34**	0.13	-0.21	0.04	-0.03	0.16
Days to 50% tasseling	-0.61**	1.000	0.40**	-0.67**	-0.78**	-0.96**	-0.39**	-0.88**
Days to 50% silking	-0.34**	0.74**	1.000	-0.46**	-0.28*	-0.98**	-0.97**	-0.96**
Kernel row per ear	0.13	-0.77**	-0.81**	1.000	0.98**	0.96**	-0.06	0.98**
Kernels per row	-0.21	-0.41**	-0.48**	0.84**	1.000	0.96**	-0.32**	0.94**
Ear length	0.04	-0.60**	-0.68**	0.94**	0.71**	1.000	0.96**	0.89**
250-kernel weight	0.03	-0.76**	-0.67**	0.13	0.18	0.41**	1.000	0.59**
Grain yield kg/ha	0.16	-0.31**	-0.21	0.16	-0.02	0.20	0.04	1.000

*, ** Significant at P≤ 0.05 and 0.01 respectively

Table 6: Results of principal compound analysis showing scores of the major characters of the first four axes of yield and yield related characters in maize genotypes over two seasons

Traits	Component score		
	1	2	3
Seed emergence	0.08	**-0.63**	0.52
Days to 50% tasseling	-0.35	**0.40**	-0.13
Days to 50% silking	-0.37	0.19	-0.12
kernel row per ear	**0.40**	0.21	0.23
Kernels per row	0.30	**0.44**	0.24
Ear length	0.39	0.20	0.02
250-kernel weight	0.25	-0.35	**-0.50**
Grain yield kg/ha	**0.45**	0.12	0.12
Eigen value	4.59	1.43	1.13
Total variation %	51.06	15.86	12.50
Cumulative variation (%)	51.06	66.92	79.42

Bold Figures: Traits with significant contribution to variation