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# Genetic variability, heritability and genetic advance studies in top-cross and three-way cross maize (*Zea mays* L) hybrids

**Sayo Sesay\*[1,2], David K Ojo[2], Omolayo J Ariyo[2], Silvestro Meseka[3]**

[1]Crop Improvement Program, Rokupr Agricultural Research Center, Sierra Leone Agricultural Research Institute, PMB 1313, Tower Hill, Freetown, Sierra Leone
[2]Department of Plant Breeding and Seed Technology, College of Plant Science and Crop Production, Federal University of Agriculture, Abeokuta, Nigeria
[3]Maize Improvement Program, International Institute of Tropical Agriculture, PMB 5320, Oyo Road, Ibadan, Nigeria
\*Corresponding author: E-mail: osaiosesay@yahoo.com

## Abstract

Understanding the genetic variability, heritability and genetic advance of traits in any plant population is an important pre-requisite for selection program. This study was designed to assess the magnitude of genetic variability, heritability and genetic advance of traits in top-cross and three-way cross maize (*Zea mays* L) hybrids evaluated at three locations in South-Western Nigeria. The trial consisted of ten genotypes each of top-cross and three-way cross hybrids arranged in randomized complete block design with three replications. Data on grain yield and other desirable traits across the three locations were used to estimate the genetic variability parameters, heritability and genetic advance (GA). Highly significant ($P \leq 0.01$) differences were detected within each hybrid class for all the traits. Traits evaluated in this study exhibited different levels of variability, heritability and genetic advance between the two hybrid classes. Low to moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded. Also, low to very high heritability and low to high GA values were recorded for all the traits measured in the top-cross hybrids, whereas the three-way cross hybrids exhibited low to moderately high heritability estimates and low to moderate GA values. Grain yield and field weight showed moderate GCV, moderately high heritability and high GA values in top-cross hybrids. These characters exhibited moderate GCV but low heritability and GA values in three-way hybrids. More characters in top-cross hybrids revealed sufficient amount of variability than in three-way cross hybrids, thus offer scope for genetic improvement through selection.

**Keywords**: genetic variability, heritability, genetic advance, maize, hybrid class

## Introduction

Maize is an important staple food in West and Central Africa (WCA), accounting for about 15% of the total calorific intake of the rural communities (Badu-Apraku et al, 2011). Average world's maize yield has increased from 4.9 tons ha$^{-1}$ in 2012 to 5.5 ton ha$^{-1}$ in 2013 (FAOSTAT, 2015). Africa's share of average maize yield was estimated to be 2 tons ha$^{-1}$ in 2012 and 2013. However, in Western Africa, average maize yield is low and estimated to increase from 1.6 tons ha$^{-1}$ in 2012 to 1.8 tons ha$^{-1}$ in 2013.

The understanding of genetic variability present in a given crop species for the traits under improvement is imperative for the success of any plant breeding program (Sankar et al, 2006). The parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in a given characteristic. The efficiency with which genotypic variability can be exploited by selection depends upon heritability and the genetic advance (GA) of individual trait (Bilgin et al, 2010). Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Akinwale

et al, 2011). Heritability provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations (Bello et al, 2012). Heritability coupled with high GA would be more useful in predicting the resultant effect in the selection of the best genotypes for yield and its attributing traits (Singh et al, 2011).

There are conflicting reports by several researchers about the heritability for genetic improvement of field crops. Ramanujam and Thirumalachar (1967) suggested that heritability estimates in the broad sense will be reliable if accompanied by a high genetic advance. Dhankhar and Dhankar (2002) argued that broad-sense heritability alone may be misleading, but should be jointly considered with genotypic coefficient of variation and genetic advance. According to Ibrahim and Hussein (2006) and Nwangburuka et al (2012) that characters with high heritability as well as high genotypic coefficient of variation and genetic advance can be explained by additive gene action and hence can be improved through mass selection. Such characters may be good predictors of yield and can be used as index to select for yield improvement in breeding programs (Murtadha et al,

2004). Therefore, this study was designed to assess the magnitude of genetic variability, heritability and genetic advance of traits in top-cross and three-way cross maize hybrid varieties.

## Materials and Methods

The experimental materials consisted of ten genotypes each of top-cross and three-way cross maize hybrids obtained from the maize improvement program of the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria (Table 1).

This study was carried out at three different locations of South-Western Nigeria during the main rainy season in 2014. The locations were, the Teaching and Research Farm of the Federal University of Agriculture, Abeokuta, Ogun State [70°14'N;30°26'E and 162 meter above sea level - (masl)]; National Institute of Horticultural Research, Ibadan, Oyo State (70°24'N;30°50'E and 184 masl); and Federal University of Technology, Akure, Ondo State (70°18'N;50°07'E and 380 masl). The mean monthly temperature for each location during the experiment (August-November) was 27°C and average monthly rainfall for Abeokuta, Ibadan and Akure were 114 mm, 196 mm, and 237 mm, respectively. At each location, the trial was arranged in randomized complete block design with three replications. Each entry was planted in a two-row plot of 5 m long, with a plant spacing of 75 cm x 50 cm. Crop management practices were applied following the standard recommendations at each location.

Data were collected on ten parameters of each hybrid class including:

a. Days to 50% anthesis (DPOL) - was recorded on plot basis in days from planting date to the date when 50% of the plants had started shedding pollens.

b. Days to 50% silking (DSLK) - was recorded in days from planting date to the date when 50% of the plants had emerged silks.

c. Plant height (PLHT) - was recorded as average height of ten randomly selected plants measured in centimeters (cm) from the base of the plant to where tassel branching began.

d. Ear height (EHT) - was recorded as average height of ten randomly selected plants measured in cm from the base of the plant to the node bearing the upper ear.

e. Field weight (FDWT) – was measured in kilogram (kg) for each entry at harvest of dehusked ears using a measuring balance.

f. Ear length (ELTH) – was recorded as averaged length of ten randomly selected dehusked ears in cm measured at harvest using measuring ruler.

g. Ear diameter (EDMT) – was computed as averaged diameter of ten randomly selected dehusked ears in millimeter (mm) determined at harvest at the middle portion of ears using a digital Vernier caliper.

h. Number of kernel rows per cob (KROW) - determined at harvest as average of ten randomly selected ears dehusked and the number of kernels rows per cob counted.

i. 100-grain weight (GWT) - was measured in gram (g) using an electronic balance from shelled grains of ten randomly selected ears for each entry dried to 12% moisture content.

j. Moisture content - was determined at harvest for each plot, grains were shelled from ten randomly selected ears and uniformly mixed to record the percent grain moisture using a digital moisture tester.

k. Grain yield (YLD) - was calculated for every entry from the data of field weight per plot in kg ha$^{-1}$ (later converted into t ha$^{-1}$) using the following formula according to Rahman et al (2007):

$$Grain\ yield\ (kg\ ha^{-1}) =$$

$$\frac{Field\ weight\ (kg\ plot^{-1})\ x\ (100 - MC)\ x\ 0.8\ x\ 10{,}000}{(100 - 12)\ x\ 7.5}$$

where: MC = moisture content in grains at harvest (%); 0.8 = shelling co-efficient, 7.5 = Area harvested plot$^{-1}$ (m$^2$), 1 hectare = 10,000 m$^2$ and 12% = moisture content required in maize grain at storage.

### Data analysis

Combined data of each hybrid class, across the three locations, were subjected to analysis of variance using SAS software version 9.1 (SAS Institute, 2000) to estimate the genetic variability parameters.

Phenotypic, genotypic and environmental variances were computed from the respective mean squares following the procedures suggested by Singh and Chaundhary (1979) and Allard (1960), thus Genotypic variance

$$\delta_g^2 = \frac{MS_g - MS_{gl}}{rl}$$

Genotype by environment interaction variance

$$\delta_{gl}^2 = \frac{MS_{gl} - MS_e}{r}$$

Phenotypic variance

$$\delta_P^2 = \delta_g^2 + \left(\frac{\delta_e^2}{rl}\right) + \left(\frac{\delta_{gl}^2}{l}\right)$$

where, $MS_g$ = mean square of genotype; $MS_{gl}$ = mean square due to genotype by environment interaction; $MS_e$ = error mean square (mean square of environment); l = number of locations; r = number of replications.

The genotypic and phenotypic coefficients of variation were estimated according to the procedure outlined by Johnson et al (1955):
Genotypic coefficients of variation

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{X}} x100$$

Phenotypic coefficient of variation

$$PCV = \frac{\sqrt{\delta^2 p}}{\bar{X}} x100$$

Table 1 - Pedigree, kernel color of top-cross and three-way cross maize hybrids obtained from IITA.

| Hybrid | Pedigree | Kernel color |
|---|---|---|
| Top-cross maize hybrids | | |
| M0926-7 | WhiteDTSTR Syn/IWD-SYN-STR-C3-46-5-BB | White |
| M0926-8 | WhiteDTSTR Syn/IWD-SYN-STR-C3-51-1-B | White |
| M0926-9 | WhiteDTSTR Syn/IWD-SYN-STR-C3-52-2-B | White |
| M1026-1 | IWDC2SynF2/1368xMi82-23-2-1-1-B*7 | White |
| M1026-11 | WhiteDTSTRSyn/IWD-SYN-STR-C3-52-4-B | White |
| M1026-13 | WhiteDTSTRSyn/IWD-SYN-STR-C3-70-2-B | White |
| M1026-2 | IWDC2SynF2/1368xMi82-23-2-1-4-B*6 | White |
| M1026-3 | IWDC2SYN/P43SRC9FS100-1-1-8-#1-B1-13-B1-B*8 | White |
| M1026-4 | WhiteDTSTRSyn/P43SRC9FS100-1-1-8-#1-B1-13-B1-B*8 | White |
| M1226-2 | DTSTR-WSYN2/IWD-SYN-STR-C3--52-3-BB | White |
| Three-way cross maize hybrids | | |
| M1124-17 | (1368/Mi82-23-2-1-2-B*7/P43SRC9FS100-1-1-8-#1-B1-13-B1-B*6)-1-1/((ACR-86-8-1-2-1-1-1-B-1-B*4/ (Babangoyo/MO17LPA/Babangoyo-28-1-2-1-B*6))-38-1/IWD-SYN-STR-C3--70-2-BB | White |
| M1124-24 | (1368/Mi82-23-2-1-2-B*7/P43SRC9FS100-1-1-8-#1-B1-13-B1-B*6)-65-1/DTPL-W-C7-S2-7-1-1-1-1-B-2-B*4/ BabangoyoxMO17LPAxBabangoyo-23-1-3-1-B*6-23-1/IWD-SYN-STR-C3--35-3-BB | White |
| M1124-27 | (1368/Mi82-23-2-1-2-B*7/P43SRC9FS100-1-1-8-#1-B1-13-B1-B*6)-58-1/DTPL-W-C7-S2-7-1-1-1-1-B-2-B*4/ BabangoyoxMO17LPAxBabangoyo-23-1-3-1-B*6-9-1/IWD-SYN-STR-C3--51-1-BB | White |
| M1124-29 | (1368/Mi82-28-1-1-2-B*7/P43SRC9FS100-1-1-8-#1-B1-13-B1-B*6)-40-1/DTPL-W-C7-S2-1-2-1-1-5-B-1-B*4/ BabangoyoxMO17LPAxBabangoyo-23-4-3-3-B*6-46-1/IWD-SYN-STR-C3--51-1-BB | White |
| M1124-31 | (KU1409/KU1414-SR/A619)-S2-2/9450xKI21-7-2-2-1-1-BB/(POP66SR/ACR91SUWAN1-SRC1/ACR91SUWAN1-SRC1-6X (MP420x4001xMP420)-3-1-3-1-B)S2-5-B*5 | Yellow |
| M1227-14 | (KU1409/KU1414-SR/KVI3)-S2-4-1-BB/9450xKI21-1-5-2-1-2-B*5/(SYN-Y-STR-34-1-1-1-1-2-1-B*5/NC354/ SYN-Y-STR-34-1-1-1-1-2-1-B*5)-S2-7-5-BB-B-B-B-B | Yellow |
| M1227-18 | (KU1409/KU1414-SR/A619)-S2-3-B/9450xKI21-1-4-1-1-2-B-B-B-B-B/(POP66SR/ACR91SUWAN1-SRC1/ ACR91SUWAN1-SRC1-6X(MP420x4001xMP420)-3-1-3-1-B)S2-5-BB-B-B-B-B | Yellow |
| M1227-21 | 9450xKI21-7-2-2-1-1-B-B-B-B-B/(KU1409/KU1414-SR/NC350)-S2-24-1-BB/(POP66SR/ACR91SUWAN1-SRC1/ ACR91SUWAN1-SRC1-6X(MP420x4001xMP420)-3-1-3-1-B)S2-10-BB-B | Yellow |
| M1227-6 | 1368 x Mi82-33-1-1-B-B-B-B-B/LATA-26-1-1-1-B-B-B-B-B-B/IWD-SYN-STR-C3--52-3-B-B-B | White |
| M1227-7 | 1368xHlx4269-1x1368-7-1-B-B-B-B-B-B-B-B-B/DTPL-W-C7-S2-1-2-1-1-5-B-1-B-B-B-B-B/IWD-SYN-STR-C3--47-1-B-B-B | White |

Source: Maize Improvement Program, IITA, Ibadan, Nigeria.

where $\overline{X}$ = mean value of the particular character.

GCV and PCV values were categorized as low when less than 10%, moderate, 10-20% and high, greater than 20% as indicated by Deshmukh et al (1986).

### Estimates of heritability and genetic advance

Broad sense heritability (H) and genetic advance (GA) for pooled data across locations for each hybrid class were estimated.

Broad-sense heritability was estimated according to the procedure suggested by Singh and Chaudhary (1985):

$$H = \frac{\delta_g^2}{\delta_p^2} x100$$

Heritability percentage was categorized as low when less than 40%, medium, 40 – 59%, moderately high, 60-79% and very high, 80% and above as indicated by Singh (2001).

Genetic advance (GA) values were determined by the formula illustrated by Johnson et al (1955):

GA= (K) ($\delta$A) (H).

where, K = 2.063 (selection differential at 5%); $\delta$A = phenotypic standard deviation of the mean yield of the hybrids and H = Broad sense heritability.

Genetic advance (GA) was expressed as a percentage of the hybrids mean. This was categorized as high when it is above 20%, moderate, 10-20% and low when it is less than 10%.

## Results

### Analysis of variance

The results of combined analysis of variance showing mean squares of traits for ten top-cross and ten three-way cross hybrids combined across three locations are presented in Table 2. Highly significant ($p \leq 0.01$) differences were detected among the genotypes, locations and genotype x location interactions for all the traits evaluated in the two hybrid classes, except for days to 50% anthesis where genotype x location interaction was not significant in three-way cross hybrids.

### Genetic variability, heritability and genetic advance

Estimates of means, range, genotypic and phenotypic variances and their coefficients of variation, heritability in broad sense and genetic advance as percentage of means among ten top-cross hybrids are presented in Table 3. High phenotypic and genotypic variance values were recorded for plant height, ear height and 100-grain weight. Moderate PCV and GCV values were recorded for ear height, ear length, 100-grain weight, field weight, and grain yield. Whereas number of kernel rows per cob recorded moderate PCV value only. On the other hand, low PCV and GCV values were recorded for days to 50% anthesis, days to 50% silking, plant height, and ear diameter. Number of kernel rows per cob recorded low GCV value only. Very high heritability estimate was observed only for ear length, whereas moderately high heritability values were recorded for ear height, 100-grain weight, grain yield, and field weight (Table 3). Characters such as days to 50% anthesis, plant

Table 2 - Mean squares of analysis of variance for ten top-cross and ten three-way cross maize hybrids combined across three locations.

| Source | DF | DPOL | DSLK | PLHT | EHT | ELTH | EDMT | KROW | GWT | FDWT | YLD |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Top-cross hybrids** | | | | | | | | | | | |
| Location (Loc.) | 2 | 200.54** | 172.93** | 7697.01** | 1802.01** | 28.64** | 5.18** | 14.15** | 335.51** | 8.75** | 10.04** |
| Rep (Loc.) | 6 | 2.76** | 4.36** | 27.64ns | 13.31ns | 0.92** | 0.49ns | 0.04ns | 1.28ns | 0.69ns | 0.17ns |
| Genotype (G) | 9 | 10.20** | 12.5** | 827.35** | 889.09** | 29.89** | 19.81** | 16.51** | 107.91** | 9.46** | 10.06** |
| Loc. x G | 18 | 3.03** | 5.76** | 259.25** | 117.67** | 1.49** | 5.08** | 3.69** | 12.54** | 1.75** | 1.58** |
| Error | 54 | 0.79 | 1.52 | 16.42 | 16.79 | 0.22 | 0.37 | 0.25 | 1.61 | 0.55 | 0.54 |
| C.V. (%) | | 1.49 | 1.97 | 2.01 | 4.67 | 2.71 | 1.26 | 3.36 | 4.19 | 11.88 | 12.1 |
| **Three-way cross hybrids** | | | | | | | | | | | |
| Location (Loc.) | 2 | 126.08** | 186.98** | 11053.7** | 4221.23** | 7.37** | 5.44** | 5.58** | 134.43** | 1.53* | 2.11** |
| Rep (Loc.) | 6 | 12.6ns | 3.34** | 48.7ns | 17.12** | 0.13ns | 0.14ns | 0.06ns | 3.66* | 0.87* | 0.77* |
| Genotype (G) | 9 | 34.69** | 23.28** | 439.4** | 637.96** | 9.72** | 27.08** | 6.42** | 59.65** | 7.16** | 6.30** |
| Loc. x G | 18 | 14.34ns | 5.69** | 78.3** | 102.78** | 2.66** | 3.91** | 1.22** | 6.01** | 2.6** | 2.29** |
| Error | 54 | 9.723 | 1.011 | 10.3 | 10.21 | 0.25 | 1.06 | 0.31 | 1.59 | 0.39 | 0.35 |
| C.V. (%) | | 5.21 | 1.63 | 1.73 | 3.85 | 2.99 | 2.13 | 3.9 | 4.21 | 10.5 | 10.32 |

DF = degrees of freedom, DPOL= days to 50% anthesis, DSLK= days to 50% silking, PLHT = plant height, EHT= ear height, ELTH= ear length, EDMT= ear diameter, KROW= number of kernel rows per cob, GWT= 100-grain weight, FDWT= field weight and YLD= grain yield. *, ** significant at 0.05 and 0.01 probability levels, respectively; ns = non-significant at P>0.05

height, number of kernel rows per cob, and ear diameter showed medium heritability values, while days to 50% silking showed low heritability value. Grain yield and field weight showed high GA, while ear length, 100-grain weight, ear height, and number of kernel rows per cob showed moderate GA. Traits such as plant height, ear diameter, days to 50% anthesis, and days to 50% silking recorded low GA values.

Table 4 shows the estimates of means, range, genotypic and phenotypic variances and their coefficients of variation, heritability in broad sense and genetic advance as percentage of means among ten three-way cross hybrids. High phenotypic and genotypic variance values were recorded for plant height, ear height, and 100-grain weight. Moderate PCV and GCV values were recorded for field weight and grain yield, whereas ear height recorded moderate PCV value only. Low PCV and GCV values were observed for days to 50% anthesis, days to 50% silking, plant height, ear length, ear diameter, number of kernel rows per cob, and 100-grain weight. Moderately high heritability estimates were recorded for plant height, ear height, ear diameter, number of kernel rows per cob, and 100-grain weight. Days to 50% anthesis and silking, and ear length showed medium heritability values. Field weight and grain yield recorded low heritability values. Moderate GA values were recorded for ear height, 100-grain weight, field weight, and grain yield. While days to 50% anthesis, days to 50% silking, plant height, ear length, ear diameter, and number of kernel rows per cob recorded low GA values.

## Discussion

The existence of variability is essential for resistance to biotic and abiotic factors as well as for wide adaptability of genotypes (Vashistha et al, 2013). The estimated genetic variability parameters observed in our study indicated that phenotypic variance was slightly higher than genetic variance for all the traits in both Top-cross and Three-way cross hybrids, except for plant and ear heights. However, there were slight differences between PCV and GCV values for all of the traits evaluated in the two hybrids classes, suggesting that there was a minimal influence of environments in the expression of these traits. Our results of genetic variability also revealed that plant height, ear height and 100-grain weight exhibited the highest phenotypic and genotypic values in the two hybrid classes. Yusuf (2010) and Nzuve et al (2014) also found highest phenotypic and genotypic variances for these traits. These results were consistent with observations of earlier workers (Alake et al, 2008; Bello et al, 2012; Nzuve et al, 2014). The higher differences observed between phenotypic variance and genotypic variance for plant and ear heights in both hybrid classes suggests that these characters were greatly influenced by the environments. The result for plant height corroborates with the findings of Ojo et al (2006) and Kashiani et al (2010).

Generally, PCV, GCV, and GA were low for most of the traits measured in three-way cross hybrids than in top-cross hybrids. Low genetic variability values were observed for plant height, days to 50% anthesis and silking, in top-cross hybrids, days to 50% anthesis and silking, plant height, ear length, ear diameter and number of kernel rows per cob in three-way cross hybrids indicate high influence of environmental conditions on these traits. Our results is part agreed with findings of Vashistha et al (2013) who observed low genetic variability for days to 50% anthesis and silking in maize cultivars. However, several characters in top-cross hybrids showed moderate PCV, and GCV values than in three-way cross hybrids, suggesting a good amount of variability among top-cross hybrids for these traits. The results of moderate PCV and GCV values observed in this study were reported by earlier researchers on plant and ear heights (Nzuve et al, 2014); kernel weight and kernels row[-1] (Alake et al, 2008) and 100-grain weight and ear diameter (Hefny, 2011). The moderate PCV and GCV values for field weight and grain yield observed in both hybrid classes revealed consistently high variability in these traits, suggesting the reliability of these traits for yield

Table 3 - Estimates of mean, range, phenotypic and genetic variability parameters, broad sense heritability and genetic advance as percent of mean for grain yield and other related traits among ten top- cross hybrids combined across three locations.

| Trait | Mean ± SE‡ | Range | $\partial^2 p$ | $\partial^2 g$ | PCV | GCV | H (%) | GA (%) |
|---|---|---|---|---|---|---|---|---|
| DPOL | 59.94 ± 0.28 | 55 - 65 | 1.63 | 0.80 | 2.13 | 1.49 | 48.93 | 2.15 |
| DSLK | 62.4 ± 0.29 | 57 - 68 | 2.33 | 0.74 | 2.44 | 1.38 | 31.95 | 1.61 |
| PLHT | 201.91 ± 1.89 | 160 - 239 | 145.89 | 63.12 | 5.98 | 3.93 | 43.27 | 5.34 |
| EHT | 87.71 ± 1.36 | 62 - 119 | 121.21 | 85.71 | 12.55 | 10.56 | 70.72 | 18.31 |
| ELTH | 17.4 ± 0.22 | 13.3 - 22.8 | 3.60 | 3.16 | 10.91 | 10.21 | 87.63 | 19.72 |
| EDMT | 48.38 ± 0.19 | 44.7 - 52.5 | 3.25 | 1.64 | 3.73 | 2.64 | 50.33 | 3.87 |
| KROW | 14.76 ± 0.18 | 11.3 - 20.0 | 2.60 | 1.42 | 10.93 | 8.08 | 54.73 | 12.34 |
| GWT | 30.29 ± 0.49 | 22 - 41 | 14.42 | 10.60 | 12.54 | 10.75 | 73.50 | 19.01 |
| FDWT | 6.25 ± 0.14 | 3.6 - 10.8 | 1.32 | 0.86 | 18.35 | 14.80 | 65.09 | 24.64 |
| YLD | 6.06 ± 0.15 | 3.5 - 10.5 | 1.35 | 0.94 | 19.17 | 16.02 | 69.79 | 27.60 |

‡SE = standard error of mean

DPOL= days to 50% anthesis, DSLK= days to 50% silking, PLHT = plant height, EHT = ear height, ELTH = ear length, EDMT = ear diameter, KROW = number of kernel rows per cob, GWT = 100-grain weight, FDWT= field weight, and YLD = grain yield; $\partial^2 p$ = phenotypic variance, $\partial^2 g$ = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H (%)= broad sense heritability, GA = genetic advance as percent of mean.

improvement in maize.

Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain (Rao and Rao, 2015). In our study, there were low to very high magnitude of broad sense heritability values recorded for traits measured in the top-cross hybrids, whereas the three-way cross hybrids exhibited low to moderately high broad sense heritability estimates. However, all the traits measured in the two classes of hybrids showed different levels of heritability estimates. Ear length, for instance, exhibited very high heritability value in top-cross hybrids but showed medium heritability value in three-way cross hybrids. Similarly, grain yield and field weight exhibited moderately high heritability values in top-cross hybrids, but low heritability values in three-way cross hybrids. Relative, moderately high heritability values were observed for plant height, ear diameter, and number of kernel rows per cob in three-way cross hybrids, while medium heritability estimates were recorded for the same traits in top-cross hybrids. Langade et al (2013) reported high to moderate heritability in maize for days to 50% anthesis and silking, ear height, ear length, and ear diameter. Ojo et al (2006) recorded the largest heritability values for ear-weight with husk and ear-weight without husk. The low heritability estimates observed in the present study indicated low genetic potential and high effects of environment in determining these traits.

Heritability of a trait is a key component in determining GA from selection (Nyquist, 1991). In this study, we observed low to high GA values for all the traits measured in top-cross hybrids and low to moderate in three-way cross hybrids. Field weight and grain yield exhibited high GA values in top-cross hybrids but revealed medium values in three-way cross hybrids. Very high heritability estimate and moderate GA values were observed for ear length in top-cross hybrids. Moderately high heritability estimates coupled with high values of GA were recorded for field

weight and grain yield in the same hybrid class suggest that these traits were governed by additive gene action and phenotypic selection for these traits will be effective. El-Badawy (2012) reported high GA with high to moderate heritability estimates for ear diameter and ear weight plant[-1] in three crosses of maize. Similarly, Hefny (2011) also reported highest GA at both planting dates and high heritability values for yield plant[-1] and 100-kernel weight.

Moderately high heritability values and moderate GA values observed, in the present study, for ear height and 100-grain weight in both top-cross and three-way cross hybrids indicate the existence of intermediate additive and non-additive gene actions, suggesting that phenotypic performance of these traits can be achieved through careful selection. Rajesh et al (2013) reported high to moderate heritability with moderate estimates of GA for grain yield, plant height, ear height, number of kernels per row and 100-kernel weight. Low heritability values and low GA observed for days to 50% silking in top-cross hybrids and low heritability values and moderate GA estimates for field weight and grain yield in three-way cross hybrid suggested that these traits were governed by non-additive gene action and direct selection may not be possible because most of the variation is attributed to the environmental effects. Wondimu et al (2014) suggested that such traits require management practices than selection to improve the traits performance. Similar findings were reported by Vashistha et al (2013). Estimate of GA is more useful as a selection tool when considered jointly with GCV and heritability values (Johnson et al, 1955). Traits such as field weight and grain yield showed moderate GCV, moderately high heritability values and high GA values in top-cross hybrids, suggesting that they were principally under genetic control. The combinations of high heritability and GA are important indicators of the predominant role of additive gene action in these characters. Predictability of high performance and selection of hybrids based on high heritability and genetic advance would lead to

Table 4 - Estimates of mean, range, phenotypic and genetic variability parameters, broad sense heritability and genetic advance as percent of mean for grain yield and other related traits among ten three-way cross hybrids combined across three locations.

| Trait | Mean ± SE‡ | Range | $\partial^2 p$ | $\partial^2 g$ | PCV | GCV | H (%) | GA (%) |
|---|---|---|---|---|---|---|---|---|
| DPOL | 59.82 ± 0.42 | 52 - 87 | 4.88 | 2.26 | 3.69 | 2.51 | 46.35 | 3.53 |
| DSLK | 61.64 ±0.31 | 55 - 67 | 3.63 | 1.95 | 3.09 | 2.27 | 53.87 | 3.43 |
| PLHT | 185.24 ± 1.88 | 153 - 221 | 63.93 | 40.12 | 4.32 | 3.42 | 62.76 | 5.59 |
| EHT | 82.9 ± 1.44 | 55 - 119 | 91.46 | 59.46 | 11.54 | 9.30 | 65.02 | 15.47 |
| ELTH | 16.58 ± 0.14 | 13.8 -19.3 | 1.62 | 0.78 | 7.67 | 5.34 | 48.54 | 7.68 |
| EDMT | 48.4 ± 0.22 | 42.2 - 53.0 | 3.64 | 2.57 | 3.94 | 3.31 | 70.67 | 5.75 |
| KROW | 14.28 ± 0.12 | 12 - 17.3 | 0.92 | 0.58 | 6.70 | 5.32 | 63.00 | 8.71 |
| GWT | 30 ± 0.36 | 20 - 37 | 7.61 | 5.96 | 9.20 | 8.14 | 78.31 | 14.86 |
| FDWT | 5.93 ± 0.13 | 3.2 - 10.3 | 1.29 | 0.51 | 19.12 | 12.00 | 39.36 | 15.53 |
| YLD | 5.75 ±0.13 | 3.1 - 10.0 | 1.13 | 0.44 | 18.51 | 11.60 | 39.27 | 15.00 |

‡SE = standard error of mean

DPOL= days to 50% anthesis, DSLK= days to 50% silking, PLHT = plant height, EHT = ear height, ELTH = ear length, EDMT = ear diameter, KROW = number of kernel rows per cob, GWT = 100-grain weight, FDWT = field weight and YLD = grain yield; $\partial^2 p$ = phenotypic variance, $\partial^2 g$ = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H (%) = broad sense heritability, GA = genetic advance as percent of mean.

successful maize breeding program.

*Conclusion*

Traits measured in this study revealed different levels of variability, heritability and GA estimates between the two hybrid classes. More characters in top-cross hybrids revealed sufficient amount of variability than in three-way cross hybrids, thus offer scope for genetic improvement through selection. However, field weight and grain yield revealed consistently high variability in both hybrid classes. Grain yield and field weight, to a great extent, were governed by additive gene effect in top-cross hybrids, as demonstrated by their moderate GCV, moderately high heritability and high GA. Whereas, in three-way cross hybrids, these traits were governed by non-additive gene action as they exhibited low heritability and GA estimates.

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