



Genetic Variability and Divergence of Drought Tolerant Open Pollinated Maize (*Zea mays* L.) Genotypes Grown Under Random Stress in Jigjiga, Ethiopia

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ABSTRACT

Low-moisture availability is one of the major causes for grain yield reduction in dry land areas. Twenty-four open pollinated maize genotypes were evaluated in a randomized complete block design at the main research station of Jigjiga Pastoral and Agricultural Research Centre to assess performance, variability and heritabilities of important traits. The recorded range and mean performances as well as significant genotypic and phenotypic variances for most of the tested traits indicated the existence of considerable amount of variability among the genotypes. Grain yield had higher genetic and phenotypic coefficient of variation coupled with the highest genetic advance as percent of mean (56.5%). Genotypes (VP05147, ZM523 and VP0713) gave the highest grain yield with promising expression in other desirable traits. Estimates of the broad-sense heritability were higher for grain yield (72.58) and other yield component traits. However, days to tasseling, anthesis, silking, maturity, anthesis-silking interval, leaf area index, plant and ear height demonstrated below 40%. In general, the observed differences in performances, variability and heritabilities in the tested traits of the populations confirmed possibility to increase maize productivity in target area through direct use and/or the best one improvement or utilizing their diversity as germplasm source for development of superior inbred-lines.

Keywords: Genetic advances, Genetic divergence, Heritability, Open pollinated maize, Variability

INTRODUCTION

Maize (*Zea mays* L.) is an annual plant belonging to the grass family Graminae or Poaceae (Tollenaar and Dwyer, 1999). It is an important cereal and fodder crop which occupies a pivotal role in the world economy (White and Johnson, 2003). Maize grows in most parts of the world over a wide

range of environmental conditions, with altitudinal ranges of 0 to 3000 meters above sea level and temperature from 5 to 45 °C (Dowswell *et al.*, 1996). Although it is widely adaptable to various climatic and soil conditions, the crop can be affected when exposed to extreme environmental factors, such as low moisture stress during its growing period.

Diversity among maize genotypes is important for identifying parental lines for successful breeding program, and hybrid development (Kostova *et al.*, 2006; Losa *et al.*, 2011). Since there is a rapid increase in climate change, there is a need to develop high yielding genotypes with tolerance to various environmental stresses. The analysis of genetic diversity provides breeders and researchers with useful information for germplasm preservation and the identification of group of inbred lines and other breeding materials that may be exploited by the production of highly heterotic hybrids (Melil *et al.*, 2013). Additionally, characterization of genetic diversity of maize germplasm is of great importance in hybrid maize breeding (Xia *et al.*, 2005).

In drought tolerant plants, there are many defence mechanisms, such as osmoregulation, antioxidant and hormonal systems, helping plants to stay alive and develop earlier to their reproductive stages (Sairam and Tyagi, 2004; Ashraf, 2010). Physiological and morphological characteristics such as osmotic adjustment, stomata behaviour, chloroplast activity, leaf water potential, root volume, root weight, leaf area and dry matter production are found different in maize cultivars grown under limited water supply (Weerathaworn *et al.*, 1992; Mian *et al.*, 1993). Changes in morphological characters are the ultimate determinants of stress effects on plants (Farooq *et al.*, 2009; Jaleel *et al.*, 2009). Drought tolerant genotypes of maize are recognized from sensitive ones by higher photosynthetic rate and short anthesis-silking interval (Olaoye *et al.*, 2009).

In Ethiopia, maize production has remained low, with the estimated national average yield of 3.1 t ha⁻¹ compared to the world average yield at 5 t ha⁻¹ due to several constraints (CSA, 2013). About 40% of the total maize growing areas is located in low-moisture stress areas but contributes less than 20% to its total production (Mandefro *et al.*, 2001). This low productivity is mainly associated with drought since about 85% of the crop production is handled by small-

scale farmers under rain-fed growing conditions. Although drought is unpredictable, maize is most sensitive to low-moisture stress during two weeks bracketing flowering that often results in barrenness and serious yield instability at farm level (Bolaños and Edmeades, 1996).

The problem of low moisture stress can be solved either by providing supplemental irrigation to the crop in rainfed areas or by developing genotypes which can produce higher and more stable yield in water-limited areas. The provision of supplemental irrigation is currently challenging for Ethiopian agriculture due to the dominance of small scale rainfed agriculture. The development of drought tolerant cultivars is the best way to cope with the drought stress. Most of the people of the Somali National Regional State mainly earn their livelihood from livestock; they practice crop production as well. Maize is the major crop cultivated and predominant in the region, particularly under low-moisture areas. This investigation needs to look deeply on the drought background for sources of genotypes, which can be effectively used as parents to develop a new variety with high yield and good agronomic traits with adaptation to drought conditions. However, in Somali National Regional States of Ethiopia, information is lacking on performance and variability of drought tolerant maize genotypes. Hence, the study was undertaken with the objectives: (1) to assess the performance, variability, genetic advance and heritabilities of desired traits in drought tolerant open-pollinated maize genotypes; and (2) to identify divergent parents from distantly related clusters for future hybridization.

MATERIALS AND METHODS

Experimental Design and Methods

The research was carried out at the main station of Jigjiga Pastoral and Agricultural Research during 2013 cropping season. It is located 628 km far away from the capital of Addis Ababa to the Eastern part of Ethiopia, situated at 09°21'7"N latitude and 42° 49'7"E longitude and also at an altitude of 1672 meter above sea level. It receives a mean annual rainfall of 722 mm, with the maximum and minimum temperature of 28 °C and 18 °C, respectively. The experimental materials included 24 drought tolerant open pollinated maize genotypes. They have been developed for drought tolerance by the International Maize and Wheat Improvement Institute (CIMMYT)

using simultaneously both managed drought stress at flowering and optimum irrigation for screening. Most of these genotypes have been released as variety for production in the Eastern and Southern Africa countries (Table 1). The experiment was conducted in randomized complete block design with three replications. The plot size was four rows with inter-row and intra-row spacing's of 0.75 m and 0.25 m respectively; the row length was 5 m and plot size of 15 m². Two seeds per hill were planted in the trial site to ensure uniform stand and then thinned to one plant per hill. The crop was raised under rain fed conditions with the recommended agronomic management (weeding, cultivation and fertilizer application) practices.

Statistical analysis

Data were subjected to analysis of variance using the procedures outlined by Cochran and Cox (1957). Significant differences among genotypes were separated by Duncan's Multiple Range Test (DMRT). Analysis of covariance was done for each pair of characters to obtain the sum of cross products to be used in covariance calculation. The randomized complete block design (RCBD) analysis of variance was used to derive variance components. The phenotypic and genotypic variance components and coefficient of phenotypic and genotypic variation were estimated based on the method suggested by Burton and DeVane (1953) as follows:

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{Msg} - \text{Mse}}{r}$$

Where, Msg and Mse are the mean squares for the genotypes and error in the analysis of variance, respectively. r is the number of replications. The Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated according to the formula outlined by Singh and Chaudhary (1977).

$$\text{PCV} = \left(\frac{\sqrt{\sigma^2_p}}{\text{grand mean}} \right) \times 100$$

$$\text{GCV} = \left(\frac{\sqrt{\sigma^2_g}}{\text{grand mean}} \right) \times 100$$

Broad sense heritability (h^2) values were estimated based on the formula of (Johnson *et al.*, 1955) as follows:

$$h^2 = \left(\frac{\sigma^2_g}{\sigma^2_p} \right) \times 100$$

Then, the genetic advance for selection intensity (k) at 5% (2.06) was estimated by the following formula (Johnson *et al.*, 1955):

$$\text{EGA} = k * \sigma_p * h^2$$

Where, EGA = the expected genetic advance under selection

σ_p = the phenotypic standard deviation

h^2 = heritability in broad sense

k = selection intensity

The genetic advances as percent of population mean (GA) were also estimated following the procedure of Johnson *et al.* (1955):

$$\text{GA} = \left(\frac{\text{EGA}}{\text{grand mean}} \right) \times 100$$

Clustering of genotypes into different groups was carried out by average linkage method and the appropriate number of clusters was determined from the values of Pseudo F and Pseudo T statistics using the SAS computer software facilities (SAS, 1999-2000). By employing the same software, F-statistics and univariate test statistics was used to test the significances of generalized squared distances between clusters and that of clusters versus traits, respectively.

The Mahalanobis generalized distances (1936 as cited in Ganesan *et al.*, 2010) was utilized to estimate the intra and inter cluster distance using the SAS computer software package as per the following formula:

$$D^2_{ij} = (X_i - X_j)' S^{-1} (X_i - X_j)$$

Where, D^2_{ij} = the distance between any two groups i and j

X_i and X_j = the vector mean of the traits for the i^{th} and j^{th} groups, respectively

S^{-1} = the inverse of the pooled covariance matrix

RESULTS AND DISCUSSION

The analysis of variance indicating source of variation and mean squares for the studied genotype based on the mean values of 16 quantitative characters are shown in Table 2. Significant ($p < 0.05$) and highly significant ($p < 0.01$) differences among the open pollinated maize genotypes were observed for three traits of days to tasseling, leaf area index and number of kernel rows per ear; and seven traits of number of ears per plot, number of ears per plant, number of

kernels per row, biological yield, thousand kernel weight, grain yield and harvest index, respectively. This confirmed the existence of sufficient genetic variability in the studied genotypes for yield and related traits.

Mean and Range

Means and standard error regarding different characters of 24 open pollinated maize genotypes and their ranges of variability are given in Table 3. Coefficients of variation (CV) were used to compare the precision of the experiment with various means (Table 2). The means with less than 20% in CV for most of the characters revealed existence of reliability of the data. Similar findings were reported by Shabbir *et al.* (2007) for grain yield, number of ears per plant, days to tasseling, days to silking and plant height. There were high coefficients of variation (CV %) for anthesis-silking interval (22.4%) and ear height (23.7%) which indicated high variability among the tested genotypes for the traits.

A range for days to tasseling was 71.3 to 80.7 with minimum values for genotypes ZM309 and VP05118,

the maximum for ZM521 with an average value of 76 days. Coefficient of variation for the variable was 4.52% and its standard error was 0.53. Days to anthesis ranged from 82 (VP05147) to 92.3 (VP051) with a mean value of 87.15 days. Its coefficient of variation was 4.52% and its standard error was 0.57. Days to silking also ranged from 76 (VP05147) to 87.3 (VP051) with an average value of 81.65 days. Its coefficient of variation was 4.9% and 0.61 standard error. These results are in line with the findings of Naushad *et al.* (2007) and Nazir *et al.* (2010). The other flowering traits, days to anthesis-silking interval ranged from 3.3 (VP0610) to 6.3 (VP05118) with an average value of 4.8 days and 0.14 standard error. Similarly like other growth stages, days to maturity ranged from 113.7 (VP05147) to 128.3 (ZM521) with an average value of 121 days indicating that the tested genotypes were early to medium maturing category. Its coefficient of variation and standard error were 4.3% and 0.82, respectively. Leaf area index ranged from 0.197 (VP0730) to 0.35 cm (ZM523) with an average value of 0.27 cm. Coefficient of variation for the variable was 16.9% and its standard error of 0.006. The findings were in line with Ali *et al.* (2010).

Table 1: List of their pedigree and production status of drought tolerant open pollinated maize genotypes used for the study.

Entry	Name	Pedigree	Released in
1	ZM309	VP047	A, ML, MO, ZM
2	ZM401	Syn01E2	T, ZM, SA
3	VP051	SynG15QSR	MX
4	VP05118	[P401,P402,ZEWAc1F2L/ZEWBc1F2P]-#	MX
5	VP05147	ZM303c2F2-#	ZM
6	VP05163	VP041-#	SA
7	VP05179	[Syn01E2/ECAEE16]F2	ZM
8	VP05194	[S99TLWQ-AB/OBATANPA-ZMSRc1F3]#-#	MA
9	VP0610	[Syn0411]H#-#	ZM
10	VP065	[Syn045]H#-#	ZM
11	VP0712	(Syn01E2/DTPWC9)F2	MX
12	VP0713	(VP041/LaPostaSeqC8)F2	MX
13	VP0716	(Syn01E2/LaPostaSeqC8)F2	MX
14	VP0720	(VP047/03SADVI)F2	SA
15	VP0721	(Syn01E2/03SADVI)F2	ET
16	VP0730	VHTA06DTSyn	MX
17	VP0731	VHTB06DTSyn	ZM
18	VP079	(VP041/DTPWC9)F2	MX
19	VP086	VHTDEF07Syn	SA
20	ZM421	ZM421-#	AN, ZA
21	ZM423	ZM423-##	AN, ZA
22	ZM521	ZM521-FLINT-##	AN, ET, K, MO, ZA, ZM
23	ZM523	ZM523-##	AN, ET, ML, MO, T
24	ZM525	02SADVE	ET, K, T

Description of the abbreviation: AN= Angola; ET= Ethiopia; K= Kenya; MA= Madagascar; MX= Mexico; ML= Malawi; MO= Mozambique; SA= South Africa; T= Tanzania; ZA= Zambia; ZM= Zimbabwe

Table 2: Mean squares of the 16 traits of open pollinated maize genotypes tested at Jigjiga Centre (2013/14).

Source of Variation	Degree of Freedom	Mean square of traits								
		DT	DA	DS	ASI	LAI	PH	EH	DM	NEP
Replication	2	155.5	213.8	244.6	1.04	0.008	2783.4	647.8	631.8	28.4
Genotype	23	25.1*	21.99 ^{NS}	28.2 ^{NS}	1.72 ^{NS}	0.004*	479.5 ^{NS}	181.7 ^{NS}	38.1 ^{NS}	40.1**
Error	46	12.02	15.7	16.3	1.2	0.0016	332.75	103.5	27.6	6.8
Total	71									
CV (%)		4.52	4.52	4.9	22.4	16.9	15.3	23.7	4.3	12.4
Mean		76.7	87.5	82.6	4.9	0.24	119.3	42.9	120.9	21.1

Source of Variation	Degree of Freedom	Mean square of traits						
		NEPP	NKRPE	NKPR	BY	TKWT	GY	HI
Replication	2	0.05	5.04	54.8	1711934.2	898.64	56816.82	41.5
Genotype	23	0.07**	3.2*	25.4**	1029164.4**	903.3**	244856.56**	226.4**
Error	46	0.01	0.93	6.8	232241.9	183.52	27382.13	34.1
Total	71							

NS, ** and * indicates not significant, highly significant at 1% and significant at 5% probability levels, respectively.

DT: days to tasseling, DA: days to anthesis, DS: days to silking, ASI: anthesis-silking interval, LAI: leaf area index (cm), PH: plant height (cm), EH: ear height (cm), DM: days to maturity, NEP: numbers of ears per plot, NEPP: number of ears per plant, NKRPE: number of kernel rows per ear, NKPR: number of kernels per row, BY: biological yield (kg/ha), TKWT: thousand kernel weights (g), GY: grain yield (kg/ha), HI: harvest index (%).

Grain yield of the genotypes ranged from 274.50 to 1323.50 kg/ha with the lowest in VP079 and highest in VP05147 followed by ZM523 and VP0713 with an average of 799 kg/ha. The coefficient of variation for the variable was 19.8% and its standard error of 44.42. Here, the highly significant difference among the maize genotypes in grain yield was clearly demonstrated. Besides, this reflected availability of genotypes with diverse genetic background. The results were in line with the findings of Grzesiak (2001) and Salami *et al.* (2007). Harvest index also ranged from 14.4 (VP079) to 48.8% (VP05147) with a mean value of 31.6%. The coefficient of variation and standard error for the variable were 17.5% and 1.16, respectively. High variation in harvest index reflected significant variability in yielding abilities among the genotypes. Besides, it is suggested that the more harvest index showed more grain yield and vice versa. Similar result was reported by Nazir *et al.* (2010).

The study identifies three open pollinated genotypes (VP05147, ZM523 and VP0713) with superior performances in grain yield and its components. On the contrary, VP079 and VP051 exhibited extremely poor performance in the traits. In addition to drought tolerance, these three maize genotypes could be used as source materials for superior inbred lines development or direct use through verification and release in target environment.

Estimates of variance components

The genetic parameters of the traits that were estimated both for genotypic and phenotypic coefficients of variation; broad sense heritability as well as genetic advance for selection is presented in Table 3. A wide range genotypic variability was recorded for the character of biological yield, grain yield, thousand kernel weights, harvest index, plant and ear height. Similar findings were reported by Anshuman *et al.* (2013) for the aforementioned characters. Although moderate for number of ears per plot, the estimates for most of the other characters were very low. Among these characters, the present observation in days to tasseling and silking was in agreement with Anshuman *et al.* (2013).

Maximum values of phenotypic variance were recorded for biological yield followed by grain yield, thousand kernel weights, plant height, ear height and harvest index. These characters showed significantly at both genotypic and phenotypic level of variances. However, the magnitudes of phenotypic variance for these traits were higher than that of genotypic variances, indicating the influence of environments in their expression.

The genotypic coefficient of variation (GCV) was less than its corresponding estimates of phenotypic coefficient of variation (PCV) for all the traits, which

indicated significant role of environment in the tested traits. Estimates of phenotypic coefficients of variation ranged from 4.61% (days to maturity) to 37.80% (grain yield). The genotypic coefficients of variation also ranged from 1.55% (days to maturity) to 32.20% (grain yield).

Magnitudes of phenotypic and genotypic coefficient of variation were the highest for grain yield (37.80 and 32.20) followed by harvest index (29.67 and 23.97). The high PCV and medium GCV were exhibited by biological yield, ear height, leaf area index and number of ears per plot. Furthermore, a high PCV and low GCV were recorded for anthesis-silking interval. Number of ears per plant, number of kernels per row and thousand kernel weights also showed intermediate amount of both parameters. However, medium PCV and low GCV were appeared in plant height and number of kernel rows per ear. Overall, the aforementioned estimations indicated the existence of substantial variability that ensures ample scope for their improvement through selection. These observations are in confirmation with the findings of Rafique *et al.* (2004), Rafiq *et al.* (2010) and Ram Reddy *et al.* (2012). However, low estimates of

phenotypic and genotypic coefficients of variation were recorded for days to tasseling, days to anthesis, days to silking and days to maturity that revealed existence of low variability among the genotypes for these characters and less chance to change their maturity period through selection. Similar results were reported for days to anthesis and days to silking by Bello *et al.* (2012).

Estimates of heritability

The estimated broad sense heritability for the studied traits varied between 11.3% for days to maturity and 72.6% for grain yield (Table 3). According to the magnitude of heritability estimates, the characters were expressed as medium, low and high. Relatively high broad sense heritability estimates were recorded in grain yield followed by harvest index, number of ears per plot and number of ears per plant. Accordingly, these characters could be improved through selection as their high dependent on genetic and low influence by environmental factors was confirmed by their high heritability. It was in agreement with the findings of Chen *et al.* (1996) and Anshuman *et al.* (2013) for grain yield and harvest index, and Wannows *et al.* (2010) for grain yield.

Table 3: Estimate of ranges, mean, genotypic (σ^2_g) and phenotypic (σ^2_p) component of variances, broad sense heritability (H^2), and genetic advance as percent of mean (GAM) of 16 characters of open pollinated maize genotypes evaluated at Jigjiga Centre (2013/14).

Traits	Range	Mean \pm SE	σ^2_p	σ^2_g	PCV (%)	GCV (%)	H^2 (%)	EGA	GAM (%)
DT	71.3 - 80.7	76 \pm 0.53	16.38	4.36	5.28	2.72	26.62	2.22	2.89
DA	82 - 92.3	87.15 \pm 0.57	17.79	2.09	4.82	1.65	11.78	1.02	1.17
DS	76 - 87.3	81.65 \pm 0.61	20.27	3.97	5.45	2.41	19.57	1.82	2.19
ASI	3.3 - 6.3	4.8 \pm 0.14	1.37	0.17	23.92	8.49	12.62	0.30	6.22
LAI	0.197 - 0.35	0.27 \pm 0.006	0.003	0.001	21.52	10.76	25	0.03	11.08
PH	99.4 - 151.3	125.35 \pm 2.50	381.67	48.92	16.38	5.86	12.82	5.16	4.32
EH	30.5 - 63.5	47 \pm 1.40	129.57	26.07	26.53	11.90	20.12	4.72	10.99
DM	113.7 - 128.3	121 \pm 0.82	31.10	3.50	4.61	1.55	11.25	1.29	1.07
NEP	12.7 - 26.7	19.7 \pm 0.50	17.88	11.11	20.04	15.79	62.14	5.41	25.65
NEPP	0.57 - 1.1	0.835 \pm 0.02	0.03	0.02	19.35	15.25	62.07	0.22	24.74
NKRPE	10.9 - 15.1	13 \pm 0.16	1.68	0.75	10.36	6.91	44.53	1.19	9.50
NKPR	17.9 - 29.3	23.6 \pm 0.44	12.98	6.21	15.59	10.78	47.84	3.55	15.37
BY	2148.1 - 4740.7	3444.4 \pm 85.97	497882.70	265641	23.38	17.07	53.35	775.5	25.69
TKWT	106.67 - 159.44	133.05 \pm 2.96	423.45	239.93	15.51	11.67	56.66	24.02	18.10
GY	274.50 - 1323.50	799 \pm 44.42	99873.61	72491.4	37.80	32.20	72.58	472.5	56.52
HI	14.4 - 48.8	31.6 \pm 1.16	98.20	64.10	29.67	23.97	65.27	13.33	39.89

DT: days to tasseling, DA: days to anthesis, DS: days to silking, ASI: anthesis-silking interval, LAI: leaf area index (cm), PH: plant height (cm), EH: ear height (cm), DM: days to maturity, NEP: numbers of ears per plot, NEPP: number of ears per plant, NKRPE: number of kernel rows per ear, NKPR: number of kernels per row, BY: biological yield (kg/ha), TKWT: thousand kernel weight (g), GY: grain yield (kg/ha), HI: harvest index (%)

Moderate heritability were observed in thousand kernel weights, biological yield, number of kernels per row and number of kernel rows per ear. On the contrary, low estimates of heritability were recorded for days to tasseling (26.62%), leaf area index (25%), ear height (20.12%), days to silking (19.6%), plant height (12.8%), anthesis-silking interval (12.6%), days to anthesis (11.8%) and days to maturity. The contribution of these characters for selection was limited due to the masking effect of the environments. The observation for anthesis-silking interval was in harmony with the findings of Anshuman *et al.* (2013), but contrary with the results of Aminu and Izge (2012) who reported high and moderate heritability for anthesis-silking interval, plant height; days to tasseling, ear height and days to silking.

Estimates of expected genetic advance

The estimated genetic advance as percentage of mean varied from 1.1% (days to maturity) to 56.52% (grain yield) (Table 3). In the present investigation, high genetic advance as percent of mean was recorded for grain yield, harvest index, biological yield, number of ears per plot and number of ears per plant. Furthermore, moderate values of genetic advance were also observed for thousand kernel weight, number of kernels per row, leaf area index and ear height. The remaining other characters exhibited low estimates.

High genetic advance associated with relatively high heritability and high genetic variance coefficients were found in grain yield and harvest index. This indicates that these characters were mostly controlled by additive gene action that can be considered as more reliable basis of selection. For grain yield, similar findings were reported by Ali *et al.* (2010), Ram Reddy *et al.* (2012) and Atnafua and Nageshwar (2014).

High heritability with moderate genetic advance was recorded for number of ears per plot and number of ears per plant, while moderate heritability with high genetic advance was registered for biological yield. Moderate estimates of heritability paired with moderate estimates of genetic advance were observed for thousand kernel weight and number of kernels per row. Unlike other yield components, number of kernel rows per ear showed moderate heritability with low genetic advance. This showed that the interference of both additive and dominance gene effects.

Leaf area index and ear height exhibited low heritability and moderate genetic advance as percent of mean. Low heritability and genetic advance were found for days to tasseling, days to silking, plant height, anthesis-silking interval, days to anthesis and days to maturity, indicated that these characters were controlled by non-additive gene action. Similar results were reported by Shabbir *et al.* (2007) for days to tasseling, days to silking and plant height.

Genetic Divergence Analysis

Clustering of genotypes

Clustering was applied using average linkage method for 24 open pollinated maize genotypes that were separated into three different clusters (Table 4). A dendrogram summarizing the homogeneities between maize genotypes based on the sixteen traits is shown in Figure 1. In this study, the distribution of genotypes into various clusters showed considerable genetic divergence on the tested maize genotypes. It was indicated that cluster I (50%) contained maximum of 12 genotypes that showed the presence of genetic similarity among themselves, followed by cluster II (45.83%) included 11 genotypes. The lowest singleton was comprised in cluster III (4.17%).

Estimates of average intra and inter cluster square distances

The pairwise generalized square distances (D^2) between all clusters (Table 5) showed highly significant variation ($P < 0.01$) indicating wide diversity among genotypes in various clusters. The maximum inter-cluster divergence was observed between clusters I and III, followed by clusters II and III, indicated that there was a wide genetic variability among the genotypes. It also showed minimum distance between clusters I and II, which revealed that narrow genetic diversity among genotypes. The maximum and minimum intra-cluster distance was observed in clusters III and I, respectively. The distance with in cluster II was as much related as cluster I, revealed that the variability of genotypes within these clusters are homogeneous in nature. Cluster III had only a single genotype and its intra cluster distance was highest.

In the present investigation, selection would be more effective from most divergent clusters and hybridizations involving from distant parents are expected to generate wide diversity and manifest for

the enhancement of high grain yield in maize. Inter-cluster distance was much higher than the intra-cluster one, indicating that there were differences and similarities of nature among the genotypes found between and within groups, respectively. Depending

up on wide inter-cluster distances (clusters I and II with III), crossing among the genotypes from different clusters would favor the chance to mate with genetic variability that increases efficiency for improvement of grain yield in maize.

Table 4: Distribution of 24 open pollinated maize genotypes into different clusters

Clusters	No. of Genotypes	Genotypes			
I	12	VP051	VP065	VP05163	VP086
		ZM401	VP0716	ZM421	VP0721
		VP0730	VP0610	VP0720	VP079
II	11	VP05118	ZM521	VP0713	VP05194
		ZM309	VP0731	VP05147	VP0712
		VP05179	ZM525	ZM423	
III	1	ZM523			

Table 5: Average intra (bold face) and inter-cluster (above diagonal) divergence (D^2) values of 24 open pollinated maize genotypes.

Clusters	I	II	III
I	1.386	96.63**	479.32**
II		1.56	175.64**
III			6.356

** = highly significant at 0.01 probability level ($\chi^2_{16} = 32.00$)

Table 6: Mean values of clusters for 16 traits of the 24 open pollinated maize genotypes.

Traits	Clusters		
	I	II	III
Days to tasseling	77.825	75.327	77.3
Days to anthesis	88.45	86.582	87
Days to silking	83.98	81.127	83
Anthesis- silking interval	4.492	5.455	4
Leaf area index (cm)	0.218	0.252	0.35
Plant height (cm)	111.325	125.082	151.3
Ear height (cm)	38.925	45.473	63.5
Days to maturity	122.07	119.73	119.7
Number of ears per plot	19.225	22.54	26.7
Number of ears per plant	0.807	0.945	1.1
Number of kernel rows per ear	12.525	12.44	13.6
Number of kernels per row	21.45	24.56	27.7
Biological yield (kg/ha)	2574.1	3346.8	4740.7
Thousand kernel weights (g)	122.99	140.87	159.44
Grain yield (kg/ha)	638.50	1013.23	1257.4
Harvest index (%)	30.375	36.791	31.9

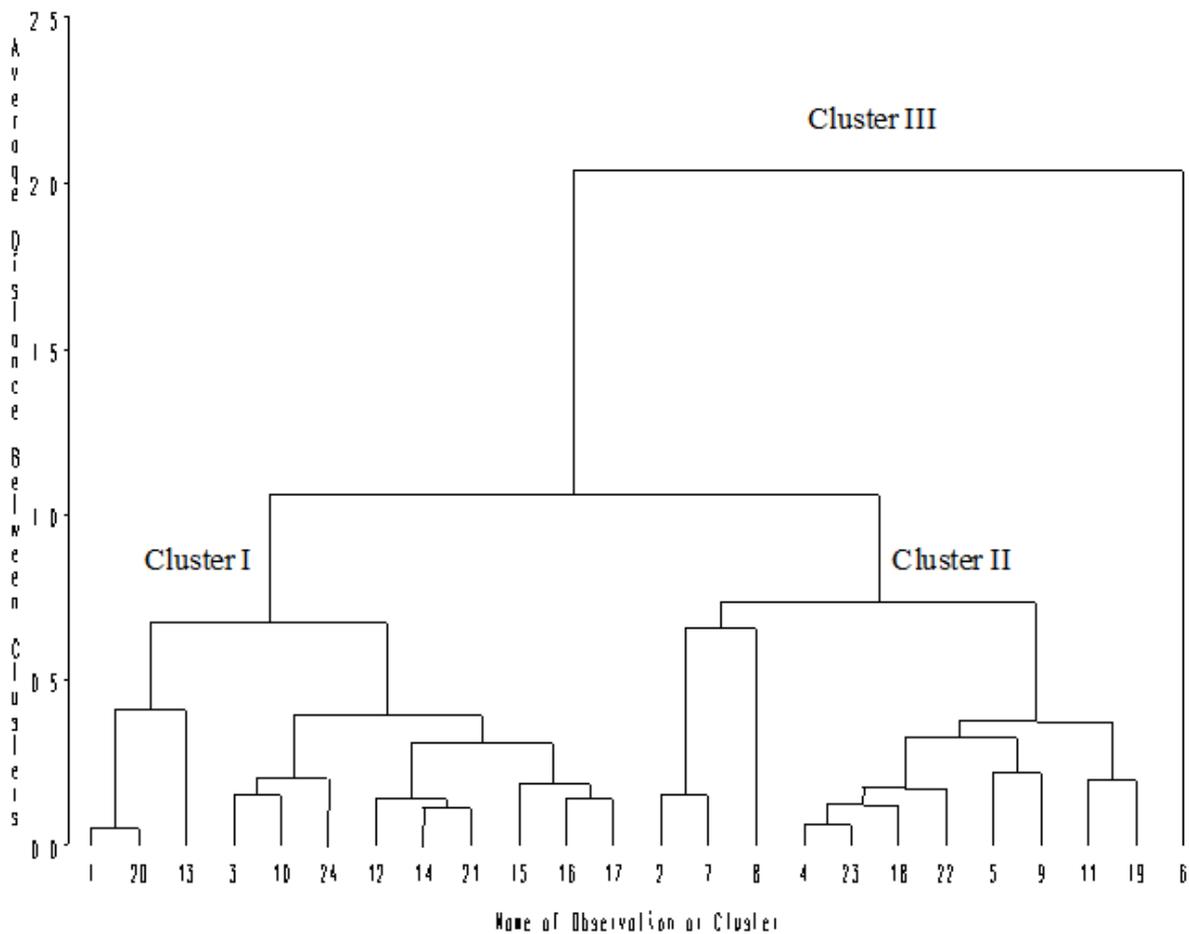


Fig.1: Dendrogram showing hierarchical clusters of 24 open pollinated maize genotypes tested at Jigjiga in 2013/14 cropping season.

Cluster means for 16 traits

The cluster mean values of the 16 characters are presented in Table 6. Varied mean values among clusters were observed in various characters. Cluster III exhibited maximum mean values for biological yield, grain yield, thousand kernel weights, plant and ear height, number of kernels per row, number of ears per plot, number of ears per plant, number of kernel rows per ear and leaf area index. The high mean values of harvest index and anthesis-silking interval were recorded in cluster II. Cluster I exhibited highest mean values for days to tasseling, anthesis, silking and maturity.

The variation of most characters in a cluster was observed with high ranges among a single (cluster III) as much as many genotypes. The contribution of traits to the wide divergence appeared with their highest

mean performances for grain yield, biological yield, thousand kernel weights, plant and ear height, number of ears per plot and number of kernels per row. The remaining traits were lowest in their mean performances. Similar results have been reported by Azad *et al.* (2012). Therefore, clustering would be preferable in selection of parents with high genetic divergence and more effective for the improvement of genotypes leading to choosing of various traits.

CONCLUSION

The present investigation revealed that wide range of genetic variability was exhibited among the tested maize genotypes. The tested traits range and mean performances, estimated genetic distance, as well as genotypic and phenotypic variance confirmed the existence of considerable amount of variability among

the tested genotypes. In terms of grain yield and components VP05147, ZM523 and VP0713 were superior in performances while inferiority observed in VP079 and VP051.

High magnitude of phenotypic (PCV) and genotypic coefficients of variations (GCV) were also recorded for grain yield and harvest index suggesting existence of sufficient variability and potential for genetic improvement through selection. Furthermore, medium PCV and GCV were obtained for number of ears per plant, number of kernels per row and thousand kernel weight which are considered as the main drought adaptive and yield related traits. Although there was substantial variability the greater magnitude of PCV values than GCV values for all the characters revealed presence of environmental influences which need caution during selection. Furthermore, the estimates of heritability, genetic advance as percent of mean and genotypic coefficients of variation were high for grain yield and harvest index which are critical to determine potential for development of superior inbred lines and/or improvement of population through selection.

The present study revealed that wide range of genetic variability was exhibited among the tested maize genotypes. Simultaneous enhancement of grain yield through selection and hybridizations obtaining from distant parents are considerable to generate wide diversity and providing for the improvement of maize grain yield.

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Conflict of Interest

The author declares that there is no conflict of interest.

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