

Genetic Variability, Heritability and Genetic advance Estimates in Maize (*Zea mays* L.) inbred lines

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Abstract: In Ethiopia Maize (*Zea mays* L.) ranks second after *Teff* in area coverage and first in total production. Present investigations were aimed to determine the nature and magnitude of genetic variability for yield and yield related traits in maize inbred lines adapted to low moisture stress area. Forty maize inbred lines were evaluated in alpha lattice design for genetic variability study between grain yield and its related traits at Melkassa Agricultural Research Center (MARC) during 2017/2018 main cropping season. The analysis of variance showed the mean square due to genotype were highly significant ($P < 0.01$) for all traits studied except number of kernel row per Ear which is significant at ($p < 0.05$). It directly implies that the existence of sufficient genetic variability and potential for selection and improvement on the traits. The highest phenotypic (PCV) and genotypic (GCV) coefficient of variations were observed in number of tassel branch, grain yield hectare, Thousand kernel weight, Ear height, Number of ear per plant. High heritability estimate were recorded for all traits which indicated that these traits were relatively less influenced by environmental factors and phenotypic selection would be effective for the improvement of these traits. Number of tassel branches showed the highest estimate of genetic advances (GA) as percent of mean at 5% selection intensity which indicated that the existence of opportunities for genetic improvement in these traits through selection.

Keywords: PCV, GCV, heritability, genetic advance, maize.

1. INTRODUCTION

Maize (*Zea mays* L.) is belongs to the tribe *Maydeae*, of the grass family, *poaceae* (Piperno and Flannery, 2001), globally it is the third important cereal crop after wheat and rice. In Ethiopia it ranks first in total production and second after *teff* in area coverage (CSA, 2016/17). Maize is consumed as a staple food in different forms, including: *injera* (alone or mixed with *teff*), porridge, bread, grits and *nefro*. It is also consumed roasted or boiled (especially at green stage). Moreover, it is brewed into tella, araki and other local spirits Berhanu et al., (2007). 75% percent of Ethiopia's landmass is categorized as dry land Kidane et al., (2010).

In the drought stressed areas of Ethiopia, which cover about half (46) % the total arable land contributes 20% of the total maize production of the country Mandefro et al., (2001). Maize grain yield is being a polygenic complex inherited character which is influenced by a number of yield contributing traits. So, the selection for desirable types should not only be based on yield, but also other yield related traits (Shengu and Tilahun, 2016).

Genetic improvement in traits of economic importance along with maintaining sufficient amount of variability is always the desired objective in maize breeding programs Ahmad et al., (2011). Variability is as the occurrence of differences among individuals due to differences in their genetic makeup or the environment in which they are raised. The development of new varieties depends on the magnitude of genetic variability in the base material for the desired trait (Burt and Austin, 2000).

Studying genetic variability is important for the success of any plant breeding. However, limited research work has been done to understand and describe the nature and extent of genetic and phenotypic variability and related genetic parameters of maize inbred lines developed for low moisture stress area of Ethiopia.

2. MATERIAL AND METHODS

2.1 Description of the study area

The experiment was conducted in the 2017/2018 main cropping season at Melkasa Agricultural Research Center (MARC) which is one of the main centers of the Ethiopian Institute of Agricultural Research (EIAR). The center is located at 8°24' N latitude and 39°21' E longitude and an altitude of 1550 m.a.s.l. The climate of the area is characterized as semi-arid with mean monthly maximum and minimum temperature of 33°C and 10.8°C, respectively. **2.2**

Experimental Materials and Procedures

The 40 inbred lines were planted at Melkasa Agricultural Research Center using alpha lattice (0, 1) design (Patterson and Williams, 1976) with two replications. The genotypes were assigned at random to each experimental unit in each block. Each replicate consisted of 10 incomplete blocks and 4 plots in each blocks. The plot length was four (4) meters and 75cm space between rows, with in 25cm spacing seeds were planted per hill in two rows per plot, thinning was done at the three to five leave stages to attain a final plant density of 53,333 plants/ha. All management practices including planting, fertilization, weeding and harvesting was performed as per the recommendations for the location.

2.3 Data were recorded for the traits

Ten plants were selected randomly for recording observations of all the quantitative traits except for days to 50 % tasseling and silking. Mean of ten plants for each entry in each replication was worked out for each trait and used for statistical analysis.

2.4 Statistical analysis

ANOVA was carried out for all the traits as per the procedure outlined by Gomez and Gomez, 1984 using SAS statistical software (9.2) (SAS, 2008). The linear model of observations in alpha design form:

$$y_{ijk} = \mu + t_i + r_j + b_{jk} + e_{ijk}$$

where y_{ijk} denotes the value of the observed trait for i^{th} treatment received in the k^{th} block within j -the replicate (super block), t_i is the fixed effect of the i^{th} treatment ($i = 1, 2, \dots, t$); r_j is the effect of the j^{th} replicate (super block) ($j = 1, 2, \dots, r$); b_{jk} is the effect of the k^{th} incomplete block within the j^{th} replicate ($k = 1, 2, \dots, s$) and e_{ijk} is an experimental error associated with the observation of the i^{th} treatment in the k^{th} incomplete block within the j^{th} complete replicate.

Estimation of variance components

Phenotypic and genotypic variances were calculated recording to Burton and de Vane (1953).

$$\text{Genotypic variance } (\sigma^2_g) = \text{MSg} - \text{MSe} / r$$

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

Environmental variance (σ^2_e) = Mean Square due to Environment effect, Where: MSg = Mean square due to genotype, MSe = Mean Square due to environment, r = the number of replications.

Phenotypic and genotypic coefficient of variations (PCV) and (GCV) values will categorize as low, moderate, and high values as indicated by Siva Subramanian and Menon, 1973 as follow.

0 - 10% = Low, > 10 - 20 = Moderate, > 20 = High

Phenotypic coefficient of variation (PCV)

Genotypic coefficient of variation (GCV), where X =trait means

Heritability in broad sense for all traits was computed using the formula given by Falconer (1996) as;

$$H^2 = \sigma^2_g / \sigma^2_p * 100 \text{ Where: } H^2 = \text{heritability in broad sense, } \sigma^2_p = \text{phenotypic variance } \sigma^2_g = \text{genotypic variance}$$

Genetic advances (GA) under selection was expected genetic advances where for each traits at 5% selection intensity was computed by the formula described by Johnson *et al.*, (1955).

Genetic Advances (GA) = $k \cdot \sigma_p \cdot H$ Where: k = constant (selection differential where k = 2.056 at 5% selection intensity), σ_p = phenotypic standard deviation H = Heritability in broad sense

Genetic advances as percent of mean was calculated to compare the extent of predicted advances of different traits under selection, using the formula.

GAM = $GA / X \cdot 100$ (Falconer, 1996). Where: GAM=genetic advances as percent of mean, GA=Genetic advances under selection, X = Mean of population in which selection will be employed.

The GA as percent of mean was categorized as low (0- ≤10%), moderate (>10≤20 and (>20) high as following by Johnson *et al.*, (1955).

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The variability among the inbred lines were determined using analysis of variance (ANOVA).The analysis of variance showed that mean squares of genotypes were highly significant (P <0. 01) for most of the traits like:- Days to 50% anthesis, days to 50% sliking, days to 90% maturity, plant height, ear height, ear diameter, ear length, number of ear plant⁻¹, leaf length, leaf plant⁻¹, tassel length, thousand kernels weight, grain yield ha⁻¹, number of kernel rows⁻¹, number of tassel branch, leaf width) except it was significant (P < 0.05) for number of kernel rows ear⁻¹ and number of node plant⁻¹ which indicated that there is variability among the genotypes (Table1). The ANOVA result is in agreement with the findings of (Maruthi and Rani, 2015) who reported highly significant (P<0.01) differences among the maize genotypes for all the traits they studied.

Similarly the work of (Ghimire and Timsina, 2015b) showed highly significant differences among the maize genotypes for all the traits studied indicating that the experimental materials were genetically divergent to each other. There is an opportunity to select desirable genotypes with increased yield components traits which may be able to perform well and give increased yield.

Table 1. Mean squares from analysis of variance of the 40 genotypes evaluated

Source of Variation	DF	DA	DS	MD	PH	EH	EL	ED	NEPP	NLPP	LL
Replication	1	15.3	13.61	1.8	17.32	10.88	9.04	3.54	0.055	9.04	5.59
Genotype	39	25.84**	28.3**	57.33**	457.98**	357.6**	2.89**	0.2**	0.098**	6.6**	50.32**
Block within Rep	18	2.64	3.19	4.76	160.9	78.28	0.52	2.21	0.078	0.53	18.3
Error	21	2.69	1.73	4.3	52.88	9.2	0.33	0.028	0.028	1.52	15.74
CV %		2.28	1.81	1.66	4.42	3.95	4.44	4.5	11.8	9.3	4.87

Table 1 continued.....

Source of Variation	DF	LW	NNP	TL	NTB	NKRPE	NKPR	TKW	GYPH
Replication	1	0.45	1.51	0.45	17.29	0.008	2.78	1301.7	26.63
Genotype	39	2.06**	1.7*	19.92**	39.13**	1.59*	15.44**	1396.5**	631805**
Block(Rep)	18	0.53	1.69	7.2	7.9	0.91	4.13	223.4	7.9
Error	21	0.34	0.78	3.0	5.0	0.72	2.08	16.5	19.2
CV %		6.4	7.9	15.3	12.7	6.1	5.24	8.85	14.2

DF = Degree of freedom, DA = Days to 50% Anthesis, DS = Days to 50% sliking, DM = Days to 90% Maturity, PH = Plant height, EH = Ear height, ED = Ear diameter, EL = Ear length, NEPP = No. Ear per plant, LL = Leaf length, NLPP = No. of leaf per plant, TL = Tassel length, NKRPE = No. of kernel row per ear, TKW=thousand kernel weight, GYPH =

Grain yield per hectare , NKPR = No. of kernel per row ,NPP = Node per plant , NTB = No. of tassel branch LW = Leaf width, CV = Coefficient of Variation, ** = most significant P [≤ 0.01], * = significant P [< 0.05], CV = Coefficient of Variation , ** = most significant P [≤ 0.01], * = significant P [≤ 0.05]

Table 2. Mean performances of maize inbred lines and variability components for 18 traits.

Traits	Range	Mean	SE	σ^2_g	σ^2_p	σ^2_e	PCV (%)	GCV (%)	H ²	GA	GAM%
DA	65-80	71.76	0.4	24.495	27.185	2.69	7.25	6.90	90.10	9.67	13.47
DS	65-81	72.2	0.48	27.435	29.165	1.73	7.48	7.24	94.07	10.48	14.51
MD	119-145	124.6	0.69	55.18	59.48	4.3	6.18	5.96	92.77	14.74	11.83
PH	132-224	144.19	2.12	431.54	484.42	52.88	15.26	14.40	89.08	40.45	28.05
EH	55-120	76.96	1.65	353	362.2	9.2	24.73	24.42	97.46	38.26	49.72
EL	10.8-16.5	12.86	0.24	2.715	3.045	0.33	13.61	12.83	89.16	3.22	25.03
ED	2.85-4.25	3.7	0.045	0.186	0.214	0.028	12.43	63.24	86.92	0.82	22.29
NLPP	9.7-20.2	13.21	0.16	6.435	6.765	0.33	13.25	12.49	95.12	3.43	26.00
NEPP	1.05-1.85	1.4	0.034	0.084	0.112	0.028	24.29	20.71	75.00	0.53	37.58
LL	70.22-99.05	81.44	0.78	42.45	58.19	15.74	9.37	7.99	72.95	11.48	14.10
LW	7.7-13.5	9.1	0.13	1.89	2.23	0.34	16.37	15.05	84.75	2.61	28.63
NPP	9.05-13.45	11.12	0.14	1.31	2.09	0.78	13.04	13.04	62.68	1.87	16.86
TL	24.7-41.3	32.5	0.48	18.42	21.42	3	14.22	13.20	85.99	8.20	25.22
NTB	10.1-35.9	17.7	0.6	36.63	41.63	5	36.44	34.18	87.99	11.71	66.15
NKRPE	10.5-15.7	13.76	0.13	1.23	1.95	0.72	10.17	8.36	63.08	1.82	13.24
NKPR	24.85-34.2	27.53	0.37	14.4	16.48	2.08	14.74	13.80	87.38	7.32	26.58
TKW	95.23-223.7	149.1	5.27	1313.75	1479.25	165.5	25.79	24.31	88.81	70.47	47.26
GYPH	1635-4115	3094	0.74	535121.5	728488.5	193367	27.59	23.64	73.46	1293.43	41.80

Standard error=(SE), Phenotypic Variance=(σ^2_p) and Genotypic Variance=(σ^2_g) , Phenotypic coefficient of variability =(PCV) and Genotypic coefficient of variability=(GCV), Broad sense heritability=(H²), Expected genetic advances=(GA) and Genetic advance as percent of mean =(GAM)

In the present study highest PCV and GCV were observed for most of the traits as shown in table (2). PCV showed a wide range of variation from 6.18 to 36.44 percent while the GCV ranged 5.955 to 34.18 percent for the different traits studied. The GCV value were generally slightly smaller than their corresponding PCV values for all the traits considered indicating the contribution of environmental variance for the expression of phenotypic variance of the trait. This is in line with the work of (Nagabhushan, 2015) who reported higher percentage of PCV as compared to GCV values. Similar finding were reported by several researchers who found out higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) for all the traits studied Langade *et al.*, (2013); Reddy *et al.*, (2012) and Shazia *et al.*, (2017).

Highest coefficient of phenotypic and genotypic variation were observed for number of tassel branches (36.44, 34.18), grain yield kg/ha (27.57, 23.66), thousand kernels weight (25.79, 24.31), ear height (24.73, 24.42) number of ear per plant (24.29, 20.714). Thus highest estimate of GCV and PCV indicates the presence of ample variation for the traits in the present material and suggests that the selection can be effective for these traits based on phenotypic and genotypic performances, respectively.

This result agrees with the finding of Ghimire and Timsina (2015b); Ghosh *et al.* (2014); Sesay *et al.* (2016) and Sarker (2015b) who reported high phenotypic and genotypic variance values for the traits like ear height ,grain yield , plant height and 1000grain weight.

Moderate value of PCV and GCV were observed for length width (16.37, 15.055), plant height (15.265, 14.40), number of kernels per row (14.74, 13.80), tassel length (14.22, 13.2) ,ear length (13.61,12.83), number of leaves per plant (13.25,12.49), number of nodes per plant (13.04, 13.04) , ear diameter (12.43,11.62), number of kernel rows per ear (10.17,8.36).

Low value of PCV and GCV were recorded for leaf length (9.37, 7.99) days to silking (7.479, 7.24), days to anthesis (7.246, 6.898), days to maturity (6.18, 5.96) respectively. So it indicates that these traits provide average chance for selection. The low GCV was observed for days to maturity (5.96%) which indicated that improvement of this traits through selection is less effective due to lack of genetic variability among the varieties. Hence such traits provide less chance for selection because they were highly affected by environment.

This result in line with the finding of Dutta *et al.* (2017) and Kumar (2008) who reported lower GCV value indicating the presence of environmental influence to some degree in the phenotypic expression of the traits they studied, thus no farther selection for future improvement of the traits.

3.2 Heritability

Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic trait can be transmitted to successive generation. Broad sense heritability (H^2), an estimate of the total contribution of the genetic variance to the total phenotypic variance of trait ranged from 62.68 for nodes per plant to 97.46 for ear height (Table 3).

High heritability estimate were recorded for traits like:- leaf width (97.46 %), days to 50% silking (94.07%), days to 90% maturity (92.77%), days to anthesis 50% (90.10%), number of leaves plant⁻¹ (95.12%), ear length (89.16%), plant height (89.08), thousand kernels weight (88.81%), number of tassel branches (87.99), number of kernels row⁻¹ (87.38%) , tassel length (85.99%), leaf width (84.75%), ear diameter (86.92%), and ear plant⁻¹ (75%), grain yield ha⁻¹ (73.64%), leaf length (72.95%), number of kernel rows ear⁻¹(63.08%), number of nodes plant⁻¹ (62.68%).

All the traits recorded high heritability in the present study indicating that these traits were relatively less influenced by environmental factors and phenotypic selection would be effective for the improvement of these traits.

According to Waqar *et al.* (2008) traits with high heritability can easily be fixed with simple selection resulting in quick progress. In consistent with these results Ghosh *et al.* (2014) and Bello *et al.* (2012) reported that traits with high heritability and moderately high genetic advance such as grain yield, number of grains per row, plant height and ear height indicate the importance of additive gene action where cautious selection may lead towards improvement for these traits.

Similarly, (Kumar ,2008; Idris and Abuali, 2011 and Shengu, 2017a) reported higher heritability values for traits like :- days to 50 percent tasseling (89.27%), days to 50 per cent silking (88.57%), plant height (93.53%), ear height (92.77%), ear length (85.97%), number of kernels per row (72.80%), 100-grain weight (84.43%), grain yield per plant (96.80%) have high heritability. Heritability for all the traits was high, indicating the low influence of environment on the studied traits.

3.3 Genetic Advance

The genetic advance and genetic advance as percent of the mean (GAM) at 5% selection intensity is presented in Table 4. It ranged from 11.83% for days to 90% maturity to 66.15% for number tassel branches. There were relatively high genetic advance expressed as percent of mean for some traits, i.e. ear height (49.72%), thousand kernels weight (47.26%), grain yield ha⁻¹ (41.80%), Number of ears per plant (37.58%), leaf width (28.63%), plant height (28.05%), number of kernels row⁻¹ (26.58%), tassel length (25.22%) and ear length (25.03%), number of leaves plant⁻¹ (26.00%), ear diameter (22.29%).

In addition to this traits such as, number of nodes per plant (16.86%), days to 50% silking (14.51%), leaf length (14.10%), days to 50% anthesis (13.47%), number of kernel rows ear⁻¹ (13.2%), days to 90% maturity (11.83%) had moderate genetic advance as percent mean. it shows the importance of genetic variability in improvement through selection.

This result agrees with Dar *et al.* (2018); Maize *et al.* (2008) and Maruthi and Rani (2015), in their studies the high genetic advance as percent of mean was recorded for plant height (23.48%), number of kernels row⁻¹ (21.38%), number of ears plant⁻¹ (20.58%), 100-seed weight (20.10%). and contrary to the present study for grain yield plant⁻¹ (18.81%), ear length (15.13%), ear height (12.95%) have moderate genetic advance. Low genetic advance as percent of mean was recorded for kernel rows ear⁻¹ (8.66%), days to silking (8.64%), days to tasseling (8.37%) and days to maturity (7.22%). Rajesh *et al.* (2013) and Nagabhushan (2015) reported that high to moderate heritability with moderate estimates of genetic advance were observed for grain yield, plant height, ear height, number of kernels per row, 100-kernel weight .

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Similarly, Sarker (2015) reported that high GA with high heritability was observed for yield/plant, ear height, grains/row and higher genetic advance for grain yield/plant, ear height, plant height, and grains/row depicts additive gene effects. Hence high heritability estimates is indicating to preponderance of additive gene action. In contrary to the present study (Ghosh *et al.*, 2014) reported low genetic advance for days to 50% silking, days to 50% anthesis and ear length.

4. CONCLUSION

Analysis of variance indicated that mean squares due to inbred lines were significant for most studied traits indicating the existence of high level of variability and the possibility of selection among the lines for grain yield and agronomic traits of interest. The highest estimate of GCV and PCV indicates the presence of ample variation for the traits in the present material and suggests that the selection can be effective for these traits.

Traits having High heritability coupled with high genetic advance indicate the traits can be improved through direct selection since the additive gene effects are predominant. Traits with a high genetic advance as percent of mean allow the improvement of these traits through selection. However, as quantitatively inherited traits are highly influenced by environmental conditions, such study should be conducted over different years and locations to come to certain conclusion.

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