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RESEARCH ARTICLE

Genetic variability, heritability and genetic advance estimation of highland adapted maize (*Zea mays* L.) genotypes in Ethiopia

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ABSTRACT

The improvements of maize hybrid rely on significant genetic variability among the parental lines used and the degree to which it is transferred to progeny. A total of fifty genotypes are being studied in this present investigation. They were used to assess genetic parameters in two representative highland maize-growing areas. For most traits, the level of genetic variation was greater than the corresponding environmental variance. The highest genotypic and phenotypic variances were found in thousand kernel weight, ear and plant height. For all traits, the PCV was greater than the GCV. The variations between the two components, were negligible. Grain yield, ear height, and ear aspect all had moderate GCV and PCV values. Plant feature, number of ears per plant and thousand kernels weight all had a mild phenotypic coefficient of variation. The other traits, on the other hand were classified as having low PCV values, implying that selection based on traits with low variation of the genotypes tested would be less successful. Grain yield, ear height, and ear aspect have greater genetic advance and heritability signifying that additive gene action was more important in these traits. Selection for these traits will provide an opportunity to improve highland maize germplasm.

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INTRODUCTION

Maize is widely grown crop in Sub-Saharan Africa (Shiferaw et al., 2011; Martin et al., 2000). It is a staple food crop in Ethiopia (Tsedeke et al., 2017; Balemi et al., 2019), growing in a variety of agro–climates ranging from moisture deficit semi-arid lowlands to moisture surplus humid lowlands, mid-altitudes and highland areas (Worku et al., 2012; Kelemu and Mamo, 2002). Because of its enormous diversity, it appears to be adaptable to a various ecological condition (Ferdu et al., 2002).

According to Dawit et al. (2010), the tactical strategy for maize breeding programmes in Ethiopia was established by dividing development areas into three ecological zones: highland (1800–2400 m.a.s.l), mid-altitude (1000–1800 m.a.s.l) and lowland (500–1800 m.a.s.l) in order to conduct research to produce genetically improved varieties. It is a highly cross-pollinated plant that responds well to genetic improvement by plant breeders.

The selecting suitable genotypes is creating considerable amount of genetic diversity and heritability data collected from a population (Tadesse et al., 2018; Sankar et al., 2006). As a result, hybridization of maize requires a substantial level of genetic heterogeneity across the parental lines (Mustafa et al., 2014) as well as a high degree of genetic transmission from the parental line to the progeny (Hussain et al., 2011; Kashiani et al., 2008).

The heritable genetic character of the material can be improved as a result of purposefully selecting genotypes with economically favourable traits (Meena et al., 2016; Khan et al., 2011). However, determining whether all observed variability is heritable or not, rather than suggesting the likelihood and/or degree of transmission into future generations, is difficult (Johnson et al., 1955).

As part of crop enhancement, it is necessary to evaluate genetic characteristics such as genetic and phenotypic variances, heritabilities and genetic advancements; GCV and PCV (Sravanti et al., 2017). The genetic heterogeneity of maize genotypes, however, has been poorly studied, especially in the highlands.

MATERIALS AND METHODS

Materials and Experimental Sites

During the 2016 cropping season, at the Ambo and Holetta Agricultural Research Centers, forty-eight new single-cross maize genotypes were created by mating locally adapted testers with inbred lines received from CIMMYT-Kenya, as well as two standard tests, for the evaluation of genetic parameters. Both Ambo (08°57'N, 38°07'E, and an altitude of 2225 m.a.s.l.) and Holetta (9000N, 38030'E, and an altitude of 2400 m.a.s.l.) typified Ethiopia's highland sub-humid maize increasing agro-ecology.

Field Management and Experiment Design

A 10 5 alpha-lattice design was used to evaluate the materials in the field. With a 5.25m plot length, 75cm and 25cm between rows and plants were used, respectively. To grow a successful and safe crop, all crop management practises were implemented according to the recommended packages of the respective locations.

Estimation of variance components

Individuals with different genetic make-ups have genotypic variation, while phenotypic variance is the number of variances caused by genetic causes and environmental influences. Phenotypic, genotypic, and ecological variations of each trait were computed using Allard (1979) & Singh and Chaundhary (1979) methods (1960). The GCV and PCV were computed by

Falconer (1989) and Singh and Chaudhary (1985), respectively. PCV and GCV readings were classified as low if they were less than 10%, medium if they were between 10% and 20%, and high if they were more than 20%. (Deshmukh et al., 1986).

The heritability estimates for each variable were calculated using components of variance (Butterfield and nuss, 2002). Using the formulas proposed by Falconer et al. (1996) and Gravois et al. (1992), heritability was defined as the ratio of genotypic to phenotypic variation.

Heritability values were classed as low (0-30 percent), moderate (30-60 percent), and strong (60 percent and above) by Robinson et al (1949). It could be measured using the method proposed by Allard (1960). Genetic advancement was measured by formulas of Souza et al. (2009) and Deshmukh et al. (1986).

Data collection and Statistical Procedures

The quantitative data collected for fourteen traits were exposed to statistical analysis by GLM Procedure using SAS software statistical package 9.3 (SAS, 2002).

RESULT AND DISCUSSION

Table 1 shows the results of the ANOVA for significant maize genotype features. Earlier research found significant changes in yield and yield-related variables among genotypes in different groups of maize genotypes, corroborating the current conclusion (Farhan et al., 2011; Nigus, 2018). Analysis of variance owing to a location in the combined result revealed very significant variances for most of the features (Table 1).

When assessed under multiple contexts, the presence of extremely significant variances shows various of environmental situations. This finding was in line with Sesay et al findings. Among the fourteen variables studied, analysis of variance owing to genotype x location interaction revealed significant differences for thousand kernels weight. For these traits, significant mean squares owing to genotype x location suggested that there were rank disparities in genotype performance from one site to the next. Farhan et al. (2011) observed significant for grain yield, days to 50 per cent anthesis, and thousand kernel weights owing to genotype x location, similar to the current result.

In crop improvement, genetic diversity is important because of it provides the foundation for developing an acceptable selection approach. The largest genotypic and phenotypic variation was reported for kernel weight, ear, and plant height, indicating the efficacy of genotype selection. Similar results were reported by Mahto et al. (2002).

The lowest estimates of genetic variance were found for the number of ear/plants, ear and plant aspect. Anshuman et al. (2013) showed a similar outcome for similar features. Except for thousand kernel weight and number of kernels/ rows, the interactions of genotype and location variance (2gl) were smaller than the genetic variances (2g) for practically all traits. Individuals with more genetic variance should produce more producing crosses or genotypes than those having less genetic variance (Kisha et al., 1997).

The PCV was larger than GCV for all of the traits examined (Table 2). There were very few differences between the two components, save from thousand kernel weight, ear length, and ear/plant. This could be owing to the environment's impact on trait inheritance (Meena et al., 2016).

Table 1. Combined ANOVA for yield and yield related traits

Traits	Sources of Variation								
	Location	Rep(loc)	Genotype	Gen X loc	Block (loc X Rep)	Pooled Error	CV (%)	R^2	LSD
	Df= 1	Df= 1	Df= 49	Df= 49	Df= 17	Df= 82			
GY	14.051**	0.18	5.863**	1.333	1.39	1.306	14.083	0.77	1.646
AD	21590.425**	40.526**	38.065**	3.254**	4.043**	1.437	1.252	0.99	1.6841
SD	28060.810**	68.445**	47.015**	6.215**	6.843**	3.021	1.781	0.992	2.44
MD	2387.435	59.424	51.354**	32.391	29.05	20.284	2.95	0.761	7.341
PH	477.412	1551.250**	1061.250**	201.419	301.651*	176.491	8.511	0.836	18.682
EH	2613.651**	1529.053**	901.281**	63.924	158.025**	58.952	5.824	0.92	10.809
EL	16.251	6.092	9.942	7.22	8.59	4.134	15.553	0.642	3.754
ED	215.019**	2.644	21.112**	2.81	2.932	2.367	3.453	0.89	2.161
EA	3.126**	0.015	0.704**	0.137	0.216	0.127	11.034	0.843	0.534
PA	5.980**	0.035	0.523**	0.163	0.224	0.139	14.73	0.738	0.614
NEPP	7.806**	0.017	0.080**	0.041	0.034	0.038	14.34	0.824	0.27
NRPE	0.062	0.072	3.063**	0.77	0.771	0.550	7.825	0.734	1.441
NKPR	814.460**	9.25	17.750**	10.153	7.843	6.125	6.69	0.824	3.483
TKW	352103.784**	930.74	5093.390**	3060.171**	2314.781	1450.124	10.96	0.872	53.55

Table 2. Combined mean range, estimates components of variances, heritability, PCV, GCV, and genetic advance

Trait	Range (phenotypic)	σ^2g	σ^2ph	σ^2e	σ^2gl	GCV (%)	PCV (%)	H^2(bs) (%)	GA	GA as (%) of the mean
GY	6.15-11.17	1.134	1.465	1.306	0.009	12.844	14.600	77.389	1.930	23.276
AD	88.25-102.5	8.702	9.517	1.437	0.911	3.083	3.224	91.439	5.811	6.073
SD	89-105.25	10.204	11.757	3.021	1.594	3.276	3.516	86.795	6.131	6.286
MD	170-186	5.239	12.836	20.284	5.054	1.294	2.026	40.810	3.012	1.703
PH	206.5-274.25	214.962	265.314	176.491	12.459	5.998	6.663	81.022	27.186	11.121
EH	94-164	209.341	225.321	58.952	2.484	10.938	11.348	92.908	28.729	21.718
EL	14.98-26.2	1.184	2.485	4.134	0.535	6.337	9.181	47.639	1.547	9.009
ED	38.94-49.35	4.574	5.278	2.367	0.225	4.794	5.150	86.656	4.101	9.193
EA	2.37-4.13	0.142	0.175	0.127	0.003	12.664	14.055	81.189	0.700	23.507
PA	2.25-4.23	0.090	0.131	0.139	0.011	9.301	11.184	69.157	0.515	15.933
NEPP	1.05-1.8	0.012	0.021	0.038	0.001	7.828	10.640	54.118	0.163	11.862
NRPE	10.83-15.5	0.574	0.767	0.550	0.111	5.760	6.658	74.853	1.350	10.266
NKPR	33.17-42.83	1.900	4.438	6.125	2.015	3.730	5.702	42.798	1.857	5.027
TKW	231-424.11	508.306	1273.349	1450.124	805.023	6.492	10.274	39.919	29.344	8.449

A moderate GCV was found in grain yield (12.844), ear height (10.938), and ear aspect (12.664). Except for these three, all of the other qualities had low GCV levels. Sravanti et al. (2017) had the highest GCV and PCV value for ear height, while Bartaula et al. (2019) had the highest GCV and PCV value for the same trait.

The PCV was considerable for grain yield (14.600), ear height (11.348), plant aspect (11.184), ear aspect (14.055), number of ears/plant (10.640), and thousand kernels weight (10.274). Other features, on the other hand, were classed as having low PCV values. Due to their restricted genetic foundation, selection based on qualities with low values of GCV and PCV of the tested genotypes would be less effective (Nigus, 2018). Rajesh et al. (2013) and Reddy et al. (2016) for days to 50% maturity, days to 50% anthesis, and days to 50% tasselling; Ribeiro et al. (2016) for thousand kernel weights. The absence of a large GCV, according to Hefny (2011), implies that environmental changes have a significant impact on the features of the studied materials.

In the broadest sense, estimates of heredity percentage ranged from 39.919 percent (thousand kernels weight) to 92.908 per cent (ear height). Nine variables had the highest heritability percentages: ear height (92.908%), days to 50% anthesis (91.439%), and silking (86.795%), ear diameter (86.656%), plant height (81.022%), ear aspect (81.189%), grain yield (77.389%), number of rows/ear (74.853%), & plant aspect (69.157).

The days to 50 per cent maturity, and thousand kernel weights exhibited modest heritability percentages in this study due to the substantial environmental impact on the expression of characteristics. According to Anshuman et al. (2013), Bishnu et al. (2018), & Ayodeji and Comfort (2019), the number of ears per plant has a low heredity estimate.

Plant aspect (15.933), plant height (11.121), number of ear per plant (11.862), and number of rows per ear (10.266) were among the traits with modest genetic advance, while grain yield (23.276), ear height (21.718), and ear aspect (23.507) had the greatest values. The current finding was validated by the findings of Sravanti et al. (2017) and Kumar et al. (2014).

The substantial mean and high heritability seen in grain yield, ear height, and ear aspect in this study are due to additive gene action. As a result, highland ecologies can benefit from direct genetic selection for this characteristic. This revealed that selecting genotypes based on these traits could be impossible, as well as determining the ideal breeding approach for maize production.

CONCLUSION

Results concluded that PCV for all characteristics were larger than the genotypic coefficients of variation, the discrepancies between the two components were minor, showing that the traits' expression was unaffected by the environment. Grain yield, ear height, and ear aspect all had low PCV and GCV. Traits with low PCV and GCV of the tested genotypes will be less effective due to their narrow genetic foundation. Owing to the substantial genetic advance of the mean, yield, ear height, and ear aspect all have a high heritability. Because additive gene action is considered to regulate all three variables, maize production for highland ecologies can be determined indirectly by choosing genotypes for grain yield, ear height, and ear aspect.

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