Genetic Variability and Correlation Studies of Grain Yield and Related Agronomic Traits in Maize

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Abstract

A total of fourty two maize hybrids produced through a full diallel mating design and seven parental inbred lines were evaluated in three sites located at different agro-ecological zones in Kenya to determine the genetic parameters governing the inheritance of grain yield and related agronomical traits. The genetic parameters studied among the traits included the mean performance, genotypic variances, phenotypic variances, genotype by environment variances, broad sense heritability and phenotypic and genotypic correlation coefficients. Significant differences were recorded for all traits studied thereby revealing the diversity of the maize genotypes. The grain yield and days to maturity which showed high heritability had low genotypic variances suggesting the involvement of non-additive gene action which could be utilized through heterosis breeding. Ear height and plant height showed the highest heritability and high genotypic variances suggesting the preponderance of additive gene action. Grain yield was positively and strongly correlated with ear height and plant height. The tall plants with high ear placement gave better yields and this could be attributed to the high dry matter accumulation function carried out by the high number of leaves possessed. The positive relationships observed in this study imply that the desirable traits in these hybrids could be exploited in further breeding activities for the development of composites and synthetics for the resource constrained maize farmers who cannot access hybrid seeds every year.

Keywords: maize, grain yield, yield components, genetic variability

1. Introduction

Maize is the third most important food crop of the world, after wheat and rice, providing 15% of the protein, and 19% of the calories for the developing countries (Shakoor et al., 2007). The maize yield character is influenced by several genes which also interact with various environmental conditions (Bocanski et al., 2009). Thus, the yield has a multiplicative effect on the end product of many factors otherwise referred to as yield components (Zeeshan et al., 2013). These yield components are simply inherited with minimal environmental deviations, and hence selection based on them is more appropriate as opposed to the yield per se (Nagabhushan et al., 2011). The assessment of performance of parental lines based on the yield components could aid in the selection of superior parents for the production of better yielding hybrids (Bocanski et al., 2009). This can successfully be achieved if the genetic parameters which govern inheritance of important agronomic traits are established (Mahiboobsa et al., 2012). In addition, the proper characterization of the physiological traits and their relationships with maize yield and yield components coupled with utilization of the revealed genetic variability could lead to improvement and broadening of the diversity of the maize gene pool (Alake et al., 2008; Al-Tabbal et al., 2012).

The mean values, genotypic and phenotypic variances, heritability, and the correlation coefficients of agronomic traits are some of the key parameters which determine the efficiency of a breeding program. The phenotypic variance explicates the total variance among phenotypes tested in different environments of interest to the plant breeder while the total genotypic variance explains the portion of phenotypic variance attributable to the failure of homogeneity among genotypes in different environments (Sujiprihati et al., 2003). The heritability measures the value of selection for a particular trait in various types of progenies (Al-Tabbal et al., 2012; Lule et al., 2012).

It encompasses the phenotypic variance attributable to genetic causes which have a predictive function in plant breeding leading to permanent genetic improvement. This is because a genotype could be selected based on the phenotype given that the environmental effect is separated from the total variability (Bello et al., 2012). The knowledge of heritability establishes appropriate selection methods coupled with the prediction of any gains from selection while also helping to establish the magnitude of the genetic effects. Larger genotypic variance is most preferred given that high heritability values can be obtained with genotypes with either small or large genetic progress. High heritability is associated with additive gene effect whereas low heritability is due to dominance and epistasis. The coefficient of variation shows the extent of variability represented by the different characters but it excludes the heritable portion. Conversely, the coefficient of correlations help to measure the level of relationships between the traits and also establish the level at which these traits are mutually different (Bocanski et al., 2009; Nagabhushan et al., 2011). The correlations also give reliable and useful information on nature, extent and direction of selection (Zeeshan et al., 2013). This study aimed at understanding the genetic parameters which govern the inheritance of maize yield and other agronomic traits.

2. Materials and Methods

2.1 Plant Materials

Seeds of seven inbred lines CML 204, CML 312, CML 373 and CML 384 from CIMMYT; TZMI 102, TZMI 711 and TZMI 712 from IITA were included in this study. Important characteristics of these genotypes are given in Table 1. These maize genotypes were grown at Kenya Agricultural Research Institute (KARI), Kiboko in season 1. At flowering, the genotypes were cross pollinated following a full diallel mating design to generate 42 single cross hybrids. The fourty two single cross hybrids and their seven parents were evaluated for grain yield performance and other traits at the three sites and the experiments were laid out in a randomized complete block design in two replicates.

2.2 Experimental Sites

Three sites located in different agro ecological zones were chosen for this study. They included Kenya Agricultural Research Institute (KARI), Kiboko; KARI, Kakamega and Field station, Kabete and their climatic conditions have been outlined in Table 2.

Table 1. Parentage, origin, genetic background, heterotic groups and ecological adaptation of the maize inbred lines used in the study

Inbred line	Pedigree/Parentage	Origin/Source	Heterotic Group	Genetic background and Ecological adaptation
CML 204	[7794]-SELF-4-1-S9-1-4-7-4-5-BB.	CIMMYT	Group B	Adapted to mid altitude and semitropical areas of Africa
				Tall, late maturing
				White grains and a dent texture.
				Good tolerance to MSV and rust
CML 312	S89500F2-2-2-1-1-B*5.	CIMMYT	Group A	Adapted to sub-tropical areas
				Tall, intermediate maturity, white semi-flint kernel
				Good resistance to GLS and *E. turcicum*
CML 373	P43SR-4⁻1-1-2-1-B-8-1-BBB	CIMMYT	Group A	Adapted to the subtropical areas
				Tall, intermediate maturity, white flint textured kernel
				Susceptible to rust, *E. turcicum* and ear rot
CML 384	P502C1#-771-2-2-1-3-B	CIMMYT	Group B	Flint textured, white grained inbred line
				Tall, late maturity, good resistance to ear rot and rust

TZMI 711	National-1 variety crossed to an IITA MSV-resistant population, TZSR. TZSR was developed through intercrossing four populations; TZB, TZPB, POP 21, and POP 22	IITA	Group B	Adapted to Tropical mid-altitude
				Has combined resistance to gray leaf spot, maize streak virus, Exserohilum turcicum and Puccinia sorghi
				Has semi-dent grain texture
TZMI 712	Pedigree - Selected from a cross between a mid-altitude inbred line (TZMI501) from IITA and an inbred line from CIMMYT (ZSR 923 Sr bulk).	IITA	Group B	Adapted to tropical mid-altitude
				Has combined resistance to gray leaf spot, maize streak virus, Exserohilum turcicum, and Puccinia sorghi
				Has semi-dent grain
TZMI 102	Pedigree is CamInb.TCSel1-13-1-1-1-B.	IITA	Group B	TZMI 102 was a parent of the best single-cross hybrid marketed in Plateau State of Nigeria as '8535-23'

Source Pswarayi and Vivek, (2004); Menkir and Adepoju, (2005); Plant inventory (2004); Generation Challenge Programme, (2006); CIMMYT is International Maize and Wheat Improvement Center; IITA is The International Institute of Tropical Agriculture.

Table 2. Agro-climatic description of the experimental sites

| Site | Agro-ecological zone | Geographic position | | | Mean annual Rainfall (mm) | Temperature (0 °C) | | Soil type |
		Longitude	Latitude	Altitude (m)		Minimum	Maximum	
KARI, Kiboko[i]	5	37°75′ E	2°15′ S	993	548	17	30.6	Ferrasols to ferric luvisol on the old peneplain and eutric fluvisol at the bottom of the river valley
KARI, Kakamega[i]	2	34°45′ E	0°16′ N	1585	1995	13	28.6	Soils are deep, friable, Basaltic loam, fertile and well drained
Kabete, Field station, University of Nairobi[ii]	3	36°44′ E	I°15′ S	1820	1000	16	23	Soils are well-drained, very deep, dark reddish brown, friable clay with acid humic top soil

Source: [i]http://www.kari.org; [ii]Jaetzold and Schmidt, 1983; KARI= Kenya Agricultural Research Institute.

Data were collected during crop growth on days to 50% female flowering and male flowering (DTFF and DTMF respectively), Stem (SL) and root lodging (RL), plant height, ear height, field weight, moisture content, diseased ears and grain yield. DTFF and DTMF were recorded as the number of days from sowing to when 50% of the plants have silked and shed pollen respectively. Stem (SL) and root lodging (RL) were recorded as the number of plants lodged at the stem and root respectively and was observed two weeks before harvest. The ear height (EH) was recorded as the height from the ground to the node bearing the uppermost ear while the plant height (PH) was recorded as the height from the soil level to the node of the flag leaf. Grain yield data was recorded as follows: the ears from each plot were harvested and weighed (field weight); Moisture content was then determined from a seed sample of ten randomly selected cobs. The harvested cobs were then adjusted to 13% moisture content while assuming an 80% shelling percentage to calculate the grain yield in tonnes per hectare.

2.3 Data Analysis

2.3.1 Analysis of Variance

Analysis of variance (ANOVA) was carried out to establish the level of significance among genotypes using the DIALLEL-SAS program. The mean values were compared using the least significant difference (LSD) procedure.

2.3.2 The Combining Ability Tests

This was done based on the Griffing's (1956) method I involving parents, F1's and reciprocals and a standard combining ability model (model 1) using the using DIALLEL-SAS program.

The statistical model was

$$Y_{ij} = m + g_i + g_j + s_{ij} + r_{ij} + 1/bc \sum \sum e_{ijkl} \tag{1}$$

Where

i, j =1,2, … n; k=1, 2, … b and l =1, 2, … c;

$Y_{ij} = 1/bc \sum \sum Y_{ijkl}$ = mean of ixj[th] genotype over k and l;

g_i = GCA effect of ith parent, g_j = GCA effect of jth parent;

s_{ij} is the interaction (SCA effect), r_{ij} is the reciprocal effect and $1/bc \sum \sum Y_{ijkl}$ is mean error effect.

The relative importance of GCA when compared to the SCA was calculated based on the Baker's Ratio (1978).

$$2\sigma^2{}_{GCA} / 2\ \sigma^2{}_{GCA} + \sigma^2{}_{GCA} \tag{2}$$

Where

$2\sigma^2{}_{GCA=}$ mean square components associated with variance of GCA;

$\sigma^2{}_{SCA=}$ mean square components associated with variance of SCA.

2.3.3 Analysis of Phenotypic and Genotypic Variance

The variability of each quantitative trait was estimated by simple statistical measures including the mean, phenotypic and genotypic variances and coefficient of variation. The phenotypic and genotypic variation and coefficient of variation were calculated following the formulae suggested by Singh and Chaundhary (1979) and Allard (1960). Phenotypic, genotypic and environmental variances were computed from the respective mean squares as indicated below.

i. Genotypic Variance ($\delta^2{}_g$):

$$\partial^2{}_g = \frac{\left(MS_g - MS_{gl}\right)}{rl} \tag{3}$$

Where

MS_g = mean square of genotype;

MS_{gl} = mean square due to genotype by environment interaction;

l = number of locations or environments;

r = number of replications.

ii. Genotype by environment interaction variance ($\delta^2{}_{gl}$):

$$\partial^2{}_{gl} = \frac{\left(MS_{gl} - MS_e\right)}{r} \tag{4}$$

Where

MS_{gl} = mean square due to genotype by environment interaction;

MS_e = error mean square.

iii. Phenotypic Variance (δ^2_p):

$$\partial^2_p = \partial^2_g + \left(\partial 2_{gl}/l\right) + \left(\partial^2_e/rl\right) \tag{5}$$

Where

δ^2_{gl} = mean square due to genotype by environment interaction;

δ^2_e = error mean square.

iv. The genotypic (GCV) and phenotypic (PCV) coefficient of variation were estimated according to the procedure outlined by Johnson et al. (1955) thus:

$$PCV = \sqrt{\partial^2_p}/X \times 100 \tag{6}$$

$$GCV = \frac{\sqrt{\partial^2_g}}{X} \times 100 \tag{7}$$

Where

X = population grand mean for the trait considered.

v. Broad-sense heritability (H^2_{BS}) was calculated as suggested by Allard (1960) for each character thus:

$$H^2_{BS} = \frac{\partial^2_g}{\partial^2_p} \times 100 \tag{8}$$

Where

H^2_{BS} = heritability in the broad sense.

vi. Phenotypic and genotypic correlations were estimated as suggested by Miller et al., (1958) and Kashiani and Saleh (2010) respectively:

Phenotypic correlation coefficient (rp_{xy})

$$rpxy = \frac{\partial^2 px}{\sqrt{\partial^2 px \times 2py}} \tag{9}$$

Genotypic correlation coefficient (rgxy)

$$rgxy = \frac{\partial gxy}{\sqrt{\partial gx \times 2gy}} \tag{10}$$

Where

rpxy = phenotypic correlation coefficient between characters X and Y and *rgxy* = Genotypic correlation coefficients between characters X and Y.

3. Results

The genotype, environment and genotype by environment interaction were significantly different for the traits studied (Table 3). The general and specific combining abilities for all the traits were significantly different. GCA by environment interaction was significantly different for grain yield, maturity, diseased ears and root lodging. The SCA by environment was significantly different for grain yield, plant and ear height, diseased ears and root lodging. The GCA: SCA comparison ranged from 0.3 to 1.7 and the GCA values were also higher than the SCA values for all traits except grain yield and root lodging (Table 3). The coefficient of variation which was used to compare the precision of the experiment with the different means showed that the data was reliable in that the %CV for the traits ranged from 0.9 to 18.7% (Table 3).

Table 3. Values of 'F' from estimates for grain yield, yield components and other agronomic traits of 7 maize inbred lines and 42 single crosses based evaluated across three environments

Traits/Parameters	Degrees of freedom	Grain Yield (tha^{-1})	DTMF (days)	DTFF (days)	Plant Height (cm)	Ear Height (cm)	Diseased ears (count)	Root lodging (%)	Stem lodging (%)
ENV	2	1450.8***	891.5***	675.5***	262.6***	270.7***	163.4***	29***	64.2***
REP(ENV)	3	17.8	4.3	3.7	3.96	4.4	1.1	1.1	0.1
HYBRID	48	19.3***	10.3***	9.7***	43.2***	34.5***	3.1***	16.7***	3.7***
ENV*HYBRID	96	4.84***	1.7**	1.4*	2.7***	2.5***	2.9***	9.1***	3.6***
GCA	6	15.3***	21.3***	20.3***	135.9***	122.5***	8.4***	7.0***	15.7***
SCA	21	39.5***	16.1***	15.7***	58.5***	42.1***	2.8**	35.3***	3.3***
GCA*Environment	6	7.9***	2.4*	1.9***	1.7	1.5	11.2***	13.1***	0.1
SCA* Environment	21	6.1***	0.6	0.5	3.0***	3.0***	3.2***	21.5***	0.21
GCA:SCA		0.6	1.1	1.1	1.4	1.5	1.5	0.3	1.7
CV (%)		18.4	3.2	3.3	5.5	7.4	3.1	0.9	1.2

Significance levels *** = P<0.0001, ** = P<0.001, * = P<0.05, ENV = Environment, REP(ENV) = replications, HYBRID = maize hybrids, ENV*HYBRID = environment by hybrid interaction (genotype by environment interaction), GCA = General combining ability, SCA=Specific combining ability, GCA*Environment = GCA by environment interaction, SCA*Environment = SCA by environment interaction, GCA:SCA = Relative importance of GCA when compared to the SCA based on the Baker's Ratio (1978), CV% = coefficient of variation; DTMF = days to male flowering, DTFF = days to female flowering.

The plant height and ear height had the highest genotypic variances, genotype by environment variances, phenotypic variances and heritabilities. The grain yield showed moderate heritability of 74.97% and low values for genotypic, phenotypic and genotype by environment interaction variances. The stem lodging and diseased ears traits had the least heritability estimates of 7% and 2% respectively. They also had the least genotypic variances and phenotypic variances. With regard to the genotypic and phenotypic coefficients of variations, the grain yield had the highest GCV and PCV estimates of 28.6% and 33.06% respectively. The plant and ear height had moderate values for GCV and PCV while days to flowering or maturity trait had the least values for GCV and PCV estimates. In this study, the PCV estimates were slightly higher than the GCV estimates (Table 4).

Table 4. Means, estimates of genetic variance, genotype by environment interaction variance, phenotypic variance, broad sense heritability, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for maize grain yield and other agronomic traits in maize

Parameters/Characters	Mean	Variances			H^2 (%)	CV (%)	
		σ^2_g	σ^2_{gl}	σ^2_p		GCV	PCV
Grain yield	8.16	5.46	4.04	7.28	74.97	28.62	33.06
DTMF	83.29	10.01	2.13	11.97	83.69	3.8	4.15
DTFF	85.1	11.5	1.26	13.32	86.3	3.98	4.29
Plant height	195.57	776.32	94.79	826.99	93.87	14.25	14.7
Ear height	97.27	275.41	37.81	297.11	92.7	17.06	17.72
Diseased ears	5	0.19	28.76	2.61	7.22	8.65	32.2
Root lodging	1.1	1.43	3.36	3.13	45.78	10.78	15.29
Stem lodging	4.3	0.06	3.3	2.66	2.08	5.52	38.23
Field weight	4.82	11.51	1.99	0.48	68.36	11.92	14.41
Moisture content	14.46	1.6	0.16	0.82	28.27	3.34	6.28

DTMF = days to male flowering, DTFF = days to female flowering; σ^2_{gl} = Genotype by environment interaction variance; σ^2_g = Genotypic Variance; σ^2_p = Phenotypic Variance; H^2 (%) = Heritability in the broad sense given as a percentage; GCV genotypic coefficient of variation; PCV = phenotypic coefficient of variation.

Grain yield was positively and strongly correlated with ear height, field weight and plant height with high genotypic and phenotypic correlation coefficients (Table 5). Grain yield had a moderate genotypic association with the days to 50% tasseling and pollen shed. The field weight was positively and strongly correlated with days to maturity, plant and ear height. There was a negative and significantly different correlation between moisture content and ear and plant height, grain yield and field weight. A strong and negative correlation was observed between stem lodging and grain yield.

Table 5. Genotypic (G) and phenotypic (P) correlation coefficients among grain yield and other agronomic traits in maize

Characters	Correlation coefficients	DTFF	DTMF	Ear Height	Grain yield	Plant height	Field Weight	Moisture Content	Root lodging	Stem lodging
DTFF	G	1	0.98*	0.19*	0.31*	0.21*	0.36*	0.13*	0.07	-0.05
	P	1	0.97*	0.18*	0.47*	0.17*	0.53*	0.1	0.07	-0.04
DTMF	G		1	0.20*	0.29*	0.24*	0.36*	0.13*	0.08	-0.02
	P		1	0.18*	0.44*	0.18*	0.51*	0.11	0.06	-0.03
Ear Height	G			1	0.61*	0.90*	0.62*	-0.31*	-0.03	-0.06
	P			1	0.60*	0.89*	0.61*	-0.31*	0.03	-0.01
Grain yield	G				1	0.63*	0.96*	-0.35*	-0.18*	-0.48*
	P				1	0.61*	0.97*	-0.36*	-0.04	-0.34*
Plant height	G					1	0.67*	-0.28*	-0.07	-0.11
	P					1	0.65*	-0.28*	-0.01	-0.09
Field Weight	G						1	-0.24*	-0.16*	-0.39*
	P						1	-0.26*	0.17	0.08*
Moisture Content	G							1	0.07	0.15*
	P							1	-0.04	-0.3
Root lodging	G								1	0.27*
	P								1	0.08
Stem lodging	G									1
	P									1

Significance levels, * = P<0.05; G = genotypic correlation coefficients; P = phenotypic correlation coefficients; DTMF = days to male flowering, DTFF = days to female flowering.

4. Discussion

The significant differences recorded for the different traits among the genotypes studied implied that the maize genotypes included in this study had diverse genetic backgrounds (vashistha et al., 2013; Reddy et al., 2012). Thus, the genetic variability recorded in this study could be exploited by plant breeders to develop varieties adapted to the diverse agricultural practices in sub Saharan Africa to improve food security status (Feuillet et al., 2012). The significant genotype by environment interaction showed a wide variability with regard to the tested genotypes and the environments involved in this study (Alake et al., 2008).

The significant GCA indicated the evidence of additive gene action while the significant SCA implies involvement of non additive gene action. Thus, the differences noted among the traits with regard to the genetic parameters were attributed to both the GCA and SCA values. The relative importance of general and specific combining ability on progeny performance was estimated based on the Baker's Ratio (1978) and it showed a preponderance of additive gene effects in the inheritance of all traits except grain yield and root lodging. Thus, the response of hybrids to these agronomic traits could be predicted based on the GCA of the parents (Gavioli et al., 2006). Thus, the additive effects could be exploited in the introgression of the yield related traits leading to enhance gains from selection (Sese et al., 2002).

The highest heritability estimates, GCA values and variances were recorded for plant height and ear height. The high heritability estimates and variances suggested that these traits were simply inherited. This also implied that the plant and ear height traits could easily be passed from one generation to the next thence enhancing the efficiency of plant breeding programmes (Shukla et al., 2006). Thus, conventional breeding for these two traits could lead to yield improvement (Lule et al., 2012). The high heritability estimates also explained the preponderance of additive gene actions in the expression of plant height and ear height traits. This is corroborated by the high GCA values for both plant ear height traits. It also indicates that these traits are under genetic control and the environmental factors did not greatly affect their phenotypic variation. Thus, there could be a rapid response to selection for these traits (Shakoor et al., 2007; Akinwale et al., 2011). The improvement or selection for these traits at early segregating generation for the fixable additive gene effects could lead to selection of elite genotypes (Manju & Sreelathakumary, 2002; Bozokalfa et al., 2010).

The grain yield showed moderately high heritability coupled with the highest GCV and PCV estimates and high SCA estimates. However, it showed low genotypic and phenotypic variances. The preponderance of the SCA effects suggested the involvement of non additive gene action in the grain yield expression. A high number of genes could be involved in the control of grain yield trait (Sujiprihati et al., 2003). The grain yield could be improved through heterosis breeding or hybridization and hybrid vigour (Govindaraj et al., 2011; Bello et al., 2012). Similar results have been reported in other studies (Manju & Sreelathakumary, 2002; Al-Tabbal et al., 2012).

A high range of genotypic, phenotypic and genotypic by environment variances, genotypic (GCV) and phenotypic (PCV) coefficient of variation were noted for plant height and ear height. The maize genotypes had sufficient variability with regard to these two traits thus genetic improvement could be achieved through selection for these traits hence their critical role in predicting the gains from selection (vashistha et al., 2013; Mustafa et al., 2013). Low GCV and PCV values were observed for days to maturity and this could probably be attributed to the phenotypic plasticity for these traits and also the presence of both positive and negative alleles in the maize genotypes leading to low genetic variation (Akinwale et al., 2011). Similar results were reported by Shakoor et al., 2007) and Manju and Sreelathakumary (2002).

The strong correlation between ear height and plant height with grain yield suggested that tall plants with high ear placement gave better yields compared to the shorter plants with lower ear placement. This could be attributed to the high dry matter accumulation function carried out by the high number of leaves possessed in the case of tall plants. It also implied that the tall lines excelled in capacity to support kernel growth through stem reserve mobilization (Sujipriphati et al., 2003; Al-Tabbal et al., 2012). Grain yield had a moderate genotypic association with days to 50% tasseling and pollen shed and this could be attributed to the differences among the breeding materials and their genetic behavior in the different environments (Shakoor et al., 2007). There was a strong inherent association between the field weight and most of the yield related traits. Selection based on field weight could lead to grain yield improvement. Generally, correlations among traits are attributed to the genetic nature (pleiotropic effects, linked genes) and environmental factors. The phenotypic correlations arise from genetic and environmental factors and can be marked out by measuring the phenotype while the genetic correlations arise from genetic factors because they give us information about level of relationship between two traits which is additive; crucial in ensuring effective selection (Bocanski, et al., 2009). The positive relationships noted among some of these traits indicated that the desirable genes influencing their inheritance in these hybrids could be exploited in further breeding activities for varietal improvement (Sujiprihati et al., 2003). From this study, there were high genotypic correlation coefficients for plant height and ear height than their corresponding phenotypic values implying presence of a strong inherent relationship implying the presence of genetic association (Zeeshan et al., 2013). Thus, an increase in those traits which show positive and significant correlations could lead to enhanced grain yield (Akinwale et al., 2011). Similar relationships have been reported in previous studies (Kabdal et al., 2003; Shakoor et al., 2007). The genotypic relationships among the traits affecting grain yield explains the true association as they exclude the environmental influences. With positive correlations, genes controlling these traits could be linked or positioned closely together on the same chromosome or could be under the control of pleiotropic genes (Bocanski et al., 2009). On the other hand, low phenotypic correlation coefficients could arise due to the modifying effect of environment on the association character at genetic level (Alake et al., 2008). The positive relationships observed in this study also indicate that favourable genes controlling these traits present in the population could be utilized for the improvement of the population sources in maize breeding programs (Sujiprihati et al., 2003). Thus, the information on correlations among traits remains crucial in improving the efficiency of breeding programs by employing the appropriate selection indices in cultivar or varietal improvement.

5. Conclusion

This study has revealed the existence of adequate genetic variability in the material studied. This knowledge could be crucial in enhancing the efficiency of maize breeding programmes in Kenya. This genetic diversity and the strong genetic association between grain yield and the agronomic traits would aid in indirect selection thus helping the breeders in the development of composites and synthetics for the resource constraint farmers with limited access to hybrid seeds. In addition, the correlation of the highly heritable traits with complex ones could help determine whether selection for one trait has any effect on another. Ear height and plant height traits which showed the highest coefficient of genotypic variability, high broad sense heritability estimates, and had strong positive association with grain yield could be used as effective selection indices for grain yield improvement.

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