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Genetic variability, heritability, genetic advance and trait correlations in selected sorghum (*Sorghum bicolor* L. Moench) varieties

ML Jimmy [*1]**, F. Nzuve**[1]**, O. Flourence**[1]**, E. Manyasa**[2]**, J. Muthomi**[1]

[1]*Department of Plant Science and Crop Protection, University of Nairobi, Nairobi, Kenya*

[2]*International Crop Research Institute for the Semi-Arid Tropics, Nairobi, Kenya*

Abstract

Study was carried out to estimate the genetic variability, heritability and genetic advance as well as association between yield and yield related traits in selected sorghum varieties. Ten sorghum varieties were evaluated in randomize complete block design with 2 replicates across two environments. Data were recorded on plant height, days to 50% flowering, number of productive tillers, panicle length, panicle width, panicle weight, 100 seed mass and grain yield. Mean squares were significant ($P \leq 0.05$) for all traits in the individual and combined analysis of variance, implying high variation in the sorghum population. Panicle length, panicle width, Dry panicle weight and 100 seed mass could be employed as target traits to improving grain yield. All the traits evaluated exhibited high genotypic and phenotypic components of variance than environmental variance, showing that characters in the population was genetically controlled and can be exploited in breeding programs. High heritability and estimated genetic advance as percentage of mean for most of the traits indicates the presence of additive genes and suggested reliable sorghum improvement through selection for the traits. Grain yield was significant and positively associated with days to 50% flowering, number of fertile tillers, panicle width, dry panicle weight and 100 seed mass.

* **Corresponding Author:** Jimmy Morris Lado ✉ Jim4wan@gmail.com

Introduction

Sorghum (*Sorghum bicolor* [L.] Moench) grain yields in Africa and Asia are generally low (0.95–1.17t/ha) compared to 3.63 t/ha reported in USA and Europe (FAOSTAT, 2011). The grain of sorghum is a major factor in the daily menu of millions of people while the stover is used to feed livestock (Devries *et al.,* 2001). Being a native crop of Africa, tremendous number of variability exists in East Africa (MoARD, 2008). However, the existence of variation alone in the population is not adequate for improving suitable traits unless the genetic variability is well understood. The grain yield is an essential and complex trait and is a function of several component traits. In the mixed structure of a plant, most of the traits are interrelated. Direct selection on yield is not effective and it has been reported that it would be better if the structure of yield is examined through its components rather than directly to realize their mutual association (Grafius *et al.,* 1964).

Genetic improvement in sorghum yield depends on quality and magnitude of genetic variability, heritability and genetic advance in the population as well as the nature of association between yield and its components. This enables simultaneous selection for many traits associated with yield (Mahagan *et al.,* 2011). Sorghum in general possesses a wide range of genetic variability (Sharma *et al.,* 2006). Adequate variability provides options from which selections are made for improvement and possible hybridization. Binodh *et al.* (2008) reported that information on trait association in crops is essential for effective selection in crop improvement. The phenotype of a plant is the result of interaction of a large number of factors and final yield is the sum of effects of several component factors (Biradar *et al.,* 1996). Correlation coefficients assist in deciding the direction of selection and number of traits to be looked at in improving grain yield.

Heritability of a trait is important in determining its response to selection. Estimates of heritability assist breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources (Smalley *et al.,* 2004). Estimates of heritability with genetic advance are more dependable and important than individual consideration of the parameters (Nwangburuk *et al.,* 2012).

When more traits are involved in correlation study, it becomes hard to determine the traits that really contribute to yield due to the existence of some amount of mutuality. The extent of variability is evaluated by GCV and PCV which provides information about relative amount of variation in different traits. According to Tah (2011) the extent of variability is measured by GCV and PCV which provide information about relative amount of variation in different traits studied. The present study was aimed to estimate the genetic variations, heritability and expected genetic advance in the selected sorghum varieties.

Materials and methods

Experimental locations

The study was carried out during the 2015 short rain season at Kenyan Agricultural and Livestock Research Organization (KALRO) - Kiboko and at the University of Nairobi Kabete Campus field stations. Kiboko station lies at altitude 960m above sea level with average annual rainfall of 548 mm and average minimum and maximum temperature of 16.6 and 29.4°C respectively. The University of Nairobi, Kabete campus Field Station lies at an altitude of 1820 m above sea level with an average annual rainfall of 1000 mm and average maximum and minimum temperature of 23 and 16°C respectively. The data for rainfall and temperature of the locations were obtained from their respective meteorological stations.

Sorghum genotypes

The seed of ten local varieties of sorghum were obtained from the International Crop Research for Semi-Arid Tropics (ICRISAT). These materials were preferred by the farmers, for their good food, feed and malting traits. The details of the varieties are presented in Table 1.

Table 1. Colour and head type of the ten local varieties of sorghum.

Variety	Grain colour	Head type
Gadam	Chalky white	Semi-compact
Hariray	Brown	Loose
Hugurtay	Brown	Compact
IESV 23008 DL	Creamy white	Semi-compact
IESV 23010 DL	Creamy white	Semi-compact
IESV 23011 DL	Creamy white	Semi-compact
ICSV 700	Creamy white	Compact
IS 1044	Creamy white	Compact
IS 2205	Creamy white	Compact
KARI Mtama-1	Creamy white	Semi-compact
Macia	Creamy white	Semi-compact
Sila	Creamy white	Semi-compact
Tegemeo	Creamy white	Semi-compact

Experimental design and layout

The ten varieties of sorghum were evaluated in a square lattice design with two replications. The varieties were sown in 4 row plots of 4m long with spacing of 0.75m between rows and 0.25m between plants in a row at each location. Two seeds were sown per hill and seedlings were thinned to one plant stand per hill two weeks after emergence. The plots were fertilized with a basal application of Diammonium Phosphate (DAP) at 100kg ha^{-1} and top dressing was carried out with urea (40kg ha^{-1}) before earting up at 30 days after emergency as recommended for both sites.

Data collection

Observations were recorded as means from 10 randomly selected plants in the 2 central rows, for plant height (cm), days to 50% flowering, number of productive tillers, panicle length (cm), panicle width (cm), dry panicle weight (g), hundred seed mass (g), sugar brix (%) and total grain yield (t ha^{-1}). These were determined at plot bases as suggested by IBPGR and ICRISAT (1993).

Statistical analysis

Data collected for each quantitative trait were subjected analysis of variance. Treatment mean compared using Fisher's protected least significant differences at P≤0.05.

Estimation of variance components

The phenotypic, genotypic and environmental variance for individual location was computed according to the formula proposed by Singh and Chaudhury (1999) as follows:

$$\sigma^2g = \frac{MS_G - MS_E}{r}$$

$$\sigma^2e = MSE$$

$$\sigma^2p = \sigma^2g + \frac{\sigma^2e}{r}$$

Where,

MS_G = mean squares due to genotype, MS_E = mean squares of error (environmental variance), r = the number of replications, σ^2e = random error variance, σ^2g = genotypic variance and σ^2p = phenotypic variance.

Variance components for the data combined across locations were estimated using the following formula (Johnson *et al.,* 1955)

$$\sigma^2e = MS_E$$

$$\sigma^2gl = \frac{MSgl - MS_E}{r}$$

$$\sigma^2g = \frac{MSg - MSE}{rl}$$

$$\sigma^2p = \sigma^2g + \frac{\sigma^2gl}{l} + \frac{\sigma^2e}{rl}$$

Where; σ^2gl = variance of genotype by location interaction, MS_E = error mean squares, $MSgl$ = genotype by location interaction mean square, MSg = genotype mean square, r = replication, l = location for traits under consideration and were categorized according to Sivasubramanian (1974) as 0 – 30% = low; 10 – 20% = moderate and above 60% = high.

Based on the analysis of variance, the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance (GA) were estimated as using formula by Burton and Devane (1953) as follows:

$$GCV = \frac{\sqrt{\sigma^2g}}{\bar{x}} X\ 100\%$$

$$PCV = \frac{\sqrt{\sigma^2p}}{\bar{x}} X\ 100\%$$

Where; $\bar{x}$ = phenotypic trait population mean.

Estimation of broad sense heritability (H²) and genetic advance as part of mean (GAM) assuming

selection intensity of 5% for individual and combined analysis of variance were computed using the formula adopted from (Johnson *et al.,* 1955). H² was classified according to (Robinson *et al.,* 1949) as follows: 0 – 30% = low; 30 – 60% = moderate; > 60% and GAM: 0 – 10% = low; 10 – 20% = medium, greater than 20%.

Correlation coefficient

Simple linear correlation coefficient (Pearson, 1986) was performed to understand the relationship among the agronomic traits studied. The correlation coefficient is defined by;

$$r = \frac{cov.x1x2}{(var.x_1)(cov.x_2)}$$

Where:

r = correlation coefficient

cov.x_1x_2 = covariance between traits x_1x_2

var.x_1 = variance of trait x_1

var.x_2 = variance of trait x_2 to calculate simple linear correlation coefficients.

Results

The results of analysis of variance revealed that the genotypes presented highly significant (P≤0.05) differences for all the traits studied in the individual and combined locations. There were no significant differences for genotype x environment interactions for plant height, panicle length and hundred seed mass (Table 2). Heritability (H2) estimates ranged from 13% for grain yield to 49% for plant height and genetic advance as per cent of mean (GAM) varied from 4.12% for days to 50% flowering to 51.6% for number of tillers.

Table 2. Analysis of variance for varieties evaluated at Kiboko, Kabete and combined locations.

Source	Degree of freedom	Plant height (cm)	Days to 50% flowering (cm)	No. of productive tillers	Panicle length (cm)	Panicle width (cm)	Dry panicle weight (g)	Hundred seed mass (g)	Grain yield (t ha⁻¹)
KIBOKO									
Replication	1	13.88	1.89	0.15	3.33	0.35	86.27	0.03	0.05
Genotype	12	5169.08	94.07	0.57	34.61	1.85	533.56	0.53	1.49
Error	12	50.83	4.14	0.07	2.97	0.50	37.88	0.07	0.04
SE±		7.13**	2.03**	0.27**	1.72**	0.71*	6.16**	0.27**	0.20**
LSD		15.53	4.43	0.58	3.75	1.54	13.41	0.58	0.44
CV %		4.1	3.50	28.80	9.10	10.50	11.70	11.10	6.6
KABETE									
Replication	1	179.42	0.62	0.02	7.76	0.11	165.51	0.24	0.50
Genotypes	12	1388.05	55.37	1.50	92.01	26.34	1711.89	0.43	1.49
Error	12	25.51	2.70	0.31	1.60	0.39	76.98	0.11	0.21
SE±		5.05**	1.64**	0.56*	1.27**	0.62**	8.77**	0.33*	0.45**
LSD		11.00	3.58	1.22	2.76	1.35	19.12	0.72	0.99
CV %		3.30	2.50	25.30	5.70	6.20	9.80	13.00	11.7
ACROSS LOCATIONS									
Replication	1	146.56	0.17	0.14	0.46	0.42	6.40	0.05	0.12
Environment	1	4801.92**	2056.33**	21.58**	145.22**	138.62**	17317.06**	0.31*	8.28**
Genotype	12	4512.15**	109.53**	1.20**	102.58**	14.25**	1089.90**	0.60**	1.48**
GXE	12	2044.98**	39.91**	0.88**	24.04**	13.95**	1155.56**	0.36ns	1.49**
Error	25	38.51	3.37	0.19	2.62	0.43	64.95	0.10	0.14
Means		164.60	64.90	1.60	20.70	8.40	71.00	2.50	3.50
CV %		4.00	2.80	27.50	7.80	7.80	11.40	12.40	10.50
H² %		49.8	49.2	45.8	49.4	49.2	48.5	45.6	47.6
GAM %		41.8	16.2	62.0	49.5	45.3	45.8	28.0	33.3

SE ± = standard error of difference of means, LSD = least significant difference of means (5% level), GXE = genotype by environment interactions, CV % = coefficients of variation, H² % = broad sense heritability, GAM % = genetic advance as % of mean, *, **= significance levels at P≤0.05 and P≤0.001 respectively.

Estimates of genotypic, phenotypic, environmental and genotype x environment variability

Table 3 shows the genotypic, phenotypic, environmental and genotype x environment variances for Kiboko and Kabete locations. Values of genotypic variances ranged from 0.3 (hundred seed mass) to 1042.7 (plant height) at Kiboko and from 0.1 (hundred seed weight) to 1436.5 (dry panicle weight) at Kabete location (Table 3). Similarly, phenotypic variances ranged

from 0.3 (hundred seed mass) to 1354.7 (plant height) in Kiboko location and 0.3 (100 seed weight) to 1439.1 (panicle weight) at Kabete location. Environmental variances in Kiboko ranged from 0.03 in hundred seed weight to 312.0 in plant height. For Kabete location, the range for environmental variances ranged from zero in hundred seed mass to 35.0 in plant height.

Table 3. Estimate of environmental, genotypic and phenotypic variance for eight traits evaluated at Kiboko and Kabete.

Traits	Mean		$\sigma^2 g$		$\sigma^2 p$		$\sigma^2 e$	
	Kiboko	Kabete	Kiboko	Kabete	Kiboko	Kabete	Kiboko	Kabete
PH (cm)	174.20	155.00	2559.13	681.27	2584.54	694.03	50.83	25.51
DF	58.60	71.20	44.97	26.33	47.04	27.68	4.14	2.70
NT/P	1.00	2.00	0.25	0.60	0.29	0.75	0.07	0.31
PL (cm)	19.00	22.30	15.82	45.20	17.31	46.00	2.97	1.60
PW (cm)	6.80	10.00	0.68	12.98	0.93	13.17	0.50	0.39
DPW (g)	52.70	89.20	247.84	817.46	266.78	855.95	37.88	76.98
SM (g)	2.40	2.60	0.23	0.16	0.26	0.22	0.07	0.11
GY (t ha⁻¹)	3.10	3.90	0.72	0.64	0.74	0.74	0.04	0.21

$\sigma^2 e$ = environmental variance, $\sigma^2 g$ = genotypic variance, $\sigma^2 p$ = phenotypic variance, PH = plant height, DF = days to 50% flowering, NT/T = number of productive tillers, PL = panicle length, PW = panicle width, DPW = dry panicle weight, SM = 100 seed mass, GY = grain yield.

Genotypic coefficient of variation, phenotypic coefficient of variation, broad sense heritability and genetic advance as per cent of mean

Genetic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), broad sense heritability (H^2) and genetic advance as per cent of mean (GAM) estimates are presented in Table 4. The highest GCV and PCV values were recorded for number of productive tillers (76.6 at Kiboko; 40.1% at Kabete) and (88.8 at Kiboko; 43.5% at Kabete) respectively, followed by dry panicle weight (34.4 at Kiboko; 37.6% at Kabete) and (35.3 at Kiboko; 37.6% at Kabete) repectively (Table 4). Percent heritability (H^2) estimates were high at Kiboko and Kabete for panicle weight (95.1, 99.8), panicle length (96.4, 96.6), plant height (87.0, 97.8), panicle width (97.60, 75.3), hundred seed weight (94.3, 66.8), days to 50% flowering (82.9, 77.0), number of tillers (74.3, 85.0) and grain yield (76.1, 72.2). The expected genetic advance ranged from 0.5% for hundred seed mass at Kabete to 78.1for dry panicle weight at Kiboko. Genetic advance as per cent of mean (GAM) ranged

from 12.7 to 136.1 for days to 50% flowering and number of fertile tillers at Kabete and Kiboko respectively. High GAM for characters studied at both sites were observed on number of tillers, panicle weight and panicle length (Table 4).

Phenotypic correlation among traits

Phenotypic correlation coefficients between pairs of trait are presented in Table 5. All the traits that had significant phenotypic association with each other also showed significant genotypic relationship. The panicle weight, panicle length, panicle width, number of tillers and grain yield were positively correlated. The results of correlation analysis as showed by their coefficients of correlation (Table 5) reveal that grain yield displayed significant ($P \leq 0.05$) positive association with days to 50% flowering (r =0.57), number of fertile tillers per plant (r =0.81), panicle width (r =0.63), dry panicle weight (r =0.76), and hundred seed weight (r =0.37). Moderate and positive relationships were observed between hundred seed mass and days to 50% flowering (r =0.25) and hundred seed mass with dry panicle weight (r =0.30).

Significant (p≤0.05) positive associations were observed between dry panicle weight with days to 50% flowering (r =0.77), number of tillers (r =0.32), panicle length (r =0.65) and panicle width (r =0.71). Panicle diameter was highly significant and positively related to days to 50% flowering (r =0.75) and panicle length (r =0.69). Highly significant positive association was recorded between panicle length and days to 50% flowering (r =0.64). There negative significant relationships between plant height and dry panicle weight (r = -0.39), hundred seed mass (r = -0.39) and grain yield (r = -0.41).

Table 4. Coefficients of genotypic and phenotypic variations; heritability and genetic advance (as % of population mean) for eight traits of sorghum at Kiboko and Kabete.

Trait	GCV%		PCV%		H²%		GAM%	
	Kiboko	Kabete	Kiboko	Kabete	Kiboko	Kabete	Kiboko	Kabete
PH (cm)	29.04	16.84	29.18	17.00	99.00	98.20	59.60	34.40
DF	11.44	7.21	11.70	7.39	95.60	95.10	23.10	14.50
NT/P	55.58	36.02	59.34	39.39	87.70	79.40	57.40	64.50
PL (cm)	20.93	30.15	21.89	30.42	91.40	98.30	41.30	61.70
PW (cm)	12.09	35.90	14.15	36.29	73.00	98.50	21.30	73.80
DPW (cm)	29.87	32.05	30.99	37.80	92.90	95.50	59.40	64.60
SM (g)	19.88	15.41	21.35	17.86	86.70	74.50	38.20	27.40
GY (t ha⁻¹)	27.42	20.49	27.80	22.11	97.30	85.90	55.80	39.20

GCV% = genotypic coefficient of variation, PCV% = phenotypic coefficient of variation, H² %= broad sense heritability, GAM = genetic advance as % of mean, PH (cm) = plant height, DF = days to 50% flowering, NT/P = number of harvestable tillers, PL (cm) = panicle length (cm), PW (cm) = panicle width (cm), DPW (g) = dry panicle weight, SM (g) = 100 seed mass and GY (t ha⁻¹) = grain yield.

Table 5. Phenotypic Correlation among traits.

Trait	PH (cm)	DF	NT/P	PL (cm)	PW (cm)	DPW (g)	SM (g)	GY (t ha⁻¹)
PH (cm)	-							
DF	0.04	-						
NT/P	-0.28*	0.33*	-					
PL (cm)	-0.10	0.46**	0.20	-				
PW (cm)	-0.15	0.55**	0.31*	0.79**	-			
DPW (g)	-0.26	0.65**	0.31*	0.48**	0.57**	-		
SM (g)	-0.26	0.02	0.10	-0.34*	-0.18	0.14	-	
GY (t ha⁻¹)	-0.17	0.51*	0.18	0.35*	0.37*	0.76**	0.31*	-

PH (cm) = plant height, DF = days to fifty per cent flowering, NT/P = number of harvestable tillers per plant, PL (cm) = panicle Length, PW (cm) = panicle width, DPW (g) = dry panicle weight, SM (g) = 100 seed mass (g), GY (t ha⁻¹) = grain yield, *, ** = significance levels at P≤0.05 and P≤0.001 respectively.

Discussion

Analysis of variance showed significant differences amongst the genotypes for all the traits tested across environments suggesting existence of adequate genetic variability among the selected materials and scope for sorghum improvement. The significant (P≤0.05) differences found for traits in the environment component indicated that the environmental factors such as rainfall amount and distribution, temperature and soil in the two locations were different. This significant interaction effect of the traits indicated that the environmental conditions in the two locations affected the performance of the genotypes leading to the differences among the sorghum varieties across the two sites. Thus, it is important to evaluate varieties across locations and over seasons to ensure their stability for usage as reliable genetic materials for crop improvement in a particular environment. However, G x E interaction was not significantly different for plant height, panicle length and 100 seed mass implying that the genotypes responded similarly for the traits in the different environments suggesting that selection for these traits do no impact on improvement. Combined analysis, revealed that most of the traits had wide range of variability. Grain yield, which is the primary concern in most breeding programs, demonstrated a wide range of variation.

This study confirmed with those of Oyiga (2011) and Mangoel (2011) who reported that these traits may possibly be under genetic control rather than environmental influence. Significant effects due to variety x environment interaction have been reported for different characters in sorghum (Ezzat *et al.,* 2010). Therefore, the presence of such range of variations of the traits revealed the presence of large amount of genetic variation among the released varieties.

The phenotypic variation was separated into genotypic and environmental variances for perfect understanding of the pattern of variation are presented in Table 3 for individual location and Table 1 for combined analysis. Generally, the results for phenotypic variance were slightly greater than that of genotypic variance at both locations suggesting that environmental variance had influenced on the expression of the traits. The results for genetic variability also showed that plant height and panicle weight displayed the highest phenotypic variance. In addition, the traits expressed higher $\sigma^2 p$ and $\sigma^2 g$ values than the $\sigma^2 e$ values showing that manifestation of most of the traits are genetic. Hence, they can be exploited in breeding programs. This finding is in agreement with observations of other researchers on several quantitative traits in sorghum genotypes (Abu-Gasim 1985; Abraha *et al.,* 2015).

GCV measures the variability of any trait due to genetic factors. The magnitude of the environmental influence on any character is determined by the extent of the differences between the GCV and PCV. Higher GCV estimates than the PCV estimates shows that the variation in phenotypic expression of the genotypes across the two locations was largely due to genetic factors. However, higher PCV values would indicate the character is influenced by the environment. High values recorded for genotypic and phenotypic variance for plant height and dry panicle weight is in agreement with the results reported in sorghum (Can and Yoshida *et al.* 1999). PCV values were higher than the GCV for all the traits suggesting the presence of environmental influence to some level

in the phenotypic expression of the traits. Similarly, the closer GCV and PCV estimates for plant height, panicle length, dry panicle weight across environments and 100 seed mass at Kiboko suggest low environmental impact for these traits and hence high heritability. Therefore, improvement of these traits through selection is possible. GCV and PCV values were moderate for days to 50% flowering, grain yield, and number of tillers but low for hundred seed mass. This result is in line with findings of Lesley (2005) and indicates that selection for these traits is less effective when compared to those traits with high GCV and PCV. High values of PCV and GCV were found for number of productive tillers, panicle weight, panicle diameter, and plant height indicating that variation in these traits contributed to the total variability. Abirami *et al.* (2005) reported similar results of PCV and GCV values for maize grain yield and other traits and Iftekharuddeula *et al.* (2001) reported moderate genotypic and phenotypic coefficients of variation for plant height, days to maturity and panicle length in nineteen rice hybrids. The minor differences observed between GCV and PCV for panicle length, dry panicle weight and overall grain yield imply the presence of adequate genetic variability for traits which may enhance selection (Yadav *et al.,* 2000).

Heritability (H^2) combined with genetic advance is a more dependable indicator for selections of traits (Ubi *et al.,* 2001). High heritability and high genetic advance as per cent of mean (GAM) due to highly additive gene effect was observed for number of productive tillers, hundred seed mass, panicle diameter and grain yield. Thus, the improvement of these traits can be made through selection. H^2 was high for all the agronomic traits measured. Consequently, all the agronomic traits examined indicated high heritability demonstrating high breeding values with more additive genes which is essential for crop improvement. Improvement of these traits through selection should quickly be achieved. High H^2 couples with relatively high GAM was observed in plant height and panicle weight.

This is an indication that most probably that heritability is due to genetic factor and selection could be effective in early generations for this traits and the possibility of improving sorghum grain yield through direct selection for grain yield and its components. For plant height and panicle weight, the high heritability estimates were accompanied by low genetic advance suggesting non-additive gene action and use of breeding methods which exploit non-additive gene action like heterosis breeding would effective. Selection for those characters with relatively high GAM would lead to increased performance of the varieties for the traits. Therefore in the current study, most of the traits have the potential to respond positively to selection across sites due to their high H^2 coupled with relatively high genetic advance. Mahajan *et al.* (2011) also described high values of expected genetic advance showed as per cent of mean (GAM) for panicle weight and grain yield. Several researchers like Arunkumar (2004); Shegro *et al.* (2013), have also made similar observations. Ali *et al.,* (2002) observed that high heritability may not always associate with high genetic advance. Thus, heritability should be considered in association with genetic advance to predict the effect of selecting superior crops varieties.

Grain yield is a complex trait and depends on other agronomic traits in crop improvement program. Therefore, associations of different agronomic traits with each other and their relationship to yield are important. The positive relationship between grain yield with days to 50% flowering, panicle width, panicle weight and 100 seed mass is justifiable as increasing panicle length and width through selection may lead to proportionate increase in grain yield. These traits could be considered as important traits for improving grain yield. The results corroborated with the findings of Abdel-Fatah, (2013) who observed significant and positive differences between panicle lengths, panicle width and total grain yield. Thus, selection for these traits can simultaneously improve potential grain yield and gather the desirable genes. On the other hand, significant but negative correlation exists between plant height with panicle

weight, hundred seed mass indicating the compensation mechanism and trade-offs between this pair of traits in determining the yield traits in sorghum. Similar outcomes were reported by Matthews *et al.* (2005) for panicle weight, Bohra *et al.* (1986) for panicle length. Previous workers have described grain yield as a function of seed mass and panicle weight (Aba and Zaria, 2000; Kambel and Webster, 1966).

Conclusion and recommendations
This study demonstrated wide range of genetic variability among the genotypes used for all of the characters tested, thus indicating high potential for use in trait improvement. Moreover, the presence of significant high heritability (H^2) and expected GAM% implied options for improvement of the traits through selection. The correlation analysis revealed that panicle length/width, panicle weight and 100 seed weight were the most important yield associated components. These traits also demonstrated high H^2 and GAM %. Hence suggesting that panicle weight, panicle length, panicle breadth and hundred seed mass are important yield contributing traits, thus selection based on these traits would be most effective. Understanding the interaction of these traits among themselves and with the environment is of great use in sorghum yield improvement.

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