Genetic Variation and Interrelation of Agronomic Character in Landraces Sorghum (*Sorghum bicolor* (L.) Moench)

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ABSTRACT

Sorghum (*Sorghum bicolor* (L.) Moench) is a crop of world – wide importance. It is unique in its ability to produce under wide array of environmental conditions. Landraces have great genetic diversity, making selection for most traits of economic importance possible. Populations of fourteen genotypes of sorghum landraces were evaluated in two locations during the 1999 and 2000 rainy seasons. Data were collected on grain yield and five morphological traits to study genetic variability, genetic and phenotypic correlation between these traits, as well as the influence of environmental factors on these genotypes. Differences between landrace genotypes for grain yield, seed mass, plant height, inflorescence length and days to anthesis were significantly different ($p < 0.01$) in all environments. Heritability estimates in the broad sense for plant height and inflorescence length 96.8 ± 0.134 and 9.2 ± 0.134 respectively were quite high; whereas, the estimates was moderate for seed mass ($h^2 = 37.9 \pm 0.134$) and moderately high for grain yield ($h^2 = 82.05 \pm 0.136$). Genetic correlation between grain yield and days to anthesis, grain yield and seed mass were smaller than phenotypic correlation, suggesting the synergistic effect of genotypes and environment in phenotypic relationship between grain yield and those traits. The difference between genetic correlation and phenotypic correlation was high in some cases, suggesting the importance of genotype x environment interaction effects on the relationships between these traits. The correlation coefficient, indicated that selection index giving proper weight to characters like seed mass, inflorescence length and days to anthesis would likely produce sorghum varieties with higher yields.

Key words: Genetic variability, heritability, genotype x environment, selection index, sorghum landraces.

RÉSUMÉ

Sorgho (*Sorgho bicolor* (L.) Moench) est une plante importante qui s'adapte aux conditions climatiques variées. Les cultivars locaux possèdent une grande diversité génétique, rendant possible la sélection des caractères économiquement importants. Un échantillon de 14 génotypes a été évalué dans deux localités pendant deux années consécutives. Les observations ont été prises sur le rendement en grain et cinq caractères morphologiques. Les coefficients de corrélation entre les différents caractères ainsi que le degré d'association phénotypique et génétique, et l'influence des facteurs environnementaux sur ces associations ont été étudiés. Les différences significatives entre les écotypes locaux ont été observées pour le rendement, le poids de 1000 graines, la hauteur des plants, la longueur de l'inflorescence et la date de la floraison. Le coefficient d'héritabilité au sens large pour la hauteur des plants et la longueur de l'inflorescence, 96.8 ± 0.134 et 9.2 ± 0.134 respectivement, étaient tout à fait élevés. Ce coefficient est modéré pour le poids de 1000 graines ($h^2 = 37.9 \pm 0.134$) et moyennement élevé pour le rendement ($h^2 = 82.05 \pm 0.136$). Les corrélations génétiques entre le rendement et la date de la floraison, le rendement et le poids de 1000 graines étaient inférieures aux corrélations phénotypiques, ce qui suggère un effet de synergie entre génotypes et environnement sur les relations phénotypiques entre le rendement et ces caractères. Les différences entre les corrélations génétiques et phénotypiques étaient importantes dans certains cas, ce qui indique l'importance de l'effet interaction entre génotypes et environnement sur les relations entre ces différents caractères. Les coefficients de corrélations obtenus suggèrent qu'on doive construire les indices de sélection bien équilibrés sur les caractères comme le poids de 1000 graines, la longueur de l'inflorescence et la date de la floraison pour l'identification des variétés de sorgho a haut rendement.

Mots clés : variabilité génétique, héritabilité, interaction génotype x environnement, indices de sélection, écotypes locaux de sorgho.

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INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) belongs to the grass family, was domesticated in various parts of Africa. It has become one of the most economically important crops in the world with over 40 million hectares of land dedicated to its cultivation (FAO, 1994). Its many uses have made it a staple world - wide agriculture for years. Its economic importance world – wide has also made it a target for improvement via genetic transformation (Arriola, 1995). The continued improvement of this important crop depends upon the utilization of genetic variability in landraces originally maintained by traditional agricultural practices. Sorghum is cultivated in the environment where rainfall is generally insufficient and erratic (Rasenberg, 1984) and soil fertility very poor (Lal, 1987). It has evolved in the dry and semi-arid region of Africa (Mann et *al.*, 1983). Sorghum landraces are known to respond differently to day length and temperature according to their specific geographical adaptation (Grenier et *al*, 2001). Farmers in the semi arid regions preferentially sow highly adaptive landraces to match the diversity of local environmental conditions (Kouressy et al., 1998). They save seed from their own crops; often selecting for genotype that will guarantee a maturity corresponding to the end of the raining season and produce substantial yield. This artificial selection coupled with natural selection for survival in the local environment have led to the establishment of ecologically well adapted landraces.

Harlan (1975) defined a landrace as a mixture of genotypes that evolved, largely by natural selection under the environmental condition in which they were grown. Landraces of sorghum generally tolerate biotic and abiotic stresses and grow under low – input, sustainable farming conditions, which ensure a fair stability of production. There is renewed interest in landraces and primitive sorghum cultivars as important sources of genetic variation, mainly because of the trend towards greater uniformity that has narrowed the genetic base of the more recently bred, high – yielding hybrid and sorghum cultivars, therefore increasing their vulnerability to biotic and abiotic stresses.

Sorghum landraces grow in heterogeneous environments and therefore have to adjust to many ecological niches. They are therefore expected to accumulate interpopulation diversity. Sabharwal et *al.*, (1995) emphasized that sorghum parents with more diversity among them are expected to exhibit a higher amount of heterotic expression and a broad spectrum of variability in segregating generation. In the semi-arid tropic environment, breeding programs seek to combine the favorable adaptive traits of landraces and old cultivars with the high yield potentials of modern genotypes. This is aimed at producing varieties of high yield stability under unpredictable variable climatic conditions. The genetic potential of crop germplasm in the region therefore needs to be adjusted to available environment resources (Kawano and Jennings, 1983). Effective utilization of these germplasm in breeding programs is more enhanced if variation is properly characterized and described.

Improvement of landraces involves exploiting the genetic variability in specific traits. Simultaneous improvement of these traits depends on the nature and degree of genetic association between traits. Complex associations between traits have been reported for most growth and yield characteristics of such crops as *Musa* spp. (Ortiz and Vuylsteke, 1996). Studies involving sorghum have been conducted in which genetic variances, heritabilities, and correlations were determined (Esechie, 1983; Ibrahim et *al.*, 1985). These studies showed that: 1. additive variance components are of greater importance than dominance variances for all traits except yield; 2. estimates of heritabilities for yield (0.09 – 0.58) and days to 50% flowering (0.25 – 0.90) depend on the population, family structure, number of environments and replications, and number of plants per plot; 3. correlations are generally positive between yield and days to 50% flowering. House (1995) pointed out that the number of traits a sorghum breeder can manage at one time is generally limited. As the number of traits increases, the gain per cycle of selection for each trait decreases. This emphasizes the problem of prioritization of traits. Therefore, knowledge on phenotypic and genetic correlations among agronomic traits is important. It may help to identify characters that have little or no importance in the selection program. This will permit the determination of the feasibility of indirect or direct selection for a trait and the corresponding correlated response to selection.

The objectives of this study therefore included the exploration of genetic variability among sorghum landraces; the estimation of the phenotypic and genotypic correlations among selected traits and the examination of the effects of genotype x environment interaction on these traits.

MATERIALS AND METHODS

Experimental environment
The study was conducted at two geographical locations, Maroua and Koza, in Northern Cameroon. The first location (Maroua) was at the Institute of Agricultural Research for Development (IRAD) farm located at Lat. $10^0 35^0$ N, Long. $14^0 20'$ E. and at Alt. 300 m. The vegetation in the area is typical of the Sudano - Sahelien zone (Windmeijer & Andriesse, 1993). Mean annual rainfall is approximately 750 mm with most of the rain falling between June and September. The length of the growing period is between 120 to 140 days, though with periodic droughts. The soil is sandy, siliceous, reddish colored and low in fertility and organic matter. The second location (Koza) was at the Agricultural Experimental Station situated at Lat. $10^0 48^0$ N, Long $14^0 35'$ E and at Alt. 1100 m. Mean annual rainfall is approximately 1000 mm, most of it falling between May and October. The length of growing period ranges from 140 to 160 days. The soil is slightly acidic, alfisol and the landscape is mountainous. The sowing periods were from mid June to early July in both years.

Genetic materials and experimental field.
The trial consisted of fourteen sorghum landraces (here after referred to as genotypes) was conducted on the field during 1999 and 2000 rainy season. These genotypes, collected from different sorghum areas of Northern Cameroon were grouped in a randomized complete block design and were replicated four times within each location. Individual plots consisted of four rows, 5 m long with 80 cm between rows, covering a plot area of 16 m². The experiment was hand planted. All rows were thinned to 20 cm between hills at two plants per hill, resulting in a population of about 125000 plants per ha. Plots were kept mostly weed- free by regular manual weeding. At each location, the same dose of fertilizer (60 N: 40 P_2O_5: 30 K_2O kg per ha) was applied as a basal dose in each experiment with further 40 kg of nitrogen per ha in the form of urea top-dressed five weeks after planting and then incorporated into the soil.

The numbers of days to anthesis were assessed on a whole plot basis and were recorded as the number of days from planting to the date when 50% of the plants in a plot were shedding pollen. Plant height (cm) was measured as the distance from the soil surface to the tip of the panicles in each plot on five randomly selected plants. The inflorescence length (cm) was measured as the length from the base of the panicle to the top. Seed mass was recorded as grams per 1000 seeds counted using a numeral electrical seed counter. The two central rows were harvested at maturity and grain yield was measured as weight of threshed grain expressed in kg per ha.

Statistical procedure
The data were subjected to a multivariate analysis of variance using the MANOVA option of the GLM procedure in SAS (SAS, 1991). Location x year interaction was considered as environment. Means of all traits and the corresponding standard errors were calculated by UNIVARIATE procedure as outlined by SAS (SAS, 1991). Data were combined over environment after a Bartlett's test for homogeneity of error variance indicated that error variances from the individual experiment were homogenous for all traits. The statistical model use was as follows:
$$Y_{ijk} = \hat{\imath} + G_i + E_j + R_{kj} + (GE)_{ij} + e_{ijk}$$ were
Y_{ijk} is the observed performance of the ith genotype in the kth replication of the jth environment (ENV) ; $\hat{\imath}$ is the general mean. G_i the effect of the ith genotype (i = 1, 2, 3,... 14); E_j the effect of the jth environment; $(GE)_{ij}$ the effect of the genotype x environment interaction and e_{ijk} the effect of the random errors associated with the ith genotype at j^{th} environment in the kth replication. The MANOVA option produces sum of squares and cross-product (SSCP) matrices of the variables for each component of the statistical model used (SAS, 1991). Mean sums of squares and cross products (MSCP) matrices were then calculated from the SSCP by dividing by the appropriate degree of freedom.

The content of the components of variance for mean sums of squares are analogous to those for covariance. Genetic components were computed by equating the genetic variances and covariance to their appropriate expected mean squares and mean cross products.

A completely random model was assumed for estimation of the variance component σ (error variance), σ_{ge}^2 (genotype x environment) interaction variances and σ_g^2 (genetic variance). Variance and covariance components were used to compute genetic and phenotypic correlations and heritability estimates in the broad sense. The genetic correlation $r_{g(xy)}$ between two traits x and y was calculated as follows:
$r_{g(xy)} = Cov_{g(xy)} / (v_x . v_y)^{1/2}$ where $Cov_{g(xy)}$ is the genetic covariance of x and y; v_x and v_y are the respective

variances for traits x and y.

Pearson's simple correlation coefficient were calculated to estimate the phenotypic associations among the traits using the formula:
$r_{p(xy)} = Cov_{p(xy)} / (V_{p(x)} \cdot V_{p(y)})^{1/2}$ where $r_{p(xy)}$ is the phenotypic correlation coefficient between x and y, $Cov_{p(xy)}$ is the phenotypic covariance of x and y. $V_{p(x)}$ and $V_{p(y)}$ are the respective phenotypic variance of x and y.

Broad sense heritability (h^2) estimates were obtained as the ratio of genetic variance (σ_g^2) to phenotypic variance (σ_p^2) according to Lothrop et al., (1985) as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_e^2 / rl + \sigma_{ge}^2 / l + \sigma_g^2} \text{ and } \sigma_p^2 = \sigma_e^2 / r\,l +$$

$$\sigma_{ge}^2 / l + \sigma_g^2$$

Where h^2 is the broad – sense heritability, σ_{ge}^2 is the variance associated with genotype x environment interaction, σ_e^2 the experimental error. The terms r and l indicate the number of replications and the number of environments, respectively.

The standard deviation of the heritability value was calculated following Vello and Vencovsky (1974):

$$Sd(h^2) = (\frac{2}{n1+2}) + (\frac{2}{n2+2}) (1-h^2) \text{ where n1 and}$$

n2 are the degree of freedom of the genotypes and error sources of variation, respectively.

The magnitude of genetic and environmental effects involved in the expression of different traits were determined by the genotypic (GCV) and phenotypic (PCV) coefficient of variation as follows:

$$GCV = \frac{\sqrt{\sigma_g^2}}{\overline{X}} x100 \text{ where } \sigma_g^2 \text{ is genetic variance}$$

and $\overline{X}$ the mean of the trait

$$PCV = \frac{\sqrt{\sigma_p^2}}{\overline{X}} x100 \text{ where } \sigma_p^2 \text{ is the phenotypic}$$

variance and $\overline{X}$ the mean of the trait.

RESULTS
Highly significant (p< 0.01) genotype differences were observed among the landrace genotypes for the various characters measured (Table 1). Environments showed highly significant (p< 0.01) differences for all the traits studied. Genotype x environment interactions were also highly significant (p< 0.01) for days to anthesis, plant height and grain yield and significant at 0.05 probability levels for seed mass.

Mean values over genotypes, range between genotypes and coefficients of variation for the recorded traits over the four environments are shown in Table 2. Wide phenotypic variation existed for most traits. The highest coefficient of variation was shown by grain yield; followed by seed mass, plant height and inflorescence length respectively. The least value was shown by developmental traits such as days to anthesis.

The variance components and estimates of genetic parameters are shown in Table 3. The highest estimates

Table 1: Means square for the selected characters of sorghum landraces grown in the four environments

Source of variation	Df	Days to anthesis	Plant height (cm)	Panicle length (cm)	Seed mass (g)	Grain Yield (kg/ha)
Environment (Env)	3	2034.52**	33593.79**	193.20**	1615.84**	42540312.35**
Rep (Env)	12	16.22*	1951.22	6.02	12.36	399526.93**
Genotype	13	266.42**	97103.71**	256.97**	57.47*	3756002.094**
Genotype x Env	39	22.69**	3022.86**	7.12	35.65*	674029.65**
Error	156	7.34	1242.76	4.71	18.54	157021.48

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

Table 2: Phenotypic variation in selected characters of sorghum landrace genotypes

Characters	Mean	Minimum	Maximum	Range	SE ±	Coefficients of variation (%)	F value for genotypes
Days to anthesis	69.9	56	85	29	0.48	3.87	36.26**
Plant height (cm)	318.06	140	531	391	5.83	11.08	78.13**
Inflorescence length (cm)	20.63	10	29	19	0.31	10.5	54.51**
Seed mass (g)	38.70	22	62.5	39.6	0.44	11.12	3.10**
Grain yield (kg/ha)	2535.13	190	5470	5280	68.15	15.63	23.92**

**, Significant at 0.01 probability level.

of PCV were observed for plant height (24.49%). The minimum estimated of PCV was observed for seed mass (4.89 %). Estimates of genetic coefficient of variation were highest for plant height (24.10%), intermediate for grain yield (17.31%) and inflorescence length (19.15%), and the lowest for days to anthesis (5.58%) and seed mass (3.01%).

The magnitude of phenotypic coefficient of variation were nearly the same as the genotypic coefficient of variation for days to anthesis, plant height and seed mass.

The heritability estimates ranged from 37.9% for seed mass to 97.2% for inflorescence length. Grain yield was found to be highly heritable ($h^2 = 0.82$) as were plant height ($h^2 = 0.96$) and days to anthesis ($h^2 = 0.91$) when data were combined over environment. Moderate estimates were observed for seed mass.

Correlation between characters
The phenotypic and genetic correlations among the various characteristics are presented in Table 4. The

Table 3: Phenotypic coefficient of variation (PCV) and genetic coefficient of variation (GCV) components of variance, heritability (H) of selected characters of sorghum landrace genotypes.

Characters	PCV (%)	GCV (%)	Estimates of components of variance				H (%)
			σ_p^2	σ_g^2	σ_e^2	σ_{ge}^2	
Days to anthesis	5.83	5.58	16.65	15.23	7.34	3.83	91.4±0.134
Plant height (cm)	24.49	24.10	6068.98	5880.05	1242.76	445.02	96.8 ±0.134
Inflorescence length (cm)	19.41	19.15	16.05	15.61	4.71	0.60	97.2 ±0.134
Seed mass (g)	4.89	3.01	3.58	1.36	18.54	4.27	37.9±0.134
Grain yield (kg/ha)	19.11	17.31	234750.12	192623.27	157021.48	129252.04	82.0±0.136

σ_p^2, σ_g^2, σ_e^2 and σ_{ge}^2 phenotypic, genetic, error and genotype x environmental variance respectively.

strongest association among the 10 possible pairs of plant or grain characteristics was between plant height and seed mass ($r_p = 0.16$), inflorescence length and seed mass ($r_p = 0.17$), inflorescence length and grain yield ($r_p = 0.17$), seed mass and grain yield ($r_p = 0.44$), plant height and inflorescence length (0.23), where phenotypic correlation (r_p) were positive and significant. The phenotypic correlations between days to anthesis and plant height, days to anthesis and seed mass, days to anthesis and grain yield were negative and significantly different from zero. In general, days to anthesis were negatively associated with others traits. Plant height and inflorescence length were consistently correlated with other traits.

The genotypic correlations of days to anthesis with plant height ($r_g = 0.58$) was positive and significant. Similarly, plant height was positively correlated with inflorescence length ($r_g = 0.29$) and seed mass ($r_g = 0.42$). Significant negative correlation coefficient was observed between days to anthesis and grain yield ($r_g = -0.61$), plant height and grain yield ($r_g = -0.62$), inflorescence length and seed mass ($r_g = -0.21$), seed mass and grain yield (-0.37).

DISCUSSION

The data presented above show that the set of landraces evaluated formed a variable pool of sorghum germplasm (Table 2). These data also suggested evidence for significant genetic and phenotypic variation for traits tested which implied that their improvement through selection is possible. The significant genotype x environment effects on most traits studied and the variation exhibited by these traits indicate that environment or location used for selection may influence selection of lines for advanced trials. In such cases, breeders have two options: either selecting for broad adaptation by searching for those genotypes with superior and stable performance across environment, or selecting for specific adaptation whereby genotypes that perform best in each environment are retained for these particular environments. The latter approach was credited with the potential of achieving greater genetic gains by some scientists (Simmonds, 1991; Annichiarico, 1992). However, Jackson and Mc Rae (1998) suggested that family selection on the basis of broad adaptation gave the highest gains in most environments. In any event selection efficiency is related to the magnitude of heritability (Johson et al., 1955). In this study, broad-sense heritability estimates ranged between 37.9% (for seed mass) and 97.2% (for inflorescence length). This implies that most of the traits examined are under genetic control. High estimates of heritability were observed for plant height and inflorescence length; these traits also possessed high estimates for GCV. This suggested that they might respond well to appropriate recurrent selection methods. Days to anthesis also exhibited high heritability estimates ($h^2 = 0.91$), but registered low value for GCV. This might indicate that day to anthesis is controlled by non-additive gene action; an improvement of this trait therefore can be achieved through exploiting the dominance effect. The moderately high heritability estimates for grain yield ($h^2 = 0.82$) suggests that environmental effects constitute an important portion of the total phenotypic variation for this trait. Therefore, selection of superior genotypes on the basis of yield *per se* would not be as effective as selection for its primary components, namely days to anthesis, seed mass. Thus, the association of these components assumes special importance as the basis for selecting high-yielding genotypes. The estimates of coefficient of phenotypic and genotypic variation were nearly equivalent for days to anthesis, plant height and inflorescence length, suggesting that there was a neutral genotypic x environment interaction effect on these traits. This implied that for these traits, selection could be successfully carried out at all environments.

Others studies with sorghum show that, although heritabilties for grain yield and most yield components usually are low on a plant basis; they are sufficiently high on a family and population basis (Ross and Hookstra, 1983). Similarly, high heritability (90%) was also reported by Nimbalkar et al., 1988), Sankara pansian and al., (1996) in sorghum grain yield and panicle length.

Genotypic correlation coefficient provides a measure of the genotypic association between traits. In some cases, the genetic correlations were nearly the same as the phenotypic correlation coefficient, whereas in most cases, the differences were higher; suggesting the important role of genotype x environment interaction effects on the relationships between these traits. A large difference, especially a change in sign, indicated that genetic and environmental sources of variation affected the traits through different physiological mechanisms (Falconer, 1989). In a few cases, the r_p value was not significant and the r_g value relatively high. For example, r_p value between seed mass and plant height, grain yield and plant height were not significant, but estimates for r_g were significant and positive. Such situations suggest

Table 4: phenotypic (r_p) and genetic (r_g) correlation coefficient across environments among various pairs of characters in landrace sorghum genotypes.

Characters		PH	IL	SM	GY
	r_p	- 0.17*	-0.03	-0.57**	-0.49**
DA	r_g	(0.58**)	(-0.10)	(-0.12)	(-0.61**)
	r_p		0.23**	0.16*	-0.02
PH	r_g		(0.29**)	(0.42**)	(-0.62**)
	r_p			0.17*	0.17*
IL	r_g			(-0.21**)	(0.09)
	r_p				0.44**
SM	r_g				(-0.37**)

*, ** Correlation coefficient statistically significant at 0.05 and 0.01 probability levels, respectively. days to anthesis (DA), plant height (PH). Inflorescence length (IL), seed mass (SM), grain yield (GY)

cautious inferences concerning these associations. The r_g values should be regarded as strengthening trends. Negative genotypic correlations between characters selected for in a breeding program may result in a reduction in the rate of improvement for some of the characters in comparison to the improvement that could be obtained if correlation were positive. For example the negative correlation between grain yield and days to anthesis, could mean that selection for early flowering genotypes could increase the probabilities of having high yielding genotypes. The phenotypic correlations among grain yield and inflorescence length, grain yield and seed mass were highly significant and positive suggesting that any one of these characters would be a reliable measure of the others.

The genotypic correlation between grain yield and days to anthesis, grain yield and seed mass were smaller than the phenotypic correlations (Table 4). Suggesting a synergistic effect of landrace genotypes and environments on phenotypic relationship between grain yield and the above traits. The genotypic correlations between plant height and days to anthesis, seed mass and plant height was higher than phenotypic correlations (Table 4), suggesting antagonistic effects of genotypes and environments on the phenotypic relationship between plant height and these characters. However, this observation may also indicate that indirect selection for high yielding genotypes could be achieved by manipulating days to anthesis and plant height.

Inflorescence length was positively correlated with plant height. This suggests that genetic improvement in one trait can simultaneously bring about an improvement

in the other trait. Most of the early flowering lines were tall stature as indicated by the negative correlation between the two traits. This may be a desirable combination in some locations as tall genotypes should produce more biomasses for feedstuff and early flowering lines are likely to produce more grain as indicated by the negative correlation between number of days to anthesis and grain yield.

In general, some of the yield components were negatively correlated with other components. This suggested that no single component character could be effectively used as guiding index for making selection for yield at early stages of a breeding program. Selection index giving proper weight to traits like seed mass, plant height, inflorescence length and days to anthesis might be the best method to produce sorghum varieties with higher yields.

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