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REVIEW ARTICLE

Assessment of Genetic Variability & Adaptation to Climate Change in Advanced Gezira Population of Sorghum (*Sorghum Bicolor* (L.) Moench) Under Four Rainfed Areas in Sudan

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Abstract

The study was conducted during two seasons (2004-2005) to study genetic variability in the population (GSP-1) at four rain-fed areas in Sudan namely; Gedarif University farm in 2004, at Gedarif Research Station at northern Gedarif in 2005 at Rahad rain-fed area Gedarif marginal environment in 2004 and Kasamor at Gedarif middle environment in 2005. With the objectives to study; 1) The genetic diversity on the population 2) Heritability estimates and gains from selection. One hundred and twenty S1 families were taken at random from the population developed and improved for five cycles using S1 family selection, the design used was a modified (RCBD) Design with replication nested within blocks. Genetic variability, expected genetic gains from selection and broad sense heritability were estimated for each of the following traits; days to 50% flowering (day), yield (Kgh⁻¹), leaf angle (°), 1000 grains weight (gm) and plant height (cm).

The combined analysis over environments revealed significant differences between environments, which indicated that four environments are contrasting for evaluating the genotypes. In average over environments the genotypes have shown significant differences for all traits studied, which mean that there is a wide range for selection. However G×E interaction was not significant for yield, indicating relative ranking of the genotypes remained constant and yield was stable over the four environments.

The mean was 53.3 day for days to 50% flowering, 1448 for yield Kgh⁻¹, 28.4 ° for leaf angle, 22.9 gm for 1000 grains weight and 85.9 cm

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for plant height. The highest expected gain from selection was given by plant height (3.1 %) and the lowest value was obtained by days to 50% flowering (0.21%). The highest heritability estimate was given by plant height, days to 50% flowering and yield (0.52-0.50) and the lowest heritability value obtained by leaf angle (0.11), this indicates the fact that plant height, days to 50 % flowering and yield Kgh^{-1} traits were targeted in the previous improvement of this advanced population, whereas leaf angle trait has not been targeted yet.

Introduction

Sorghum bicolor (L.) Moench belongs to the family Poaceae, and the tribe Andropogoneae; the subtribe is Sorghastrae. The genus sorghum is characterized by a wide diversity of types. The greatest variability is found in the north-east quadrant of Africa, which includes the Sudan, Ethiopia and the neighboring countries. Most evidence points to this area as the centre of origin of the crop [1], but later Doggett with others suggested that initially, sorghum was probably domesticated in Ethiopia and Congo. Secondary centers of origin were India, Sudan and Nigeria [2-4]. Referring to the individual geographic origins and diverse spikelet and head types, Harlan and de Wet [5] differentiated between the five basic races: Dura, Khafir, guinea, bicolor, and caudatum, and the respective hybrid races. Furthermore, Highland, Temperate and Lowland Tropical Sorghum can be distinguished. These ecotypes differ in their adaptability to drought stress, low and high temperatures and the length of vegetative period, where highland sorghum was 180 to 200 days and lowland sorghum was 90 to 130 days [2,6-8].

Sorghum is among the few crops that cope with climate warming and attendant water problems, it can adapt to various conditions and is particularly resistant to limited inputs [9]. But limited knowledge is available about the effects of population buffering, and their interaction on the performance of sorghum grown under severe, unpredictable stress conditions. The present study was, therefore, designed to study: 1) The genetic diversity on advanced Gezira random mating sorghum population (G

S P-1) under rain-fed conditions of Sudan. 2) Heritability estimates and gains from selection.

Materials and Methods

Experimental material

One hundred and twenty S1 families were taken at random from an advanced random mating Gezira Sorghum Population (G S P-1) developed and improved for six cycles using S1family selection, at Rain-fed Crop Research Centre for Arid and Semi-Arid areas (RCRCASA) in the University of Gezira, Wad Medani Sudan. The experiments were conducted during two seasons (2004-2005) at four rain-fed environments namely; Gedarif University farm at northern Gedarif environment(2004), Gedarif Research Station at northern Gedarif environment(2005), Rahad Scheme rain-fed at marginal Gedarif environment(2004) and Kasamoor North east Gedarif (2005). Each family was grown in one row 5.0 m long, 0.6 m between rows and 0.2 m within row spacing. After 3 weeks from sowing, plants were thinned to 2 plants /hole. Weeds were controlled manually when necessary. No fertilizer or other inputs were added. At harvest, a 3.0 m length in the middle of each row was marked as experimental unit. All data were then based on 3.0 m of row length except days to 50% flowering, which were estimated from the entire row. Harvesting and threshing were done manually.

Experimental layout

The design used in this study was a modified randomized complete block (Replications-in-block) design; the hundred and twenty S₁

families were divided into 6 sets of 20 families each. Each block contained two replications of the same set from the population. Blocks were assigned at random, and replications were assigned at random within each block. The 20 families, representing a group from the population, were assigned at random to each replication. A modified randomized complete block (Replications-in-block) design has been used because it was more efficient than a blocks-in-replication design for controlling the experimental error and it allows loss of whole blocks only, if necessary, rather than the loss of whole or an entire replication.

Parameters studied

Days to 50% flowering (Bloom): The number of days from planting to the date when, approximately 50% of the plants in the row were at half-bloom (had their flowers open). The earliness in each variety is considered drought escaping traits.

Grain yield (kg h^{-1}): Panicles were harvested by hand from a three-meter section in the center of each row, where total panicle weight and total grains weight were measured and used to estimate grain yield and threshing percent. Weight of actual grain yield was taken to estimate total grain yield in kg h^{-1} .

Harvested area = $3.0 \times 0.6 = 1.8 \text{ m}^2$.

Estimated grain yield (kg h^{-1}) = Yield from harvested area $\times 10000$

1.8×1000

Leaf angle ($^\circ$): The mean of the angle between the stem and leaf midrib was measured for the second and third leaf, the smaller leaf angle means the leaf is erect, narrower leaf area exposed to the sunshine and thereby low Evapo-Transpiration (ET^0) or drought tolerant trait.

1000-Grains weight(g): It is weight in grams of 1000 seeds taken at random from each family.

Plant height (cm): The average of heights, taken at random from each family was measured from the soil surface base of the plant to the tip of the panicle for representative plants in each plot.

Statistical Approach

The least squares method was used in genetic variability analyses, utilizing the Statistical Analysis System (SAS) as outlined by Jane T. Helwig and Kathryn A. Council (1997 [10]) as in the following;

Analysis of variance of data from for each trait in each environment

Data collected from each environment for each trait were analyzed separately. The linear additive model underlying the analysis of variance was as follows:

$$Y_{ijk} = u + b_i + r_{ij} + f_{ik} + e_{ijk}$$

where:

Y_{ijk} : The observation on the k^{th} family

At the j^{th} replication within the i^{th} block.

u : The grand mean of all families.

b_i : The random effect associated with the i^{th} block; $i = 1, 2, \dots, 6$.

r_{ij} : The random effect associated with the j^{th} replication within

the i^{th} block; $j = 1, 2$.

f_{ik} : The random effect associated with the k^{th} family within the i^{th}

block; $k = 1, 2, \dots, 120$.

e_{ijk} : The random error effect associated with the Y_{ijk} observation.

Since the design had nested features, the effects of the parameters in the model were computed as deviations about the next mean

up in the hierarchy, *i.e.*, the block effect was computed as the deviation of the individual block from the grand mean, replication effect as the deviation of the replicate value from the block mean in which the replicate was located, and the family effect was calculated as the deviation of the observed family value from the block mean in which it is nested.

Genetic differences among families nested with blocks were tested by the null hypothesis:
 $H_0 : \sigma^2_{f/b} = 0$

The appropriate F-test was used: $F = (M_{f/b}) / M_e$

with $b(f-1), b(r-1) (f-1)$ degrees of freedom.

Variance components

The genotypic and phenotypic variance components were estimated by equating the observed mean square values to their expectations. Accordingly;

1/The genotypic variance was estimated as follows:

$$\sigma^2_{f/b} = (M_{f/b} - M_e) / r, \text{ and}$$

2/The phenotypic variance of the family means was estimated as:

$$\sigma^2_p = (M_{f/b}) / r$$

The standard errors (SE) associated with these estimates were computed using Anderson and Bancroft (1952) method as:

$$(1/r^2) [2M^2_{f/b} + 2M^2_e]^{1/2}$$

$$SE (\sigma^2_{f/b}) = \pm b(f-1) + 2 b(f-1) (r-1) + 2$$

and

$$SE (\sigma^2_p) = \pm (1/r^2) [2M^2_{f/s}]^{1/2}$$

$$b(f-1) + 2$$

3/ Heritability of each trait was computed as:

$$h^2 = \sigma^2_{f/b} / \sigma^2_p$$

The SE associated with h^2 was computed as:

$$SE_{h^2} = \pm (SE \sigma^2_{f/b}) / \sigma^2_p$$

Coefficient of variation

The Coefficient of Variation (C.V.) was calculated as follows:

$$C.V = (M_e^{1/2} / \text{mean}) \times 100.$$

Phenotypic Coefficient of Variation (P.C.V.):
 The Phenotypic Coefficient of Variation (P.C.V.) of each trait was calculated as follows:

$$P.C.V. = \sqrt{\sigma^2_p / \text{mean}} \times 100$$

Genotypic Coefficient of Variation (G.C.V.):
 The Genotypic Coefficient of Variation (G.C.V.) of each trait was calculated as follows:

$$G.C.V. = \sqrt{\sigma^2_{f/b} / \text{mean}} \times 100$$

Predicted response to selection: While recognizing the biases associated with genotypic and phenotypic variances, an estimate of the predicted response to selection was computed as follows:

$$Gs = (k\sigma^2_{f/b}) \sigma^-_p$$

Where: Gs : The predicted gain from selection.

K : The standardized selection differential which has the value of

1.755 at 10 % selection intensity.

$\sigma^2_{f/b}$: The estimated genotypic variance of the trait considered.

σ^-_p : The estimated phenotypic standard deviation of a family mean for the trait under consideration.

Analysis of variance of data for each trait combined over different environments

A combined analysis for each trait in each environment was performed. The additive linear model assumed was:

$$Y_{ijkl} = u + L_i + b_j + Lb_{ij} + r_{ijk} + f_{il} + Lf_{ijl} + e_{ijkl}$$

where:

Y_{ijkl} : The observation on the l^{th} family at the k^{th} replication within

the i^{th} block in the i^{th} location(environment).

U : The overall mean of all families.

L_i : The random effect associated with the i^{th} environment; $I = 1,$

$2, \dots, 4.$

b_j : The random effect associated with the j^{th} block; $I = 1, 2, \dots, 6.$

Lb_{ij} : The random effect of the interaction between the

i^{th} environment and j^{th} block.

r_{ijk} : The random effect of the k^{th} replication within the j^{th} block in

the i^{th} environment.

f_{il} : The random effect associated with the l^{th} family in the

j^{th} block.

Lf_{ijl} : The random effect resulting from the interaction of the

l^{th} family in j^{th} block with the i^{th} environment.

e_{ijkl} : The random error effect associated with the plot containing

the l^{th} family in the k^{th} replication within the j^{th} block in the

i^{th} environment.

As mentioned, the various effects in the model were computed as deviations about the mean within which they were nested, so that the sum of the deviations about the mean adds to zero. The form of the analysis of variance pertinent to the assumed model is given in table 1.

The Coefficient of Variation (CV) was calculated as: $C.V = (M_e^{1/2})/\text{overall mean} \times 100.$

Genetic differences

Genetic differences among families in blocks over environments

were determined using the F-test as:

$F = M_{f/b}/M_{sf/b}$ with $b(f-1)$ $b(e-1)$ $(f-1)$ degrees of freedom.

Where: s is for site (environment).

The interaction between the families and environments

It was computed using the F-test as:

$F = M_{sf/b}/M_e$ with $b(s-1)$ $(f-1)$, $s b(f-1)$ $(r-1)$ degrees of freedom.

Where: s is for site (environment).

The various parameters and their SE's for the combined environments data from each of the populations were estimated as follows:

Genetic variance

$\sigma_{ef/b}^2 = (M_{f/b} - M_{sf/b})/rs$ and its SE as:

$$[(1/r^2 s^2) (2M_{f/b}^2 + 2M_{sf/b}^2)]^{1/2}$$

$$SE(\sigma_{ef/b}^2) = (b(f-1) + 2)b(f-1)(r-1) + 2)$$

Phenotypic variance

$\sigma_p^2 = (M_{f/b})r s$, and its SE,

$$[(1) (2M_{f/b}^2)]^{1/2}$$

$$SE(\sigma_p^2) = (r^2 s^2) (b(f-1) + 2)$$

Génotype x environment interactions variance

$\sigma_{sf/b}^2 = (M_{sf/b} - M_e)/r$, and its SE,

$$SE(\sigma_{sf/b}^2) = [(1) (2M_{sf/b}^2 + 2M_e^2)]^{1/2}$$

$$r^2 b(f-1) (s-1) + 2 s b(f-1) (r-1) + 2$$

Table1: Mean squares for the combined analysis of variance for five traits in 120 families sorghum population evaluated at four low input areas in Sudan.

Sources of Variation	Symbol df	df	Days to flowering	Yield Kgh ⁻¹	leaf angle (°)	1000 grains Weight(gm)	Plant height (cm)
Environ.(E)	e-1	3	44951***	149372712***	4644***	535***	3077***
Block(B)	b -1	5	60.7***	1270447***	27.8 N.s	16.5*	4127***
EXB	(e-1) (b-1)	15	22.2***	3180420***	76.4***	13.7**	296.5**
Replic./B	e b	24	16.9***	506770***	84.4***	11.9**	837.1***
Families (F)/B	b(f-1)	114	11.7***	51671***	35.7***	11.67***	343.3***
G(EXB)	b(f-1)(e-1)	342	5.7 *	25837 n.s	31.9***	7.95*	164.2**
Residual	(r-1)(f-1)be	456	4.83	23595	21.57	6.52	131.6

*, **, *** are the levels of significance 0.05, 0.01, and 0.001 respectively.

Broad-sense heritability

The estimation of narrow-sense heritability (h^2), its SE, the Coefficient of Variation (C.V), and the predicted gain from selection for each trait in the population were computed in the same manner as those in the individual environment estimates.

Results and Discussion

Genotypic and phenotypic variability in the population

Genetic variability in a population is essential to secure the success of any breeding program. Selection is not effective unless a considerable genetic variation is present in the population. Evidence for the existence of considerable amount of variability in sorghum had been reported by many investigators, only 3% of 40000 accessions is utilized, while as largely as 97% is unexploited.

Analysis of variance

Analysis of variances for the four environments in Gedarif explained that, there was significant genetic variation among genotypes for all traits studied. For example, (Tables 2,3) Days to 50% flowering ranged from 29-71 days with an average of 53.3 days. This indicates that the population is suitable for selection of early maturing genotypes, thereby

suitable for growing under the short rain season prevailing in Gedarif, the main sector for sorghum production in the country. Plant height range was 49-169 cm with an average of 85.9 cm. This explained the possibility of selecting for dwarf genotypes which facilitates the mechanical harvesting and resists lodging, therefore reduces cost and effort of manual harvesting. Leaf angle range is between 10° and 90° with average of 28.4°. This furnishes the opportunity to select for an erect plant that reduces water loss in drought prone areas. As regards 1000 grains weight, the obtained range was 14.3-34.8 gm with an average equal 22.9 gm. This may be attributed to the fact that the population is improved for earliness, therefore short grain filling period occurred. Considering the yield scored, the range was from 983 to 3490 kgh⁻¹ with an average of 1448 kgh⁻¹. This indicates the chance of high yielding early maturing and dwarf genotypes in northern Gedarif. The coefficients of variation were reasonable and acceptable for rain-fed areas; all C.V values were in the range of 4.1% in bloom to 16.4 % in leaf angle. This emphasized the precision of the measurements. In population breeding families are usually produced and evaluated as varieties or parents of hybrids. For quantitative traits genetic variability among families of different generations of selfing is a function of the mode of gene action of trait in question, the proportion of non-additive variance with respect to additivity

Table 2: Estimates of genotypic(σ^2_{fb}), Phenotypic(σ^2_p) variance components, and G×E interaction their Standard Errors (SE) and coefficient of variation for five traits combined over four environments at low input areas in Sudan.

Source of variation	Day to50% flowering	Yield Kgh ⁻¹	Leaf angle (°)	1000 grains weight(gm)	Plant Height (cm)
Families (F)/B	11.7 ***	51671***	35.7 ***	11.67***	343.3***
G(EXB)	5.7 *	25837 N.s	31.9 ***	7.95*	164.2 **
Residual	4.83	23595	21.57	6.52	131.6
σ^2_{fb}	0.75	3229.3	0.475	0.465	22.4
σ^2_{fb} SE±	0.237	883	0.66	0.206	5.85
σ^2 G×E	0.44	1121	5.2	0.715	16.3
G×E SE ±	0.135	628	0.705	0.186	3.8
σ^2_p	1.46	6458.9	4.46	1.46	42.91
σ^2_p SE±	0.192	848.10	0.586	0.192	5.6

*, **, *** are the levels of significance 0.05, 0.01 and 0.001 respectively.

Table3: Range, grand mean, standard error, standard deviation from the mean and coefficient of variation for five traits in 120 families sorghum population combined over four environments at low input areas in Sudan.

Parameters	Days to lowering	Yield Kgh ⁻¹	leaf angle(°)	1000 grains weight(gm)	Plant height (cm)
Range	29-71	983-3490	10-90	14.3-34.8	47-169
GM	53.3	1448	28.4	22.9	85.9
C.V.(%)	2.19	153.6	4.64	2.55	11.5
SE±	4.1	10.6	16.4	11.1	13.4
R2	0.981	0.98	0.77	0.68	0.71
Std dev	12.14	750.3	6.62	3.097	14.8

of a selected trait and the proportion of epistasis regarding additive variance as mentioned by Goldringer IPB, et al. [11].

The selection of important traits like grain yield, earliness and dwarfness, has to be optimized according to the relative importance of the variance components, the type of the crop pollination and the type of variety that a breeder is selected for (Model of plant that the breeder looking for or requested ideo type). The estimates of genotypic and phenotypic variance components and their standard errors were summarized in table 2. Genotypic variances in days to 50% flowering, yield, leaf angle, 1000 grains weight and plant height were 0.75, 3229.3, 0.475, 0.465 and 22.4 respectively, while their corresponding standard errors were 0.214, 984.2, 0.786, 0.232 and 6.24. Their genotypic coefficients of variation were 1.63, 3.92, 2.43, 2.98 and 5.5 respectively. On the other hand, phenotypic variance components in days to 50% flowering, yield, leaf angle, 1000 grains

weight and plant height were 1.46, 6458.9, 4.46, 1.46 and 42.91. Whereas, theirs corresponding standard errors were 0.192, 848.1, 0.586, 0.192 and 0.704, while their corresponding phenotypic coefficients of variation were 2.27, 5.55, 7.44, 5.28 and 7.63 respectively. The G×E variance components in days to 50% flowering, yield, leaf angle, 1000 grains weight and plant height were 0.44, 1121, 5.2, 0.715 and 16.3 respectively. Whereas, theirs corresponding standard errors were 0.192, 848.1, 0.586, 0.192 and 0.704 sequentially.

Combined analysis of variances explained that; 1) Significant differences among families for all traits studied ($p = 0.01$), but the G×E interaction was not significant for yield differences, while they were significant for leaf angle, days to 50% flowering, 1000 grains weight and plants height (Table 1). This means that the population is stable for yield or can be treated as adapted for specific zones such as Gedarif and similar environments, the population families interact

differently. But each family kept on its ranked order in the population across the different environments. Also Leaf angle, days to 50% flowering and leaf number were significantly different in environments x families interaction which means that the genotypes were not yet stable in their performance for those traits.

2) The difference between sites (Environments) was highly significant ($p < 0.01$), which means that the four sites represent contrasting environments to examine the performance of the genotypes.

3) There were significant differences among these genotypes, where all of the characters revealed high phenotypic and genotypic variability. Characters that showed wide range of variability also had high phenotypic and genotypic coefficients of variation. This suggests that there might be a direct relationship between wide range of variability and high phenotypic and genotypic coefficient of variation. These findings were in agreement with that reported by Osman HEL, et al. [12].

4) In the present study, the 120 families of sorghum population exhibited significant differences in all characters studied under different environments. Such variations can be attributed to genetic as well as to environmental factors. Similar conclusions were detected by many workers in different cereal crops under different environments [13-19]. But days to flowering, yield, leaf angle, 1000-grain weight and plant height estimates of environmental variances were higher than their respective genotypic ones at the four locations. This indicates that a large proportion of the phenotypic variance could be attributed to the environmental causes.

5) Different patterns of interaction between Genotype and Environments (GxE) were detected. The significant differences in GxE

of the studied characters (Except yield), indicates the importance of these components in affecting the phenotypic performance of the evaluated sorghum genotypes. On the other hand, the non-significant GxE interactions, for yield trait, indicate that the increments of responses of the genotypes to the changes of environment were similar. Thus, these components had not contributed to the phenotypic variances of the different genotypes. These findings are in agreement with those reported by many breeders [20-22].

6) In general, the studied characters had lower genotypic variances than their respective environmental ones, indicating that most differences among the genotypes under study were due mainly to the environmental factors as well as the interactions of these genotypes with the environment. The grand means of all characters showed differences within and between the four locations. The change in means of these characters was due to the interactions of genotype with the environment. Also this indicates that the differences among the sorghum genotypes for these traits can be due to genetic causes as well as their interactions with the environment. These findings are in agreement with those reported by Parasad SG, et al. [23], AbrahamMJ, et al. [24] in finger millet, Fadlalla HA, et al. [15] in maize.

7) Comparing the estimates of genotype x environment interaction component of the different characters (Table 4), yield (1121) gave the highest interactions followed by plant height (16.3) and leaf angle (5.2). Weight of 1000 grains (0.715) and number of days to 50% flowering (0.44). Yield genotype environment interaction were non-significant, while the remainder traits showed significant interactions. This shows that different characters react in different

Table 4: Estimates of genotypic (GCV%) and Phenotypic (PCV%) coefficient of variation, heritability (h^2), standard errors and expected gains from selection (Gs) at 10% selection intensity for five traits combined over four environments at low input areas in Sudan.

Source of variation	Days to 50% flowering	Yield Kgh ⁻¹	Leaf angle (°)	1000 grains eight(gm)	Plant height (cm)
GCV %	1.63	3.92	2.43	2.98	5.5
PCV %	2.27	5.55	7.44	5.28	7.63
H ²	0.514	0.50	0.107	0.318	0.522
Sd dev	12.14	750.3	6.62	3.097	14.8
Gs= $k\delta^2fb/\delta p = K=1.755$	0.11	7.6	0.13	0.26	2.66

patterns with the different environments, also it shows that yield was the least affected characteristic by genotype-environment interactions, while number of days to 50% flowering was the most affected one.

8) All traits have not reached stability at the same time, while yield reached the stability where its GE1 was not significant, all of the other traits have not reached stability where, they showed different levels of significance, plant height was significant ($p = 0.01$), leaf angle was significant at (0.001), 1000 grains weight and days to 50% flowering were significant at (0.05). This can be attributed to that yield stability in such environment is dependent on drought traits, which affect each other. The flexibility of drought traits is the main factor that leads to yield stability. For example, plant adjusts its angle and flowering according to environment, thereby it gains sustainable average yield across different environments (Tables 1-3).

Conclusion

The breeding method followed in generating the current populations (Recurrent selection) presenting cyclic improvement of population, has led to concentration of favorable alleles that increased the probability of extracting elite lines for variety development or parents for hybrids.

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