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STUDIES ON GENETIC VARIABILTY IN SOME SWEET SORGHUM (Sorghum bicolor L Moench) GENOTYPES

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Studies were carried out to estimate the extent of genetic variability in some cultivated genotypes of sweet sorghum (sorghum bicolor L Moench). Thirty genotypes were evaluated in 2011 rainy season across two locations, to obtain more information on their genetic and morphological diversity. Significant mean squares were obtained for 10 traits in the individual analysis and also for the combined analysis across locations, suggesting that this sweet sorghum population was highly variable for some of the characters and as such will respond to selection. Mean performances for the combined analysis identified ICSV 93046, (SW DAURA 06-5-2 &ICSV700), SPV 422, ICSV700, (SW DAURA 06-5-2 & 38A x NR71182), SW DAURA 06-5-2, (SW DAURA 06-5-4 & E36-1), 38A*NR71182, and (SW KEBBI 07-5 & SPV 422) as the best genotypes in terms of days to 50% flowering, plant height, stem thickness, number of nodes, number of leaves, panicle weight, 1000 grain weight, grain yield and sugar content.

Key words: Variance, heritability, sweet sorghum

INTRODUCTION

Sweet sorghum (*Sorghum bicolor* (L) Moench) is the same species as grain sorghum, grass sorghum and broom sorghum (Doggett, 1970). Sorghum grain is the fifth most important cereal in the world after wheat, rice, maize and barley. In Africa it comes second after maize in terms of production (FAO, 2011). According to FAO (2011) estimates, the average world production of sorghum amounted to 66 million tonnes. Also according to Agricultural performance Survey of 2011 Wet Season in Nigeria, Sorghum production decline slightly from 7.02 to 6.89 million tons because the land area under cultivation decreased slightly from 5.04 million hectares to 4.89 million hectares. There is a need to improve overall income from sorghum through improving productivity or increasing value by locating and exploiting alternative uses. Sweet sorghum is similar to commonly grown grain sorghum with an increased potential to accumulate sugars in the stalk. The global energy demand and volatile prices of fossil fuels has forced nations to search for new alternative energy sources. Sweet sorghum, with its short growing period (four months), low water requirement, high biomass and alcohol production potential and greater income potential from cultivation, is thus a preferred raw material for generating energy. In addition to its sweet-stalk, it has a grain yield of about 2.0 to 6.0 t ha^{-1} (which can be used as food or feed) when harvested. Progress in plant breeding, depends on the extent of genetic variability present in the population. Therefore the first step in any breeding program is the study of the genetic variability present This cannot easily directly measured as the phenotypic expression reflects non-genetic as well as genetic influences. The genetic basis must be inferred from the phenotypic observations which are the results of interactions of genotype and environment.

MATERIALS AND METHODS

Thirty genotypes were used for this study: seven of these

Table 1. Description of the Sweet sorghum varieties and the hybrids

GENOTYPES/ VARIETIES	SOURCE	DESCRIPTION
SPV 422	ICRISAT	High stalk yield, high grain yield and high sugar content.
ICSV 700	ICRISAT	Low stalk production
NTJ-2	ICRISAT	Lowest stalk yield, high yielding in post rainy season. Resistant to leaf diseases.
E 36-1	ICRISAT	High stalk sugar
ICSR 903034	ICRISAT	High yielding post rainy season, high sugar content and late maturing.
64 DTN	ICRISAT	High stalk sugar
ICSV 93046	ICRISAT	Moderate sugar content, tolerant to shoot fly, stem borer and leaf diseases.
ICSV 24001 X Samsorg 38	Hybrid	
ICSA 344 X Samsorg 38	Hybrid	
ICSA 24001 X Samsorg 41	Hybrid	
ICSA 344 X Samsorg 41	Hybrid	
ICSA 344 X Samsorg 39	Hybrid	
ICSA 24001 X E 36-1	Hybrid	
ICSA 24001 X NTJ-2	Hybrid	
38A X Samsorg 39	Hybrid	
38A X Samsorg 38	Hybrid	

were obtained from India, eleven locally collected across Nigeria, nine genotypes resulted from crosses done and three non-sweet varieties were included from the Institute for Agricultural Research (IAR), Samaru, Zaria.

The genotypes/varieties were planted during the 2011 rainy seasons at two locations for evaluation in replicated trials. The Research Farm of the Institute for Agricultural Research (IAR), Ahmadu Bello University (ABU) Samaru Zaria (11 011'N, 07 0 38'E, 686 m above sea level) in the northern Guinea Savanna ecological zone of Nigeria; and the Irrigation Research Station, Kadawa of IAR/ABU (11 0 39', 080 027' E and 500 m above sea level), in the Sudan Savanna ecological zone of Nigeria.

At each location, the 30 genotypes/varieties were grown in a randomized complete block design with three replications. Each of the 30 plots consisted of 4 ridges each of which measured 5m long and were spaced 0.75m apart with 0.25m within row spacing. Proper local agronomic practices for sorghum were carried out. The two inner rows were used for data collections and observation for each plot. The data collected include:

Days to 50% flowering: - the number of days from sowing to the time when 50% of the Plants flowered.
Number of leaves: - was taken by counting the number of leaves from the base to the flag leaf of 6 plants taken from the two central rows and taking the average.
Plant height: -was measured in cm using meter rule from the base of the plant to the top of the panicle.
Stem thickness: - the diameter of the stem of six ramdomly selected plants per plot and the mean taken. It was measured in cm using vanier caliper.
Number of nodes: -number of nodes on the plant from base to top taking 6 plants from the two central rows by counting the nodes.
Panicle length: - the length from the base of the panicle to the tip measured in cm using a meter rule.
Panicle weight: - weight of the total number of heads harvested from the two central rows in grams using measuring scale.
Grain yield/plot: - after threshing and adequate drying, record the grain weight per plot to the nearest grams from the two central rows.
1000g grain weight: - the weight of 1000gram grains after threshing.
Percentage sugar content: - some parts of the stem were taken within each plot and analyzed at the Product Development Programme Unit Laboratory of IAR.
The genotypes used for this study are listed in Table 1 and 2.

The data obtained were subjected to analysis of variance for each location based on plot means followed by combined analysis of data across the two locations; these were done according to methods described by Singh and Chaudhary (1985). Mean separation was carried out according to Duncans multiple range test (DMRT) described by Duncans (1955). Also components of variance (σ^2p, σ^2e, σ^2g) were used for the estimation of coefficients of variation (PCV, GCV) as described by Singh and Chaudhary (1985)

RESULTS AND DISCUSSIONS

The significant mean values obtained from the analysis of variance for the individual location suggests that differences existed the sorghum genotypes/ varieties for most traits, indicating that they are highly variable (Table

Table 2. Sweet sorghum germplasm collected from five northern states of Nigeria.

s/n	Institute assigned name	Place of collection	State
1	SW daura 06-2	Daura	Katsina
2	SW daura 06-5-1	Daura	Katsina
3	SW daura 06-5-2	Daura	Katsina
4	SW daura 06-5-4	Daura	Katsina
5	SW samaru 06-4	Samaru	Kaduna
6	SW makarfi 06-3	Makarfi	Kaduna
7	SW kebbi 07-1	unguwar lawal	Kebbi
8	SW dansadau 07-2	Dansadau	Kebbi
9	SW bodinga 07-3	Bodinga	Sokoto
10	SW bungudu 07-1	Bungudu	Zamfara
11	SW bungudu 07-6	Bungudu	zamfara

Non sweet sorghum varieties.
Samsorg 41 (ICSV111)
Samsorg 39 (NR71182)
Samsorg 38 (NR71172)

Table 3. Mean square values for the ten traits measured at Samaru and Kadawa of 30 different sorghum genotypes in 2011.

SOURCE OF VARIATION	DF	DTF	PLHT	ST	NN	NL	HDWT	PL	TGWT	GYLD	PSS
Rep	2	14.27	76.42	0.07	0.01	0.04	0.0007	0.72	2.42	0	0.14
Location	1	96.8*	58056.42**	8.49**	68.45**	72.20**	113.21**	0.78	1496.75**	52.08**	68.76**
Rep(Location)	2	12.35	53.19	0.36	0.05	0.05	0.0003	0.86	0.06	0.002	0.09
Genotype	29	319.99**	12331.95**	3.69**	17.58**	18.82**	1.54**	232.09**	40.81**	0.74**	28.39**
Genotype*Location	29	95.25**	884.0**	0.49**	1.54**	1.41**	0.63**	2.58**	21.44**	0.34**	1.38**
Error	116	8.27	131.48	0.13	0.07	0.07	0.01	0.92	2.55	0.005	0.05

DF= degrees of freedom, DTF= Days to 50% flowering, PLHT=plant height, ST=stem thickness, NN=no of nodes, NL=no of leaves, HDWT=head weight, PL=panicle length, TGWT=1000 grain weight, GYLD=grain yield, PSS=% stem sugar, ** significant at 1%, * significant at 5 %

3). The significant mean square values obtained for the location (Table 4), for some of the traits indicated that the conditions in the two locations were not similar in many ways and that is why the genotypes/ varieties did not perform in the same way in the locations. The significant effects of genotype × location interaction mean squares that were observed (Table 5) in most traits also suggest that the environmental conditions in the two locations influenced the performance of the genotypes, thus suggesting the need to test genotypes over different locations across years to ascertain their stability for use as reliable genetic materials for crop improvement practices. To minimize error and consequently increase the

Table 4. Mean square values for the ten traits measured across the two locations and 30 sorghum genotypes in 2011.

SOURCE OF VARIATION	DF	DTF	PLHT	ST	NN	NL	HDWT	PL	TGWT	GYLD	PSS
Rep	2	14.27	76.42	0.07	0.01	0.04	0.0007	0.72	2.42	0	0.14
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Table 5. Mean performance for 30 genotypes of the 10 traits across the two locations in 2011.

GENOTYPE	**DTF**	**PLHT**	**ST**	**NN**	**NL**	**HDWT**	**PL**	**TGWT**	**GYLD**	**PSS**
sw bungudu 07-1	69jk	200de	6d	7g	9i	4.33abcd	17.46jk	23.27hij	0.94kl	7.14abcd
sw daura 06-5 2	82bc	304a	6d	10c	11.5c	7.35a	32.23a	24.86efgh	0.9l	6.9abcd
sw samaru 06-4	80cd	187ef	6d	9d	11d	5.35abcd	18.63ijk	21.59jk	1.54bc	7.33abc
sw daura 06-5-1	69n	158hi	5e	5m	6m	4.96abcd	19.51hij	26.01efgh	1.0jk	5.76k
sw daura 06-2	67kl	161hi	5e	7g	9i	6.03abcd	24.74bcdefg	24.99efgh	1.05j	6.68hij
sw kebbi 07-5	65lm	209d	5e	6k	8k	4.22abcd	17.14jk	22.05ijk	0.94kl	7.52a
sw daura 06-5-4	67kl	210d	5e	6l	9i	6.15bcd	25.04bcdefg	29.81a	0.62o	7.53a
sw dansadau 07-2	79cdef	182fg	6d	8e	9i	3.79bcd	11.37l	26.01defg	1.0jk	7.14bcde
sw bodinga 07-3	60n	255b	6d	11b	13b	6.13abcd	26.64bcdef	26.01defg	0.95kl	6.84fghi
sw makarfi 06-3	73hij	162hi	6d	8e	10f	3.63cd	10.8l	28.02abc	1.26gh	7.37ab
sw bungudu 07-6	81bc	238c	6d	9d	11d	5.49abcd	24.92bcdefg	26.01cdef	0.51p	7.37ab
spv 422	73hi	236c	8a	11b	13b	6.46abcd	26.04bcdef	28.23ab	1.04j	7.49a
ntj 2	67kl	158hi	7bc	9d	11d	5.5abcd	19.95hij	26.33bcde	1.2hi	7.36ab
e 36-1	79cdef	162hi	6d	8f	10f	5.94abcd	23.55efgh	29.24a	1.58bc	7.26abcd
icsr 93034	69jk	206d	7bc	9.d	11d	6.19abcd	23efgh	28.09abc	1.6b	6.5j
64 dtn	62mn	169gh	7bc	9d	11d	5.18abcd	19.52hij	28.28ab	1.17i	5.96k
icsv 93046	91a	265b	7bc	11b	13b	3.72cd	15.65k	28.04abc	0.71n	7.26abcd
icsv 700	84b	304a	6d	13a	15a	3.13d	10.86l	21.97ijk	0.6o	6.92efgh
1csa24001*nr71176	73hij	173gh	7bc	9d	11d	6.76abc	27.42bc	24.61efgh	0.79m	7.26abcd
icsa 344*nr71176	75fgh	206d	6d	8f	10f	6.98abc	26.21bcde	24.14efgh	1.31fg	7.02defg
icsa 24001*icsv111	80cde	164hi	8ab	9d	11d	6.67abc	24.06cdefg	23.82fghi	1.5cd	6.69hij
icsa 344*icsv111	77defg	137k	6d	8e	10f	5.39abcd	22.47fgh	20.94k	0.95kl	7.28abcd

Table 5. Continues

icsa344*nr71182	71ij	132k	6d	7g	9i	6.06abcd	21.68ghi	21.32jk	1.43de	7.03cdefg
icsa24001*E36-1	81bc	205d	6d	9d	11d	5.82abcd	23.57defg	21.37jk	1.25gh	6.62ij
icsa24001*ntj-2	76efgh	196def	7bc	8f	10f	5.88abcd	26.96bcd	26.02defg	0.89l	6.94efgh
38A*nr71176	74ghi	229c	6d	8f	10f	7.3ab	26.06bcd	26.15bcde	1.91a	7.07bcdef
38A*nr71182	75fgh	152ij	7bc	8f	10f	7.51a	28.33b	21.23jk	1.85a	6.75ghij
icsv111(samsorg 41)	77defgh	162hi	6d	7g	9i	6.35abcd	23.81cdefg	26.02cde	1.44de	0
nr71182(samsorg 39)	76efgh	139jk	7bc	9d	11d	5.9abcd	23.93cdefg	23.77ghi	1.008jk	0
nr71176(samsorg 38)	72ij	197de	7bc	7g	10f	6.2abcd	24.45cdefg	27.72abcd	1.38ef	0

DTF= Days to 50% flowering, PLHT=plant height, ST=stem thickness, NN=no of nodes, NL=no of leaves, HDWT=head weight, PL=panicle length, TGWT=1000 grain weight, GYLD=grain yield, PSS=% stem sugar, ** significant at 1%, * significant at 5 %. Means with the same letter are not significantly different

precision and reliability of estimates Allard and Bradshaw (1964) suggested increasing the sample size and number of locations or years during the trials. However, the disadvantage of this suggestion would be increased costs and delayed release of results, see Table 3, 4, 5 and 6.

Comparative performance of the 30 genotypes across the two locations for the 10 traits studied (Table 5) provides a clear indication of the superiority of some of the genotypes over others. All “sweet sorghum” genotypes were sweet with sugar concentrations ranging from 6-7.5% sugar. Good breeding potential therefore exists for genotypes such as ICSR 93034, E 36-1, samaru 06-4 and crosses/hybrids between ICSA24001 × ICSV111, 38A × NR71182, 38A × NR71176 as these performed very well for both yield and yield components across the two locations. Depending on the breeding objective, there was a wide range of genotypes to choose from. For instance if the breeding objective is to produce high yield and early maturing sweet sorghum varieties, then hybridization between ICSV 93046 × SAMARU 06-4 or ICSV93046 × E 36-1 or ICSV 700 × SAMARU 06-4 or DANSADAU 07-2 × SAMARU 06-4 which are early maturing and high yielding genotypes respectively could be promising.

Table 6. Shows estimates of variance components obtained from the analysis of variance. The estimates of the phenotypic, genotypic, environmental variances with their standard errors are given. All of the ten traits studied showed positive genotypic variance. Genotypic variances had relatively higher estimates compared to environmental variance estimates. For all but head weight (1.5%) and 1000 grain weight (56%) genotypic variance was > 75% of phenotypic variance.

Phenotypic and error variances estimates were all positive for all traits and they had very low standard errors. Plant height, head weight, 50% days to flowering, panicle length and thousand grain weights had large estimates of phenotypic, genotypic, and error variances. The variance components showed that most of the characters had higher phenotypic and genotypic variance estimates than the environmental variance estimates.

The variance components for the two locations showed that most of the traits had high phenotypic and genotypic variance estimates (Table 6). Therefore expressions for most of the characters were genetic, which indicates advances can be achieved in breeding programs. This finding is in agreement with the findings of Bello D. *et al*. (2007), Basu (1981), and Abu-Gasim and Kambal (1985) for several quantitative traits in sorghum genotypes. Zaveri *et al*. (1989) also reported similar results in pearl millet. Bello *et al*. (2007) and Lukhele (1981) observed that higher error or environmental variance estimate for some traits similar to what was obtained in this study could also be attributed to sample size.

CONCLUSION

The success of any breeding program depends upon the genetic variation in the materials at hand. The greater the genetic variability, the higher would be the heritability. Hence the better the chances of success to be achieved through selection. Ten traits involving the leaves, stem, seed and other agronomic parameters were used

Table 6. Estimate of phenotypic (σ^2p), genotypic (σ^2g) and environmental variance for the 10 traits over the 2 locations (Samaru and Kadawa) in 2011.

Traits	σ^2_{ph}	σ^2_g	σ^2_e
50% DTF	45.4172	37.4567	7.9605
plant height	2149.78	1907.99	241.78
stem thickness	0.69	0.5332	0.1568
no of nodes	2.748	2.673	0.075
no of leaves	2.9119	2.8433	0.0686
head weight	6.0791	0.0883	5.9908
panicle length(cm)	31.4402	24.4783	6.9619
1000 grain weight	5.7801	3.2283	2.5518
Grain yield	0.0713	0.0667	0.0046
sugar content	4.2442	3.95	0.2942

for this study. There was considerable variability present in the materials used. As such these results will be useful for choosing populations to be used in developing new breeding strategies to improve sweet sorghum productivity. The variations could be effectively manipulated with appropriate breeding methods to develop improved varieties, synthetics and hybrids for use by farmers and industries.

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