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Assessment of genetic parameters and yield trait stability in sweet sorghum genotypes through AMMI and GGE biplot approaches

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ABSTRACT

Biofuel from sweet sorghum is an alternative and viable source of renewable energy. This study was conducted to determine the interaction between genotype and environment on yield traits, assess stability and identify the most suitable sweet sorghum genotypes for biofuel production. Genotypes comprised of 80 sorghums (*Sorghum bicolor* (L.) Moench) genotypes (63 sweet sorghum genotypes, 12 improved grain sorghum and 5 sweet sorghum landraces) grown in four environments in the Sudano–Sahelian region of Nigeria. The combined analysis of variance of the sweet sorghum genotypes in two years (2018 and 2019) over the two environments revealed that year(Y), genotype(G), environment(E) and genotype by environment interaction (G × E) were significant in the entire biofuel yield attributes except the Brix at maturity and bagasse. AMMI analysis of variance effects of G, E, and G × E. These significant effects of G, E, and G × E were used to identify the best-performing, most adaptable and most stable genotypes. Genotype contributed 77.2% of the total sum of squares for Brix, followed by environment (1.37%) and interaction (0.47%). For grain yield, environmental effects accounted for 89.5% of the total sum of squares, whilst genotype and interaction accounted for 3.6% and 1.1% respectively. Genotypic variances for stalk fresh yield are 5.5% and those for environment and interaction are 88.3% and 0.8%, respectively. The total sum of squares of the environment for juice volume is 39.5%, with genotype contributing 32.4%, and the interaction contributing 4.2%. Environment and interaction contribute to bagasse are 82.6% and 1.4% respectively, and that of genotypes is 7.1%. This suggests a better chance of progress in the genetic improvement of these traits. The genotype SEREDO, SPV 422-NB, IESV 92008 DL, ICSB 324 and F7.5SSM09-5-3/3-2-2-2 combined high yields with stability in grain, juice, stover, bagasse and Brix, respectively, according to the stability index ranking across environments. On the other hand, genotypes SERENA-ML and Gwaram, though high-yielding, were unstable according to AMMI stability value scores.

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INTRODUCTION

Sweet sorghum (*Sorghum bicolor* (L.) is an opportunity crop for smallholder farmers. The plant resembles grain sorghum, except that it exhibits rapid growth and accumulates a substantial amount of sugary juice in the stalk. It is a multipurpose crop grown for food, feed and fuel (Regassa and Wortmann, 2014). It has great potential for ethanol production. As a drought-tolerant crop, it remains the most desirable alternative to other cereals. Sweet sorghum accumulates a large amount of fermentable sugars in the stem, and the ethanol from sweet sorghum is cleaner than ethanol from sugarcane when mixed with gasoline (Belum *et al.*, 2010). Sweet sorghum produces eight units of energy for every unit of energy invested in its cultivation and production (Udoh *et al.*, 2018). The crushed stalks or the bagasse could be used for cellulosic ethanol production, and the grain may be used for ethanol production from the starch (Rajvanshi *et al.*, 2007). Sweet sorghum stalks can be crushed to extract juice for ethanol production, and the leftover crushed stalks (bagasse) can be used as livestock feed.

The biofuel produced from agricultural biomass offers a sustainable and eco-friendly energy option that fosters environmental sustainability as compared to other renewable sources. This led to economic considerations in the production of sweet sorghum with emphasis on high grain yield, high stalk yield, and sugar yield. Plant breeding procedures require conducting yield trials of crop genotypes in multiple environments. Such trials provide valuable information on the performance, adaptation, and genotype-by-environment interactions of genotypes, which are essential for cultivar selection. Since yield and yield attributes are controlled by complex polygenes, their expression strongly depends on environmental conditions. Multi-environment trials (MET) are conducted to evaluate the yield stability and performance of genetic materials under varying environmental conditions (Yan and Rajcan, 2002). A genotype grown in different environments will frequently show significant variation in yield performance. These changes are influenced by the genotype-by-environment interaction (G × E). G × E sometimes complicates the selection of superior genotypes (Ramagosa *et al.*, 2013), making ranking of genotypes or correlation between genotype and phenotype difficult. Yield stability analysis, therefore, is an important step in developing cultivars for a wide range of environments or for a specific location. AMMI analysis is used to determine the stability of genotypes across locations by utilising the principal component axis (PCA) scores, AMMI stability value (ASV), and biplot. The purpose of this study was to investigate the interaction between genotype and environment on yield traits, assess stability, and identify the most suitable sweet sorghum genotypes for biofuel production in the Sudano-Sahelian areas of Nigeria.

MATERIALS AND METHODS

The experiment was conducted in the 2017, 2018 and 2019 rainy seasons at the ICRISAT research field in Bayero University, Kano (BUK) and the Centre of Agriculture and Pastoral Research (CAPAR) of Usmanu Danfodio University, Sokoto (UDUS) research farm. The locations are at latitude 11.97691, longitude 8.41934, altitude 450m and latitude 12.76439, longitude 5.42808, altitude 288m in the Sudano-sahelian zone of Nigeria, respectively.

Eighty sorghum (80) genotypes were used for the study (63 sweet sorghum genotypes, 5 sweet sorghum landraces and 12 improved grain sorghum varieties from ICRISAT as checks) were evaluated for genetic variability. The genotypes were planted in an incomplete alpha lattice design with two replications under each growing condition. A plot consisted of two rows, each 5 m long. At each site, the land was double-harrowed and ridged at a depth of 0.75m. Five to six seeds were planted at an intra-row spacing of 0.30m on top of the ridge. It was thinned to two plants per hill at 2-3 weeks after planting. A basal dose of NPK fertiliser at 30N:30P:30K was applied at planting time, followed by another dose of 30N as top-dressing using urea at 35-40 days after planting. 2-3 manual weeding using hoes was conducted to control weeds as and when necessary. The observations recorded in 19 traits *viz.* plant seedling vigour, days to 50% flowering, chlorophyl content using SPAD at 4 and 8 weeks after planting, days to physiological maturity, plant height (cm), stem diameter (mm), number of internodes, fresh stalk weight (ton/ha), bagasse weight (ton/ha), juice volume (L/ha), juice weight (kg/ha), panicle length (cm), Panicle number, Panicle weight (kg/ha), 100 grain weight (g), grain yield (kg/ha), Brix reading at maturity and Brix reading at dough.

Observations were recorded on five randomly selected plants in each genotype from each replication. The data were subjected to analysis of variance using Genstat software, 19th Edition, to determine the significance of the main effects and interactions. A combined analysis of growth and yield parameters across different growing environments was also done. Broad heritability (H) and Variance components (genotypic, phenotypic, and environmental, as well as genotype x environment variances) were estimated from the respective mean squares obtained from the analysis of variance table, following the method outlined by Ntawuruhunga and Dixon (2010). The rainfall patterns of these areas were monomodal and erratic, with an annual mean of 738 mm. The rains usually begin in April-May, end in October, and are followed by a long dry season (5–6 months). Intermittent dry spells usually occur even during the rainy season.

Phenotypic and genotypic variances were estimated using the following formula, as used by Falconer and Mackey (1996).

$$\sigma^2 g = \frac{\sigma^2{}_v - \sigma^2{}_e}{r}$$

$$\sigma^2{}_p = \sigma^2{}_g + \sigma^2{}_e$$

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to Mukherjee *et al.* (2016) as follows:

GCV (%) = $(\sqrt{\sigma^2 g}/\ddot{X}) \times 100\%$,

PCV (%) = $(\sqrt{\sigma 2p}/\ddot{X}) \times 100\%$,

Where $\ddot{X}$ is the grand mean.

Heritability (h²)

Heritability, in a broad sense, was computed as the ratio of genetic variance to total phenotypic variance, as suggested by Hanson *et al.* (1956) and expressed as a percentage.

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where:

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_p$ = Phenotypic variance

h^2 = Heritability

$\sigma^2 e$ = pooled error

r = number of replications.

Stability analysis

The additive main effect and multiplicative interaction (AMMI) model, as presented in GenStat 19th edition, was used to determine the stability of the genotypes across environments. The AMMI model first fits the additive effects for the genotypes and environments (two environments and two seasons), as well as the multiplicative term for genotype-by-environment interactions. AMMI stability value (ASV) was calculated for each genotype according to the relative contributions of the principal component axis scores (IPCA1 and IPCA2) to the interaction sum of squares (Purchase *et al.*, 2000).

The AMMI stability value (ASV)

$$ASV = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(SSIPCA1\ score)\right]2 + (SSIPCA2\ score)^2}$$

Where

$\frac{\text{IPCA1}}{\text{IPCA2}}$ is the weight from dividing the sum of IPCA1 square by the sum of IPCA2 square.

Where IPCA1Sum of squares/IPCA2Sum of squares is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares (from the AMMI analysis of variance table) by the IPCA2 sum of squares. The larger the IPCA score, whether positive or negative, the more adapted a genotype is to a specific environment. Smaller ASV scores indicate a more stable genotype across environments (Farshadfar *et al*., 2011).

The yield stability index (YSI) was also calculated by summing the ranking based on yield and the ranking based on the AMMI stability value.

Yield stability index (YSI)

YSI = ASV + RMY

Where;

ASV = rank of genotypes based on the AMMI stability value

RMY = rank of genotypes based on average yields (mean) across environments

The genotype with the least YSI (i.e., high mean yield and low ASV) is considered most stable (Tumuhimbise *et al*., 2014).

YSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Tumuhimbise *et al*., 2014; Bose *et al*., 2014).

RESULTS

The environments differed in total rainfall amounts, as well as minimum and maximum temperatures (Tables 1 and 2). The total rainfall recorded in 2018 was higher than that recorded in the 2019 season for both locations. For the UDUS farm in 2018, 867.9 mm was recorded, which was higher than in 2019 (788.2 mm). A higher amount of rainfall was also recorded at BUK farm in 2018 (685.95 mm) than in 2019 (609.30 mm). Mean monthly temperature records at UDUS farm were higher than at BUK farm in both years.

There was a highly significant (p < 0.001) effect of genotypes and environment for all the traits studied (Table 3). Genotype × environment effect was also highly significant (p < 0.001) for the traits studied (bagasse, days to maturity, grain yield, juice volume, Brix at maturity and stover fresh weight).

The AMMI analysis of variance indicated highly significant (p < 0.001) effects of genotype, environment, and interaction for all traits (Table 4). Genotypic factors accounted for a larger proportion of the treatment sum of squares for all the traits (bagasse, days to maturity, stem girth, grain yield, juice volume, plant height, Brix and stover fresh weight). Genotypic effect accounted for 5.457% of the treatment sum of squares (SS) for stover fresh weight (ton/ha), whilst environment and interaction accounted for 88.29% and 0.82% respectively. The first two interaction principal component axes (IPCA1 and IPCA2) accounted for 2.23% of the interaction sum of squares. For juice volume (litres), the genotype effect contributed 32.40% of the treatment sum of squares, while environment and interaction effects accounted for 39.47% and 4.15%, respectively. The IPCA1 accounted for 7.03% with IPCA2 accounting for 3.38%. A greater proportion of the treatment sum of squares for Brix was attributed to the genotype effect (77.22%), while the environment had a very small effect on Brix (1.37%) and the interaction effect (0.47%). The first two interaction principal component axes accounted for a total of 1.35%.

Genotype effects accounted for 7.06% of the treatment sum of squares for bagasse, whilst environment and interaction effects accounted for 82.64% and 1.36%, respectively. The IPCA1 accounted for 2.95% of the interaction sum of squares, with IPCA2 accounting for 0.67%. For grain yield, the environment contributed a greater proportion (89.52%) of the treatment sum of squares compared with the genotype effect (3.59%) and interaction (1.07%). Principal component axes (IPCA1 and IPCA2) accounted for 2.31% and 0.59% of the interaction sum of squares, respectively.

The most stable genotype based on mean yield for bagasse is F7.5SSM09-5-3/3-2-1-4, IS 23562, F5.3SSM10-1/1-3 and Maijankai; while F5.3SSM10-7/3-4, 104GRD and IESV 93042 SH for grain yield. ICSV 93046 ML, SDSL 90167, ICSR 93034-ML and IS 2331 for juice volume; while ICSR 93034-ML, F5.3SSM10-1/1-3 and ICSB 324 for Brix and F5.3SSM10-19/1-1, ICSV 700-ML, F5.3SSM10-31/2-3 and F7.5SSM09-1-1/9-2 for stalk fresh yield.

Table 1. Mean monthly minimum and maximum temperature and rainfall for BUK

Month/ Variables	2018			2019		
	Min. Temp (°C)	Max. Temp (°C)	Rainfall (mm)	Min. Temp (°C)	Max. Temp (°C)	Rainfall (mm)
January	13.22	28.6	0	15.23	32.73	0
February	19.37	36.6	0	16.75	33.16	0
March	21.3	39.6	0.7	22.61	38.96	0.3
April	25.52	41.28	0	25.66	41.37	0
May	25.03	37.87	40	25.59	38.54	18.8
June	23.67	35.06	98.5	23.75	34.82	67
July	22.06	31.68	41.9	22.29	31.7	203.85
August	21.52	30.57	320.4	21.85	29.63	186.45
September	22.08	32.46	182.15	22.56	33.02	82.4
October	21.71	35.53	2.3	21.89	32.99	50.5
November	15.11	32.66	0	18.52	36.89	0
December	15.51	29.52	0	13.65	31.9	0
	20.51	34.29	685.95	20.86	34.64	609.30

Table 2. Mean monthly minimum and maximum temperature and rainfall for UDUS

Month/ Variables	2018			2019		
	Min. Temp (°C)	Max. Temp (°C)	Rainfall (mm)	Min. Temp (°C)	Max. Temp (°C)	Rainfall (mm)
January	12.96	32.38	0	13.62	34.51	0
February	18.63	37.69	0.51	15.35	35.76	0
March	20.24	41.18	0	21.11	40.77	2.03
April	24.16	41.78	4.57	23.41	42.92	0
May	27	39.61	32.76	26.54	39.15	29.21
June	24.56	35.74	89.92	24.41	35.74	140.47
July	22.38	31.4	319.52	22.85	32.19	146.05
August	22.33	30.66	199.9	22.57	30.9	299.97
September	22.14	32.91	165.87	22.88	33.69	97.03
October	21.65	36.3	54.86	22.25	34.09	73.4
November	14.49	36.95	0	15.63	38.73	0
December	13.66	32.63	0	12.23	36.08	0
	20.35	35.77	867.91	20.24	36.21	788.16

Table 3. Combined analyses of variance for six traits evaluated on 80 genotypes of sorghum in the Sudano-sahelian savanna of Nigeria

SOV	d.f.	Bagasse	Days to maturity	Girth	GRNWT	JQ	PH	SC@Mat	STFWT
E	3	8518.9***	65784.4***	37.53***	64679226***	341400***	827392.33***	13280***	33373.24***
G	79	3787.8***	1894.7***	5.92***	61184051***	15790***	12356.39***	8.931***	20545.67***
E × G	237	4938.4***	16240.2***	23.26***	57896512***	131100***	229671.11***	242.4***	15109.78***
Residual	320	1107.12	2389.5	3.035	4814797	4566	3814.5	23.13	1315.44
Total	639	18352.20	86308.74	69.75	1885746	492800	1073234.33	13560	70344.13

E=Environment, G=Identification, SOV=Source of variation; *** = significant at $p < 0.001$, df = degree of freedom, GRNWT = grain weight (kg/ha), JQ = quantity of juice (ltr), STFWT = stover fresh weight (t/ha), PH = plant height, SC@Mat = Brix at maturity

Additive main effect and multiplicative interaction (AMMI) stability value (ASV) ranked the genotypes based on the lowest score. Low scores based on the ASV represent the most stable genotypes. The most stable sweet sorghum genotypes using AMMI stability values (ASV) were F7.5SSM09-5-3/3-2-2-2, SERENA-ML and IS 23525 for stalk fresh yield; bagasse had F5.3SSM10-20/2-1 and E 36-1; F5.3SSM10-31/5-1; IESV 92058/2 SH and SPV 422-NB for juice volume; ICSV 93046-ML and IS 2331 for Brix, while grain yield had NTJ 2 and IESV 92165 DL. The environment revealed that Kano II had the lowest IPCA2 score for both bagasse and grain yield, while Kano had the highest juice volume and stalk fresh yield, and UDUS II had the highest Brix; hence, these environments were the most interactive and stable for the economic traits.

Table 4. AMMI analyses of variance for 80 sorghum genotypes evaluated in sudano-sahelian savanna of Nigeria for sugar and yield traits

		Bagasse			
Source	d.f.	SS	MS	Explained %	Variable
Total	639	18352	28.7	-	
Treatments	319	17245***	54.1	3.54	16.48
Genotypes	79	8519***	107.8	7.06	32.86
Environments	3	3788***	1262.6	82.64	71.87
Block	4	70	17.6	-	5.35
Interactions	237	4938***	20.8	1.36	6.35
IPCA 1	81	3649***	45.1	2.95	13.73
IPCA 2	79	806***	10.2	0.67	3.11
Residuals	77	483***	6.3	-	1.91
Error	316	1037	3.3	-	
Grain yield					
Source	d.f.	SS	MS	Explained %	Variable
Total	639	188574586	295109	-	-
Treatments	319	183759788***	576049	2.53	38.23
Genotypes	79	64679226***	818724	3.59	54.34
Environments	3	61184051***	20394684	89.52	1525.18
Block	4	53488	13372	-	0.89
Interactions	237	57896512***	244289	1.07	16.21
IPCA 1	81	42695290***	527102	2.31	34.98
IPCA 2	79	10546932***	133505	0.59	8.86
Residuals	77	4654290***	60445	-	4.01
Error	316	4761310	15067	-	-
Juice volume					
Source	d.f.	SS	MS	Explained %	Variable
Total	639	4928326944	7712562	-	
Treatments	319	4882662184***	15306151	11.48	106.91
Genotypes	79	3413607258***	43210218	32.40	301.83
Environments	3	157922049***	52640683	39.47	495.14
Block	4	425260	106315	-	0.74
Interactions	237	1311132877***	5532206	4.15	38.64
IPCA 1	81	759497154***	9376508	7.03	65.5
IPCA 2	79	356301949***	4510151	3.38	31.5
Residuals	77	195333774***	2536802	-	17.72
Error	316	45239500	143163	-	
Brix					
Source	d.f.	SS	MS	Explained %	Variable
Total	639	13558	21.22	-	
Treatments	319	13535***	42.43	19.48	590.44
Genotypes	79	13283***	168.15	77.22	2339.91
Environments	3	9***	2.98	1.37	28.2
Block	4	0	0.11	-	1.47
Interactions	237	242***	1.02	0.47	14.23
IPCA 1	81	228***	2.81	1.29	39.14
IPCA 2	79	10***	0.13	0.06	1.8
Residuals	77	4ns	0.06	-	0.78
Stalk fresh yield					
Source	d.f.	SS	MS	Explained %	Variable
Total	639	70344	110.1	-	
Treatments	319	69029***	216.4	2.79	54.17
Genotypes	79	33373***	422.4	5.45	105.76
Environments	3	20546***	6848.6	88.29	514.75
Block	4	53	13.3	-	3.33
Interactions	237	15110***	63.8	0.82	15.96
IPCA 1	81	11740***	144.9	1.87	36.29
IPCA 2	79	2217***	28.1	0.36	7.03
Residuals	77	1153***	15	-	3.75

Table 5. Estimate of variance components, broad sense heritability, PCV, GCV for 12 traits in 80 sweet sorghum genotypes from four environments

Characters	F pr.	Grand Mean	Lowest Value	Highest value	LSD	CV%	Genotypic	Phenotypic	H2	GCV	PCV
Bagasse	<.001	14.5	5.0	24.8	3.7	12.8	52.2	160.0	32.6	49.8	87.2
Days_Maturity	<.001	114.0	93.0	149.0	5.4	2.4	412.6	420.1	98.2	17.8	18.0
DFLW	<.001	84.0	67.0	109.0	4.0	2.4	280.1	284.3	98.5	19.9	20.1
Girth	<.001	1.8	1.5	2.5	0.2	5.3	0.2	0.2	96.1	26.2	26.8
GRNWT	<.001	1133.0	408.0	1,895.0	241.3	10.8	401839.0	1220563.0	32.9	55.9	97.5
INTNN	<.001	12.0	9.0	14.0	1.7	7.2	5.1	5.9	87.4	18.9	20.2
JQ	<.001	3872.0	506.0	9,511.0	743.2	9.8	1.5	5.8	33.3	0.03	0.06
NHP	<.001	18.0	5.0	27.0	5.1	14.9	83.5	257.4	32.5	50.8	89.1
PANL	<.001	23.0	9.7	36.6	2.7	6.0	110.0	111.9	98.3	45.6	46.0
PH	<.001	219.0	150.0	317.0	6.8	1.6	5230.7	5242.6	99.8	33.0	33.1
SC_at_Mat	<.001	8.4	0.5	15.7	0.5	2.7	47.6	47.6	99.9	82.1	82.1
STFWT	<.001	25.5	9.5	46.4	4.0	8.0	209.2	631.6	33.1	56.7	98.6

The most stable sweet genotype for grain yield is S 35 - NB, as it's the most highly stable, having the lowest ASV ranking (i.e., the lowest ASV score), while F5.3SSM10-7/3-4 was ranked the least stable because it had the highest ASV score. In terms of stover fresh yield, F7.5SSM09-5-3/3-2-2-2 and SERENA-ML had the highest rank and hence was the most stable. Juice yield had F5.3SSM10-31/5-1 as the highest ranked and most stable, while Gwaram was ranked the least and was the least stable. The most stable genotype for Brix was ICSV 93046-ML, as it had the highest ASV ranking. In contrast, F5.3SSM10-14/2-1 was ranked the least stable, due to its lowest ASV ranking. In contrast, F5.3SSM10-14/2-1 was ranked the least stable due to its highest ASV score. The sum of the yield and stability rankings (YSI) also ranked NTJ 2 as the genotype that combined high yield with stability on grain yield. Gwaram and Kwandage-1, though high-yielding for sugar and juice, were unstable due to their low rank according to the YSI. IS23525, ICSV 93046-ML and SPV 422 – NB were found to be high-yielding and stable in terms of stover fresh yield, Brix and juice yield, respectively. Three genotypes, ICSV 93046-ML and NTJ 2, can be considered as high-yielding and stable for sugar content and grain yield across all environments.

A large proportion of the phenotypic variance for grain yield and plant height was accounted for by the genotypic variance (Table 5). All the traits studied were primarily influenced by their genotype or environment, rather than the interaction between genotype and environment, except for juice volume, which exhibited a slightly different response to the influence of genotype and environment. The estimates of broad-sense heritability varied for all traits and were especially low for bagasse (32.6%) and the number of harvested panicles (32.5%) (Table 5). Relatively high broad-sense heritability estimates were observed for Brix (99.9%), plant height (99.8%), days to 50% flowering (98.5%), panicle length (98.3%) and days to maturity (98.2%). The phenotypic coefficient of variation (PCV) for all traits was higher than the corresponding genotypic coefficient of variation (GCV). Wide differences were observed between PCV and GCV for juice volume, grain yield, stover fresh yield, number of harvested panicles, and bagasse. PCV ranged from 0.06% to 98.6% for juice volume and stover fresh yield, respectively. GCV varied from 0.03% (juice volume) to 82.1% (stover fresh yield). Moderate PCVs (10–20) were observed for days to maturity, days to 50% flowering and number of internodes, whereas high PCV (>20) was recorded for stover fresh yield, grain yield, number of harvested panicles, bagasse, Brix, panicle length, plant height and stem girth.

IESV 91018 LT is the sweet sorghum with the highest plant height (289 cm), although some checks have higher heights (CSR 01 and CSR 01, 342 cm and 310cm, respectively), with genotypes F5.3SSM10-14/2-1 and Ent#64DTN having the shortest plants across all environments. The lowest Brix was identified in genotypes F5.3SSM10-1/1-8 (7.3), but the grain checks don't have it. The genotypes Kwandage-1 and NTJ-2 had the highest with 21.2 and 19.9, respectively. The average stem diameter (girth) ranged from 1.41cm (ICSV 700-ML) to 2.20cm (ICSR 93034-ML), although the grain check had a diameter of up to 2.61cm (CSR 01). Average grain yield for all genotypes across the four environments was 1,133 kg/ha (Table 5). Maijankai, a local sweet sorghum check (2,016 kg/ha), and F5.3SSM10-7/3-4, an improved sweet sorghum genotype (1,852 kg/ha), had the highest overall grain yields, while Gwaram and Kwandage-1 have the lowest grain yields (469 and 438 kg/ha, respectively). Three genotypes (F5.3SSM10-1/3-3, Gwaram and Kwandage-1) had significantly higher juice yields of 11,105, 9,572, and 8,926 litres, respectively. In contrast, F5.3SSM10-31/6-3, a sweet sorghum genotype, yielded the lowest quantity of 1,688 litres, although this is higher than almost all the checks. Stover fresh yield also varied from 9.9 t/ha (CSR 03H) to 48.1 t/ha (Gwaram), the result follows the same trends in quantity of bagasse.

The maturity period ranges from 149 – 94 days for SAMSOR 17 and ICSV 111 across environments.

In the study, genotypes IESV 92008 DL, Zauna Inuwa, CSR 02 and ICSV 700 - NB for stover fresh yield (Fig. 1), Gwaram, ICSV 93046 – ML, Kwandage-1 and F7.5SSM09-5-3/3-2-1-4 for juice yield (Fig. 1), Deko, F5.3SSM10-7/3-4 and IESV 92038/2 SH for grain yield, ICSR 93034 – ML, F5.3SSM10-14/2-1 and F7.5SSM09-6-2/3-1-2PL for sugar yield (Fig. 1) were generally high yielding as they were placed on right-hand side of midpoint of IPC1 axis (representing grand mean). Similarly, BUK seasons I and II were considered superior in stover fresh yield (Fig. 1), while Kano and UDUS II are identified as having similar environments. All sites produced high juice and sugar yield (Fig. 1). However, Kano l and ll performed better in terms of grain yield (Fig. 2). The genotypes located on the vertex of a polygon are the ones that gave the highest yield for the environment that falls within that quadrant.

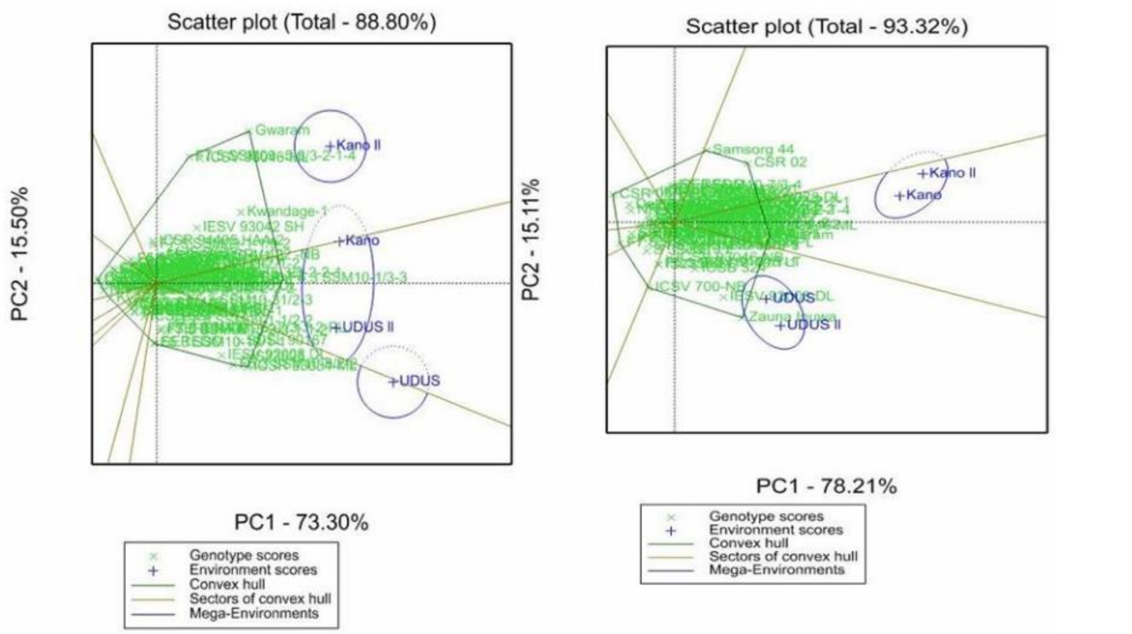

Fig. 1. GGE biplot of stover fresh yield and juice yield

The vertex genotypes for stover fresh yield were ICSV 700-NB, CSR 02, SAMSORG 44, Gwaram and IESV 92008 DL. Genotype IESV 92008 DL and Zauna Inuwa recorded the highest fresh stover in UDUS farm in seasons I and II, while Gwaram and CSR 02 gave the highest stover in Kano farm. The polygon environments. This indicates that NTJ 2 has a poor stover yield, making it unsuitable for either environment. The GGE biplot for juice yield (Fig. 1) indicates that Gwaram and F7.5SSM09-5-3/3-2-1-4 are suitable for cultivation in Kano farm in seasons II, while Kwandage 1 and F5.3SSM10-1/3-3 were better adapted to Kano season l and UDUS season ll. ICSR 93034 ML recorded the highest juice volume in UDUS in season 1. Some genotypes fall into sectors where there were no locations, these genotypes are poorly adapted to all tested environments. Locations in one sector have these genotypes that are poorly adapted to all tested environments. Locations in one sector have the best-performing genotype, which can be considered as mega environments for that genotype.

The GGE biplot for grain yield (Fig. 2) indicates that F5.3SSM10-7/3-4 and F5.3SSM10-14/2-1 are suitable for cultivation in Kano farm during season's l and II, while IESV 92038/2 SH and Zabuwa were better adapted to UDUS season l and ll. ICSR 93034 ML recorded the highest juice volume in UDUS in season 1. Genotype ICSR 93034 ML and F5.3SSM10-14/2-1 recorded the highest Brix in a mega environment of both Kano and UDUS farm for seasons I and II.

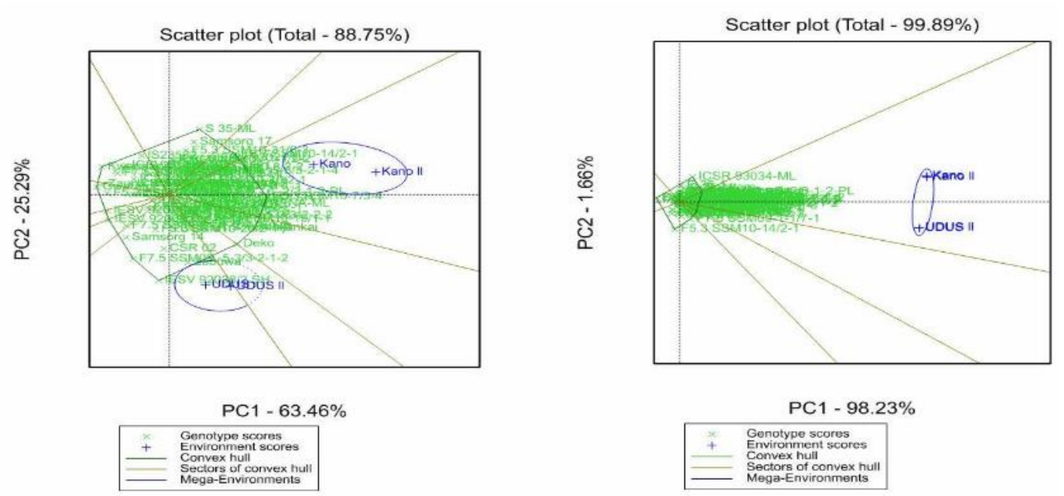

Fig. 2. GGE biplot of grain yield and sugar content

Biplots were divided into ten sectors in Fig. 2. Genotypes which fall in the same sector as the environment are said to be adapted to those locations. In the present study, genotypes IESV 92038/2 SH, F7.5SSM09-5-3/3-2-1-2, SAMSORG 14, CSR 02 and Zabuwa were adapted to UDUS farm seasons I and II. F5.3SSM10-14/2-1 is suitable for cultivation in the Kano farm for all seasons. Gwaram had the highest Juice yield in Kano season ll. All grain checks were poor performers for juice yield and were not suitable for the tested environments. Genotype ICSR 93034 ML, F5.3SSM10-14/2-1 and CSR 02 had the highest IPCA1 score for both juice, grain, sugar, and stover fresh yield, indicating that they are high-yielding genotypes and specifically adapted.

DISCUSSION

The performance of sweet sorghum lines is influenced significantly by genotype, environment, and the interaction between genotype and environment (Olweny *et al.*, 2016; Lekgari and Dweikat, 2014). Significant genotypic variations were observed for growth parameters such as grain yield and plant height, indicating an opportunity for selection.

Therefore, ICSV 93046 ML, SDSL 90167, ICSR 93034-ML and IS 2331; ICSR 93034-ML, F5.3SSM10-1/1-3 and ICSB 324, F5.3SSM10-19/1-1, ICSV 700-ML, F5.3SSM10-31/2-3 and F7.5SSM09-1-1/9-2 can be chosen for wider stability and adaptability for juice volume, Brix and stalk fresh yield, respectively, across environments. The GGE biplot was applied by Rao *et al.* (2011) to explain the interrelationship among the environments and genotypes. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them; environments with a small angle between them are highly positively correlated, and they provide similar information on genotypes. This study reveals, that some low-performing genotypes are stable and have wider adaptability, whereas some high-performing genotypes are less stable. A study by Abubakar and

Bubuche (2013) found that genotype by environment interaction had a significant influence on sorghum plant height.

Differences in plant height can result in variations in stalk yield across environments; therefore, genotypes adapted to specific locations have to be selected. Biomass yield and plant height have been identified as major contributors to economic yields in sweet sorghum (Bahadure *et al.*, 2014). Furthermore, ANOVA revealed a significant effect due to a genotype-by-environment interaction. This indicates that genotypes performed differently at each site, which is expected due to differences in soil composition, rainfall and temperature.

Ideal cultivars and environments are those having large PC1 scores (high mean yield) and small PC2 scores (high stability) (Frashadfar *et al.*, 2012). Based on this, Kano I and UDUS were found to be ideal environments, whereas ICSV 93046 ML was an ideal genotype for juice production. Genotypes Kwandage-1, NTJ 2 and Gwaram were the winning genotypes for Brix in Kano and UDUS; therefore, they are suitable for these environments.

High Brix was recorded for Kwandage-1, NTJ 2 and Gwaram genotypes, for both Sokoto and Kano in all the years. The results are closer to what was observed by Reddy *et al.* (2005) of 16 to 23% Brix and slightly higher than that observed by Woods (2000) of 11.0 to 18.5% Brix among genotypes evaluated. Combined analysis of variance revealed highly significant ($p \leq 0.001$) variations among environments, genotypes and genotype × environment interaction. This result revealed differential yield performance among sweet sorghum genotypes across testing environments. Maarouf and Moataz (2009) reported variation between sorghum genotypes with respect to fodder yield. This indicates that simultaneous selection for girth, Brix% and stalk yield is not possible across the four environments and that selection for each location must be carried out separately. This limits their wider utilisation, as reported by Begna (2021), who stated that significant G × E for a quantitative trait is known to reduce the usefulness of the genotype means over all locations or environments for selecting and advancing superior genotypes to the next stage of selection. Across locations, analysis of variance revealed that genotypes differed significantly ($p < 0.001$) for all sugar-related traits. Location × variety interactions were significantly different ($p < 0.001$) for girth, stalk weight, and juice volume. Chapman *et al.* (2000) reported that most of the G × E in sorghum was a result of the genotype by location by year, but suggested that breeders deal with the genotypes by location type over a field number of seasons. This difference among seasons can be attributed to the heavy rains received in 2018.

When the interaction between environments and genotypes was significant, further analysis was done using the Additive Main Effects and Multiplicative Interaction (AMMI) model to determine the adaptive response of specific genotypes to specific locations (Annicchiarico, 2002; Egesi and Asiedu, 2002). Analysis of variance for the Additive Main Effect and Multiplicative Interaction (AMMI) model revealed significant differences amongst treatments, genotypes, environments and interactions between genotypes and environments ($p<0.001$). These variations are closer to the ones reported by (Olweny *et al.*, 2016) while studying G × E for sugar and biomass using 18 sweet sorghum genotypes of diverse origin across environments. He found that variations in Brix were more due to genotypes than to interactions or environment.

Stability analysis methods are often used by breeders to identify genotypes that have stable performance and respond positively to improvements in environmental conditions Farshadfar *et al.*, 2011 AMMI stability value (ASV) indicates the stability of genotypes. Genotypes having low ASV are considered more stable, whilst those with high values are less stable genotypes (Hagos and Abay 2013). CTSIA 110, MM96/1751, and TME 435 were the most stable for root yield. Stability alone for yield performance does not warrant selection since a consistently low-yielding genotype can still be stable (Yan and Tinker, 2006). In some cases, the most stable genotypes do not always have the best yield performance (Oliveira and Godoy, 2006). Therefore, high grain yield is considered with stability in the estimation of yield stability index (YSI). The YSI, which is similar to genotype stability index (GSI) proposed by Fardshadfar 2008, integrates both yield and stability across environments into a single index to select varieties. The YSI sums the rank of mean yield across environments with the rank of the ASV of genotypes ((Farshadfar *et al.*, 2011; Baraki *et al.*, 2014).

Genotypes with lower YSI are desirable since they combine high mean yield performance with stability (Farshadfar *et al.*, 2011; Tumuhimbise *et al.*, 2014; Baraki *et al.*, 2014; Bose *et al.*, 2014). Based on the YSI, genotypes IS 23525, ICSV 93046 – ML, SPV 422 – NB, F5.3SSM10 – 19/1-1 and E 36 -1 were selected as combining high yield performance with stability for stover yield, Brix, juice yield, grain yield and bagasse, respectively. Genotypes such as Maijankai, Gwaram, Kwandage-1, IESV 92008 - DL and IS 2331 are high yielding for grain yield, juice volume, Brix, stover yield and bagasse, respectively, and have high ASV scores, resulting in high YSI scores, though not stable. However, they can be recommended for specific environments where they performed well. The range of variation in the favourable environments (Kano in 2018 and 2019) was larger than in the poor environments, indicating that genotypes were better able to exploit their full potential yield in the good environments (Przystalski *et al.*, 2008).

CONCLUSION

Genotype, Environment, and genotype × environment interactions had a strong effect on the yields of sweet sorghum genotypes. The significant G × E interactions for stover and juice yield observed in this study's analysis of variance indicate that sweet sorghum genotypes respond differently when grown in varying environmental conditions. The results from this study indicate that IS 23525, ICSV 93046 – ML, SPV 422 – NB, F5.3SSM10 – 19/1-1 and E 36 -1 were selected as they combined high yields with stability for stover yield, Brix, juice yield, grain yield and bagasse, respectively, were most stable and best genotype across environments. The best-performing genotypes in terms of yields were Maijankai, Gwaram, Kwandage-1, IESV 92008 - DL and IS 2331 for grain yield, juice volume, Brix, stover yield and bagasse, respectively, although not stable. It is evident that the performance of sweet sorghum is attributed to both its genetic makeup and environment.

RECOMMENDATIONS

The study indicated that selection for juice, grain, bagasse, and stover yields cannot be carried out across all four environments, suggesting that selection for these traits must be carried out separately in each environment.

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