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Identifying Suitable Dual Purpose Sorghum OPVs Lines using GGE Biplot across Three Agro-Ecological Environments in Niger Republic

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Abstract

Objectives: Shortages in animal feed are common in Niger, often resulting in livestock death. Among adaptation strategies for this crisis, some dual-purpose sorghum lines suitable were developed for both grain and fodder. The aim of this study was to identify the ideal genotypes for southern Niger republic using GGE Biplot model.

Methodology and Results: Thirty sorghum elite lines were evaluated in three locations (Tarna, Aderaoua and Bengou) for the dual-purpose traits (grain and fodder) and for yields stability in Niger. The traits were implemented following an Alpha Lattice design with three replications. Data on grain yield (GY) and fodder yield (FY) were collected and used as variables in this study. A combined analysis of variance showed a highly significant effect of the genotypes, environments and genotypes x environment interaction. The GGE Biplot model was performed to identify the most stable lines across environments. The results showed two megaenvironments for GY while for FY three megaenvironments were identified. For GY the genotypes that performed well in each environment based on the "which-won-where" polygon were G1 and G3 in Bengou megaenvironment and G28, G26 in Tarna-Aderaoua megaenvironment. For FY G25 was the vertex thus best genotype at Tarna, G10 at Aderaoua and G4 at Bengou. The site comparison biplot revealed that Aderaoua was the best environment for evaluating dual purpose sorghum genotypes in Niger.

Conclusions and application of findings: For dual purpose (GY and FY) production in southern zone of Niger G25 (MDK), G20 (ICSX14 018 BCJP-14-1-SB6) and G4 (CSM63E) recorded a good and stable potential production for both GY (1310 kg/ha to 1740 kg/ha) and FY (10484 kg/ha to 12889 kg/ha), and are therefore recommended for scaling up and further breeding activities.

Keywords: Sorghum, Dual Purpose, GGE-biplot, Megaenvironment

Introduction

In the SSA region, the pressing demand for fodder coupled with the importance of the grain of sorghum for people, makes imperative to reconsider the present mono-commodity breeding strategy of sorghum (Suad *et al*., 2015) [1].

In Niger, farmers growth sorghum as a dual-purpose crop therefore, breeding for dual-purpose sorghum lines which combine high grain yield with reasonable dry stover yield is a strategic way for improving the livelihood of rural farmers (Diakite, 2019) [6]. It is also important for the breeding program to select dual purpose sorghum varieties that have a wide adaptability and stability in different agroecological zones of the country.

The Genotype and Genotype × Environment (GGE) model is a statistical tool that helps researchers to identify stable and high-yielding genotypes, genotypes with stable yield across multi-environments, and genotypes that perform well in each location. The discrepancies in arable lands due to pedoclimatic conditions, therefore, lead to the Genotype × Environment interaction (GEI) effect, thus causing crops to not perform uniformly in the environments. For these reasons, plant breeders and agronomists give much attention to GEI studies to provide lasting solutions to this problem by applying GGE approaches (Alizadeh *et al*., 2017; Oladosu *et al*., 2017) [4, 13].

The GGE method provides three important aspects such as megaenvironment analysis, genotype evaluation, and test site for target environment (Yan *et al*., 2007) [12]. It is an effective tool for:

(1) Mega-environment analysis (e.g., "which-won-where" pattern), whereby specific genotypes can be recommended to specific mega-environments;

(2) Genotype evaluation (the mean performance and stability), and
(3) Test-environmental evaluation.

In this study, thirty sorghum elite lines were evaluated in three locations in Niger republic for the dual-purpose yield stability using GGE biplot analysis.

The objectives of the study were (i) to select dual purpose sorghum varieties which are stable and adaptable in the Southern agroecological zones of Niger and (ii) to identify the most adapted dual purpose sorghum variety to a specific environment and (iii) to determine the ideal location for evaluating new dual purpose sorghum cultivars in this region.

Methodology

Experimental sites and materials

The experiment was conducted in the southern ecological zone of Niger republic in 3 locations (Tarna, Aderaoua and Bengou) during the rainy season 2021. Geographical information of the sites is presented in Table 1. Thirty (30) sorghum varieties, including two local checks, three national checks and 25 new improved cultivars were evaluated for grain and fodder yield in this study (Table 2). The experiment was laid out in Alpha Lattice Design with 3 replications.

Seeds were planted in four rows of 5m long, 0.80 m between rows, and 0.40 m spacing between hills. Data were collected on the two central rows. The observed parameters were grain yield (GY), fodder yield (FY), date of physiological maturity and plant height.

Statistical analysis

A combined analysis of variance (ANOVA) was computed using Genstat 18th Software to evaluate the genotype effect across multi-environments and test the presence of genotype by environment interaction. GGE Biplot analysis was performed to discriminate the stable genotypes and the ideal Environment as well as the 'which won where' pattern.

The formula of GGE biplot model was given by Gauch (2006) [3] as follow:

$$Yhij = \mu + Eh + Gi + GEhi + Bj(h) + ehij$$

Where μ is the population mean, Eh is the environmental effect, Gi is the genotypic effect, GEhi is the genotype × environment effect, Bj(h) is the block effect, and ehij is the random error.

This model considers a GGE (i.e., G + GE) biplot, which is constructed by the first two symmetrically scaled principal components (PC1 and PC2) derived from singular value decomposition of environment-centered MET data. The GGE biplot graphically displays G plus GE of a MET in a way that facilitates visual genotype evaluation and mega-environment identification (Yan *et al*., 2007) [12].

Table 1: Characteristics of the experimental sites

Characteristics	**Site**		
	Tarna	**Aderaoua**	**Bengou**
Coordinates	13.460562°N and 7.107694°E	13.40236°N and 6.524°E	11.980519°N and 3.557733°E
Annual rainfall	400-600 mm	500-600 mm	800 – 1000 mm
pH (H2O) 1:2.5	5.4	6.9	5.6
OC (%)	0.3	0.53	0.34
%N	0.25	0.06	0.2
Meh P (ppm)	4.22	28.24	0.85
K (cmol+/kg)	0.1	0.28	0.12
%Sand	72	31	46
%Silt	11	36	30
%Clay	17	33	24
ECEC (cmol+/kg)	2.31	13.51	2.5

pH (H_2O): pH measurement performed with a soil-to-water mixture
OC: *Organic Carbon*
%N: *percentage of total Nitrogen in the soil*
Meh P: *Phosphorus extracted using Mehlich-3 solution*
K: *potassium*
ECEC: *effective cation exchange capacity*

Table 2: List of the tested dual purpose sorghum genotypes

Genotype	**Variety**	Source
G1	014-SB-EPDU-1004	IER Mali
G2	Ariho	ICRISAT Mali
G3	BC1F6-11	IER Mali
G4	CSM63E	ICRISAT Mali
G5	DU-37	IER Mali
G6	Fagolo	ICRISAT Mali
G7	Gnossiconi	ICRISAT Mali
G8	ICSV 1460010	ICRISAT Mali
G9	ICSV 1460011	ICRISAT Mali
G10	ICSV 1460013	ICRISAT Mali
G11	ICSV 1460014	ICRISAT Mali
G12	ICSV 1460016	ICRISAT Mali
G13	ICSV 1460018	ICRISAT Mali
G14	ICSV 1460024	ICRISAT Mali
G15	ICSV 1460025	ICRISAT Mali
G16	ICSV 1460028	ICRISAT Mali
G17	ICSV 1460050	ICRISAT Mali
G18	ICSWC 14RS 00018-1-79-1:201704	ICRISAT Mali
G19	ICSX14 001 BCJP-35-1-SB9	ICRISAT Mali
G20	ICSX14 018 BCJP-14-1-SB6	ICRISAT Mali
G21	ICSX14 027 BCJP-21-1-SB11	ICRISAT Mali
G22	L28	INRAN Niger
G23	Hakorin karoua (Local check-1)	INRAN Niger
G24	Koni kirey (Local check-2)	INRAN Niger
G25	MDK	INRAN Niger
G26	Mota Maradi	INRAN Niger
G27	Nando	ICRISAT Mali
G28	Seguifa	IER Mali
G29	Soubatimi	ICRISAT Mali
G30	Tiokala	ICRISAT Mali

Results

1. Combined Analysis of variance for GY and FY

The result of the combined analysis of variance over environments, genotypes and GEI showed a significant effect ($p < 0.001$) of these factors on grain and fodder yield of the studied dual-purpose sorghum (DPS) genotypes (Table 3).

The mean square (MS) and F. probability (F.Pr.) of GY and FY for the environment component indicated a highly significant difference ($p \leq 0.01$) among the three locations. This showed an impact of the agro-ecological properties of these environments on the dual-purpose yields of the tested accessions. Similarly, it was observed a highly significant effect ($p \leq 0.01$) of the genotype component on GY and FY. This result revealed that the thirty (30) DPS accessions performed differently in the three testing locations. The significant differences observed for genotype-by-environment interactions, illustrated the differences in performances of genotypes from one location to another.

The highly significant effect of Environment, genotype and GEI showed that the main proportion of total phenotypic variation in GY and FY in this study was attributed to the environment, the genotypes and the interaction of the two. Definitely, the variance component analysis was not sufficient to elucidate all the attributes of the genotype-by-environment interaction.

Table 3: Mean squares (MS) of combined analysis of variance of dual-purpose sorghum yield and yield components in three locations

		GY		FY	
Source of Variation	df	MS	F Pr.	MS	F Pr.
Rep	2	24357	/	1.37E+06	/
Genotype	29	1566272	<.001	6.23E+07	<.001
Environmemt	2	11437600	<.001	1.07E+08	<.001
Genotype.Environment	58	943574	<.001	2.59E+07	<.001
Residual	178	94232	/	7.81E+06	/

2. Principal component analysis

Identification of megaenvironments

For the grain yield, the polygon view of the biplot classified two locations (Tarna and Aderaoua) as megaenvironment-1 (Fig 1). Bengou stand alone as megaenvironment-2. For fodder yield (FY) the result of GGE biplot analysis showed three megaenvironments (Tarna, Bengou and Aderaoua representing the three experimental sites (Fig 1). This result indicated that the genotypes behaved differently in these locations according to the two kinds of products (grain and fodder). Therefore, selection of dual purpose sorghum varieties should consider genotypes performing well for GY and FY for a specific location or stable across several locations.

The "which-won-where" patterns

Fig 1 shows a "which-won-where" polygon view of the biplot presenting the locations and the best performing dual purpose sorghum genotypes in each sector. For the GY, the polygon was divided in six sectors. In the sector of megaenvironment-1 (Tarna and Aderaoua) the two vertices G26 (Mota Maradi) and G28 (Seguifa), which are improved varieties developed in Niger and Mali respectively, were the best yielding sorghum genotypes. G1 (014-SB-EPDU-1004) and G3 (BC1F6-11) topped in GY in megaenvironment-2 (Bengou). For fodder yield the GGE biplot "which-won-where" patterns classified the biplot into seven different sectors. G25 (MDK) as vertex was the best genotype for FY at Tarna, G10 (ICSV 1460013) at Aderaoua and G4 (CSM63E) at Bengou. On other hand it was observed that, no environment fall in the sector where G17, G27 and G23 were the vertex genotypes for GY and G1, G19 and G27 for FY, demonstrating that these genotypes were the lowest yielding genotypes in this study.

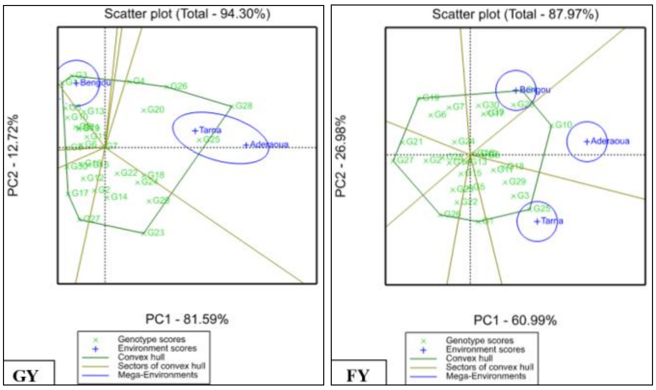

Fig 1: GGE biplot showing Mega-Environments for sorghum grain yield (left) and fodder yield (right)

Determination of ideal environment for evaluating genotypes

The comparison biplot showed that for GY performance Tarna and Aderaoua being near the arrow center of the concentric circles were good environment for genotype testing (Fig 2-left side). G28 (Seguifa) performed well in this ideal environment. For FY performance, Aderaoua was found to be the ideal environment (Fig 2-right side) with G10 as best performing genotype. Therefore, for dual purpose sorghum evaluation in southern zone of Niger, this study showed that Aderaoua could be considered as an ideal environment.

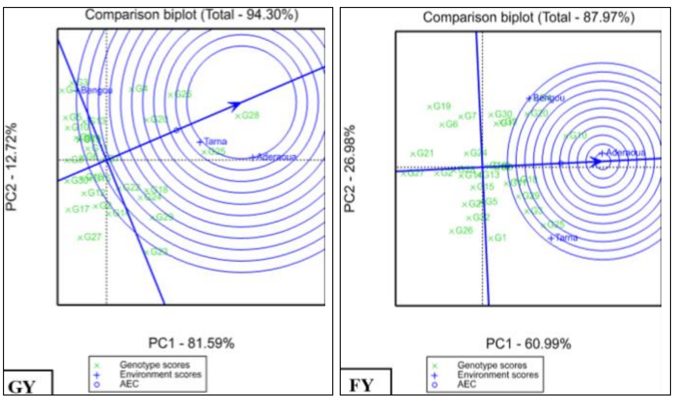

Fig 2: Environment comparison biplot showing the ideal environment for genotype testing

Analysis of stability of genotypes across environments

In this study the analysis of GY performance showed that genotypes G26 (Mota Maradi) being near the center of the concentric circles was the most stable genotype (high GY and stability) across the two megaenvironments (Fig 3-Left side), followed by G28 (Seguifa), G25 (MDK), G20 (ICSX14 018 BCJP-14-1-SB6) and G4 (CSM63E) which could be classified as good genotypes. The low yielding genotypes were G17, G27, G23 and G3 because these genotypes appeared far from the center of the concentric circle of the biplot. In contrary to this result, G27, G15, G12, G7 and G2 were the stable but low yielding genotypes.

Regarding the FY performance (Fig 3-right side), G10 (ICSV 1460013) and G18 (ICSWC 14RS 00018-1-79-1:201704) were the ideal genotypes (stable and high yielding) across the three megaenvironments. Genotypes G20, G25, G4, G18 (ICSWC 14RS 00018-1-79-1:201704), G29 (Soubatimi), G3 (BC1F6-11) were high yielding with medium stability meaning these genotypes are suitable for cultivation under particular agro-climate. In contrary genotypes G27, G2 and G21 were stable but low yielding. Therefore in this study, the good sorghum genotypes for dual purpose production in southern zone of Niger would be G25, G20 and G4 because of their good and stable potential production for both GY and FY.

The visualizing graphic of genotype means and their stability shows different genotype groups classified into four groups. Group one is highly desirable with high yield and high stability for both GY and FY (G4, G20 and G25). G26 and G28 were ideal genotypes for grain production while G10 was an ideotype for fodder production. The group with high yield but low stability is desirable for specific selection for instance G1 and G3 can be recommended for Bengou whereas genotypes with low yield and low stability (G23, G27 for GY and G19 and G26 for FY) may be for special breeding purposes (selection for drought resistance etc.). The most undesirable group is low yield but high stability (G17 and G30 for GY and G21 and G27 for FY).

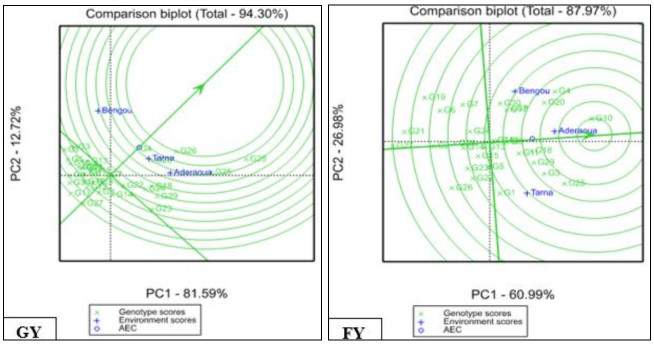

Fig 3: GGE biplot showing the stable genotypes accross Environment

Mean vs. stability

The abscissa and the ordinate of the average environment coordinate (AEC) are the two blue lines passing through the origin of the biplot (Fig 4). The AEC abscissa showed a single direction arrow indicating the ideal genotype main effect, while the AEC ordinate illustrated greater GEI effect and lower stability. The ordinate divides the genotypes into two groups: those that yielded above and below average. The following are the genotypes toward the arrow that yielded above the average means: G4, G20, G26, G28, G25, G18, G24, G29 and G23 for GY and G4, G30, G20, G9, G25, G10, G18, G29, G3 and G1 for FY. The projection on the abscissa toward the ordinate of the AEC is a measure of stability, so a genotype with zero projection or very short direction from the ordinate is considered the most stable, while a genotype with the longest projection from the abscissa is unstable. So for dual purpose selection four genotypes were selected for GY, FY and stability: G20, G25, G4 and G29.

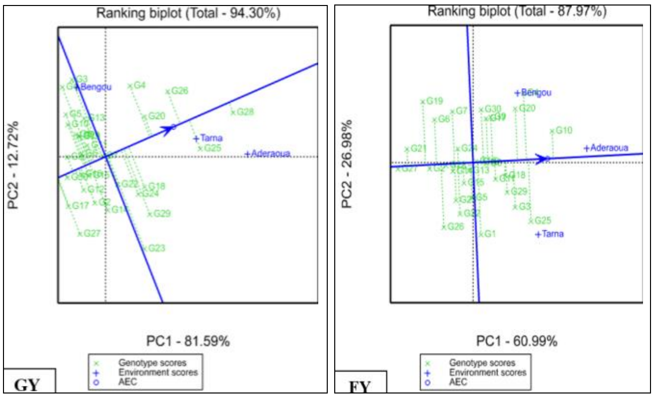

Fig 4: Genotypes comparison biplot for GY (left) and FY (right) using average environment coordinates (AEC)

Discussion

The significant differences observed for genotype-by-environment interactions, illustrated the differences in performances of genotypes from one location to another. The highly significant effect of Environment, genotype and GEI showed that the main proportion of total phenotypic variation in GY and FY in this study was attributed to the environment, the genotypes and the interaction effects. But the variance component analysis was not sufficient to elucidate all the attributes of the genotype-by-environment interaction. This implies that the yield of the tested genotypes in each environment varies significantly, which is in agreement with the finding of Linus *et al*. (2023) [15], who found significant interactions between genotypes and environments in response to yield. As evidence, in this study, the climate (rainfall) and soil properties in each location were different (Table 1). Therefore, more statistical tools and models such as principal component analysis (PCA) could be more beneficial to determine which component has a larger proportion of variation and then explain the separate effect of the two variables and their interaction as suggested by Esan *et al*. (2022) and Oladosu *et al*. (2017) [13].

The identification of megaenvironments helped to group locations that behaved similarly in terms of genotype response. Production of grain was in the same range at Tarna and Aderaoua but not at Bengou. However, genotypes produced fodder disproportionally in each location.

The "which-won-where" analysis is an approach that facilitates the visualization of the interaction patterns between genotypes and environments, thereby enabling the identification of crossover GEI, megaenvironment differentiation, and specific adaptation (Yan *et al* 2006) [11]. Sorghum genotypes located at the corners of the polygons in a "which-won-where" polygon were the outstanding genotypes in that environment. Similar interpretation was reported in various studies, including those by Linus *et al*. (2023) [15], Esan *et al*. (2023) [9], Karimizadeh *et al*. (2013) [8] and Yan *et al*. (2006) [11]. This result could be used for scaling up of some dual-purpose sorghum genotypes in specific location for instance G26 and G28 for Tarna and Aderaoua and G1 for Bengou.

According to Aremu *et al*. (2019) [14] the environment constitutes the primary source of diversity in plants. In this study, the identification of Aderaoua as ideal environment for dual purpose sorghum evaluation in southern zone of Niger might be explained by the pedoclimatic properties of this site having a clay texture and receiving in average 600 mm of annual rainfall, suitable for sorghum production, as explained by Dedi *et al*. (2021) [7].

The identification of the ideal sorghum genotypes in this study was performed according to previous findings from several authors (Yan and Kang (2003); Dedi *et al* (2021)) [10, 7] who described the ideal genotype as the highest yielding and the most stable, meaning the highest vector length and low G× E. Also, our results are consistent to Khan *et al*. (2021) who defined the genotype closer to the arrow head in the innermost circle is considered as the most ideal genotype.

In same line as the current study previous authors ((Kaplan *et al*., (2017); Yan and Tinker (2006); Esan *et al*. (2023)) [5, 11, 9] used the biplot graph to identify the best-performing genotypes adapted at the specific location or stable genotype for multiple locations and even determines the most representative locations megaenvironment) for a genotype. These results could serve as basis to propose some dual-purpose sorghum varieties for human consumption and animal feed.

Conclusion and Application of Findings

In this study the thirty dual purpose sorghum genotypes expressed different variations in their responses to the three test environments due to the effects of GEI and their different genetic makeup that control the grain and fodder yields. Two megaenvironments were identified for GY performance while for FY each location represented a megaenvironment. G28 and G26 were the highest grain yielding genotype while G10 produced the highest FY.

G20, G25, G4 and G29 were high yielding and the most stable across the environments for both GY and FY. These genotypes should reserve a particular attention by sorghum breeders to develop and disseminate superior dual purpose sorghum lines in the country. Aderaoua was the most discriminating and representative location and is therefore classified as the superior environment.

The genotypes that adapted well and uniquely to each environment were also identified. G1 and G3 recorded the highest yields in Bengou. G26 and G28 were the best in Tarna and Aderaoua while G10 outperformed in Aderaoua. These genotypes could also be used as parental lines for specific target area in breeding programs.

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