Original Research Article

Genotype x environment interaction and stability of gran yield of maize hybrids across Sudanian and Sudano-sahelian agro-ecological zones in Burkina Faso

ABSTRACT

Maize is an important staple crop for millions of people in Sub-Saharan Africa and particularly in Burkina Faso where it ranks first among cereals since 2020. However, available maize varieties are still low yielding, therefore, to enhance maize production, SEMAFORT, a seed company recently in Burkina Faso, introduced three-way hybrids for seed production and commercialization. The present investigation was performed to assess 128 hybrids in 2018 and assess twenty best hybrids for genotype-by-environment (G×E) interactions for grain yield in 2019. The study was conducted in one location (Farako-Ba) during the first year of evaluation using an alpha lattice design and in five locations during the second year using a randomized block design. The second year of the study was conducted in two different agro-ecological zones of Burkina Faso. The data were subjected to genotype and genotype by environment interaction (GGE) biplot analysis, using GenStat statistical package. The analysis revealed four mega-environments which discriminated the hybrids according to yield potential. In each mega-environment, the best yielding hybrids were identified and could be released for production in specific conditions. The most stable genotype in the high yielding and stable environment was SX8-121. It could be broadly cultivated across Sudan and Sudano-sahelian zones of Burkina Faso.

Keywords: *Biplot, Genotype by Environment Interaction, Grain Yield, Maize Hybrids, Stability, Burkina Faso*

1. INTRODUCTION

Maize (*Zea mays* L.) is the third most important crop in the world in terms of growing area, after wheat (*Triticum aestivum* L.) and rice (*Oryza sativa* L.) and it ranks first in Burkina Faso in terms of production (FOASTAT 2022) [1]. Maize originated in the southern region of Mexico, and then spread throughout America, Europe, Africa and Asia. This cereal is a cross-pollinated crop and belongs to the poaceae family. It is broadly grown all over the world due to its adaptability to wide range of environmental conditions (Bazniger and cooper, 2001) [2]. In fact, maize can be cultivated at 50˚ N- 40˚ S, from sea level (0) to 3,300 m above sea level (asl). In Burkina Faso, maize is grown in all the three agro ecological zones of the country, namely: Sudanian, Sudano-Sahelian and sahelian Zone with a rainfall ranging from 600 mm to 1200 mm.

In Sub-Saharan Africa, maize is a major staple crop for millions of people (Sibiya *et al*., 2013) [3] and plays an important role in enhancing food security in the sub-region due to its high yield potential, broad adaptability and relative ease of cultivation (Badu-Apraku *et al*., 2011) [4]. According to Edmeades (2013) [5], more than 160 million hectares of maize is produced on nearly 13 million hectares of land in West and Central Africa (WCA) under rain-fed conditions (FAOSTAT, 2014) [6]. The success of maize cultivation is linked to the application of inputs that maintain the environment and agricultural production. Among those inputs, are good soil cultivation, suitable maize varieties, adequate fertilization, insect and disease control.

Productive maize varieties are important for breeders and seed producers and distributors on the one hand, and farmers on the other hand (Babic *et al*., 2010) [7]. All of these participants in the maize value chain desire varieties that are adapted and be high yielding in a given location. Babic *et al*, (2010) [7] reported that farmers look for small genotype x year interaction while breeders, seed producers and distributors look for broadly adapted genotype that will be successful across wide area. The genotype by environment interaction (GEI) helps to identify stable genotypes that are well adapted to specific target areas (Abay and Bjørnstad, 2009) [8] which corresponds to the need of farmers. GEI through GGE plot analysis has the ability to show the which-won-where pattern and identify different mega-environments which are a group of sites that share the same and best genotypes. This approach can match the need of breeders, seed producers and distributors.

A maize seed production and distribution company, SEMAFORT, establish in Burkina Faso recently plans to register new hybrids adapted to the three different agro ecological zones of the country. The registration of new varieties in the national catalog requires evaluation of the performances of candidate hybrids in value for cultivation and use (VCU) trials. Such VCU trials are required by the Ministry of Agriculture, Animal and Halieutic Resources (MAARH) to identify useful genotypes under different cropping environments. These trials provide information about hybrid adaptation and performances across different environments in order to facilitate their registration and commercialization. The objectives of this study were to (i) evaluate grain yield performance across sites in Burkina Faso, (ii) assess the presence of GEI using GGE biplot analysis and (iii) identify high yielding and stable hybrids with potential success for commercialization.

2. MATERIEL AND METHODS

2.1. Study sites

The field studies were conducted in one location (Farako-Bâ) in 2018 and in five locations (Farako-Bâ, Kamboinse, Saria, Fada and Kouare) in 2019. The study sites are all located in different research stations of INERA during 2018 and 2019 rainy seasons. These sites are located in the Sudanian and sudano-sahelian agro ecological zones and were chosen based on an increasing rainfall gradient from North to South. Farako-Bâ is located in the Sudanian climatic zone. Saria and Kamboinse are located in the central part of the transition zone (Sudano-sahelian), Kouare is located in Eastern part of the transition zone and Di is located in north-western part of the transitional zone. Geographical coordinates about study sites are provided in Table 1.

Tableau 1: Sites geographical coordinates, rainfall and planting data

	Rainfall (mm)		Planting date		Longitude	Latitude	Altitude
Year Sites	2018	2019	2018	2019			
Farako-Ba	1382,6	1308,5	05/07	18/07	04°20’ E	11°06 N	405 m
Di		825,5		30/07	03°25’ E	13°10 N	258 m
Saria		800		14/07	2°09' E	12°16 N	300 m
Kamboinse		782,5		09/07	1°32’ E	12° 28’ N	296 m
Fada		681,5		13/07	0°17' E	11°56' N	400 m

2.2. Plant material

During the first-year trial, study materials were composed of 128 maize varieties including 120 hybrids from SEMAFORT seed company. The hybrids from SEMAFORT were coded as SX8-121 to SX8-240. Four 4 from Syngenta were coded as MAZ-20, MAZ-21, MAZ-23, MAZ-24. The remaining three (3) entries were local varieties (SR21, Bondofa and Komsaya) used as checks. During the second-year trial, materials were composed of the twenty (20) best hybrids from the first-year trail. SR21 is a composite variety resistant to maize streak viruses and originated from pop 21 of CIMMYT material. Bondofa is a white top-cross hybrid obtained from cross between EV8444 SR and SR22. Its yield ranges from 6,5 to 7 t/ha. Komsaya is a yellow top-cross hybrid obtained from cross between EV8444 SR and SR22 with yield ranging from 8 to 9 t/ha.

2.3. Experimental design

During rainy season 2018, an alpha lattice experimental design (4x32) with three (03) replications was used to evaluate 128 genotypes. Each replication was composed of four (4) blocks and each block contained 32 entries. In the second year (2019), the experimental design was a randomized complete bloc design with four (4) replications. Each replication contained 20 hybrids and each hybrid was planted on four (4) rows of five (5) m. Distance between rows was 0, 8 m and 0, 4 m between hills on each row with a total of 13 hills per row. Between three (3) and four (4) seeds were sown by hand in each hill, in 3-cm deep holes in all four locations. Seeds were sown only after receiving at least 20 mm rainfall.

2.4. Trial monitoring

Two weeks after sowing, plants were thinned to two plants per hill after hand weeding and then NPK (14-23-14) fertilizer was applied at a rate of 300 kg/ha. Fifteen days later, the trial was hand weeded again and urea (46%) fertilizer was applied at a rate of 100 kg/ha. Finally, urea was applied forty-five dap at a rate of 50 kg/ha and trial was hilled to avoid lodging.

2.5. Data collection and analysis

Data collected included germination rate (Ger), days to 50% tasseling (DT), days to 50% silking (DS), plant height (PH), ear height (EH), lodging (Lg), lodging at maturity (LgM), maturity time (Mat) and grain yield (GY). Grain yield was measured in tons per hectare adjusted to grain moisture content at 12%. Days to 50% tasseling and silking was recorded by counting the number of days from planting to when 50% of the plants in a plot emitted tassels or silks.

2.6. Data analysis

Descriptive and multivariate (principal component (PC) and Hierarchical Ascendant Classification (HAC) analysis were conducted using XLSTAT for data collected during first year evaluation.

Descriptive statistics helps to describe and understand the features of a specific data set and are focused on the measures of central tendency on one hand and the measures of variability on the other hand. Therefore, it was necessary to conduct a principal component analysis to reveal keys variable that would help to discriminate hybrids between them. From the principal components analysis, the variables associated with PC1 (Plant height and grain yield) and days to silking associated with PC2 and strongly correlated to days to tasseling and plant maturity time were used for hierarchical cluster analysis.

SAS 9.1 software was used for analysis of the effect of location, genotypes, and their interactions on response variables. Means were calculated from collected data and GGE biplot analyses in GenStat version 12 were performed to identify high yielding and suitable hybrids for grain yield across five different environments for second year evaluation.

3. RESULTS

3.1. Descriptive analysis of studied variables

In this study, measures of variability exhibited a wide dispersion of data around the mean for plant lodging at early stage (lg=6) and lodging at maturity (LgM=2) as shown by their large coefficients of variation (Lg=181.72 and LgM=203.51). These parameters showed a variation ranging from 0 % to 80% for plant lodging at early growth stage and 0% to 31% for lodging at maturity. Compared to lodging variables, the germination rate was higher (90%), but its variation among hybrids ranged from 33% to 100% with a weak coefficient of variation (11.13) which showed a strong significant difference between them. For plant height, the variation was considerable among hybrids for both ear height and plant height. The plant height ranged from 0.8 m to 3 m with a mean of 1.5 m while the ear height ranged from 0.3 m to 1.9 m with a mean of 0.8 m. Compared to other variables, low variation was observed for plant cycle traits (days to tasseling, days to silking and maturity time), but variation was significant allowing for distinction between hybrids. The Grain yield varied from 0.5 t/ha to 10.4 t/ha with a mean of 5.8t/ha. This variation is confirmed by the coefficient of variation (32.02) (Table 2).

Table 2: Descriptive analysis of studied variables

Variables	Min	Max	Me	CV	F
Ger (%)	33	100	90	11.13	1.7***
PH	0.8	3.0	1,5	16.14	3***
EH	03	1,9	0 ;8	26.05	2.6***
Lg	0	80	6	181.72	1.3ns
LgM	0	31	2	203.51	1.5**
DT	50	66	56	5.47	1.7***
DS	51	69	59	5.45	1,3*
Mat	101	110	105	2.22	2***
GY	0.5	10.4	5.8	32.02	2.7***

Ger: germination rate; DT: days to tasseling; DS: days to silking; PH: Plant height; EH: Ear height; Lg: lodging; LgM: Lodging at maturity; Mat: Maturity time; GY: Grain yield; ns: non significative at 5 %; *: significative difference at 5 %; **: highly significative difference at 5 %; ***: very highly significative at 5 %; F: Fisher probability at 5%; Max: maximum; Min: minimum; Me: mean; CV: coefficient of variation

3.2. Principal component analysis (PCA) of studied variables

The PCA demonstrated the relationship among variables and revealed that three (3) axes (PC1, PC2 and PC3) explained 61.45% of variability observed among hybrids. The first axis contributes to 31.15% of variability among hybrids, the second axis explains 17.56% of variability while the third explains 12.73% of the variability. The plant height and grain yield explained, respectively, 0.669 and 0.8 of axis 1 contribution while, the plant cycle parameters (days to tasseling (-0.743), days to silking (-0.8) and maturity time (-0.438) contribute negatively to the explanation of the axe. In the axe 2, only two parameters (ear height and days to tasseling) contributed slightly to the explanation of variability among hybrids. In the third axis, two parameters (lodging at early stage and lodging at maturity) contributed highly but negatively to the explanation of the axis (table 3). Figure 1 illustrates the contribution of different variables to the discrimination of hybrids. This figure combined with data in table 3 indicate that plant height (PH), grain yield (GY) in axis 1 with days to tasseling and days to silking are the mains components that significantly discriminate hybrids in this study.

Table 3: Eigen vectors of three principal components used to determine principal variables discriminating hybrids

Variables	PC1	PC2	PC3
Ger	**0.276**	0.045	0.231
PH	**0.669**	0.409	0.301
EH	0.436	**0.695**	0.188
Lg	0.238	0.486	**-0.500**
LgM	0.099	0.409	**-0.706**
GY	**0.800**	0.102	0.307
DT	**-0.743**	0.519	0.239
DS	**-0.800**	0.471	0.181
Mat	**-0.438**	0.147	0.187
Eigen value	2.804	1.581	1.146
Variance (%)	31.154	17.564	12.732
Cumulative	**31.154**	**48.718**	**61.450**

3.3. Hierarchical cluster analysis

A dendrogram constructed to group hybrids according to their mean revealed three major clusters. The cluster I was composed of short hybrids that emitted tassels and silks around 56 dap and 59 dap respectively. The hybrids within this cluster had low yield (2.5 t/ha) and were tolerant to lodging at early grow stage and also at maturity. The cluster II was composed of medium height hybrids that emitted tassels and silks around 55.7 dap and 58.8 dap respectively. These hybrids had a grain yield mean of around 6.2 t/ha and were lightly susceptible to lodging compared to cluster I hybrids. The last cluster (III) was composed of tall hybrids that emitted tassels and silks around 54.7 dap and 57.8 dap, respectively. Hybrids in this cluster had high yield potential (7.5 t/ha) and were tolerant to lodging (Figure 3).

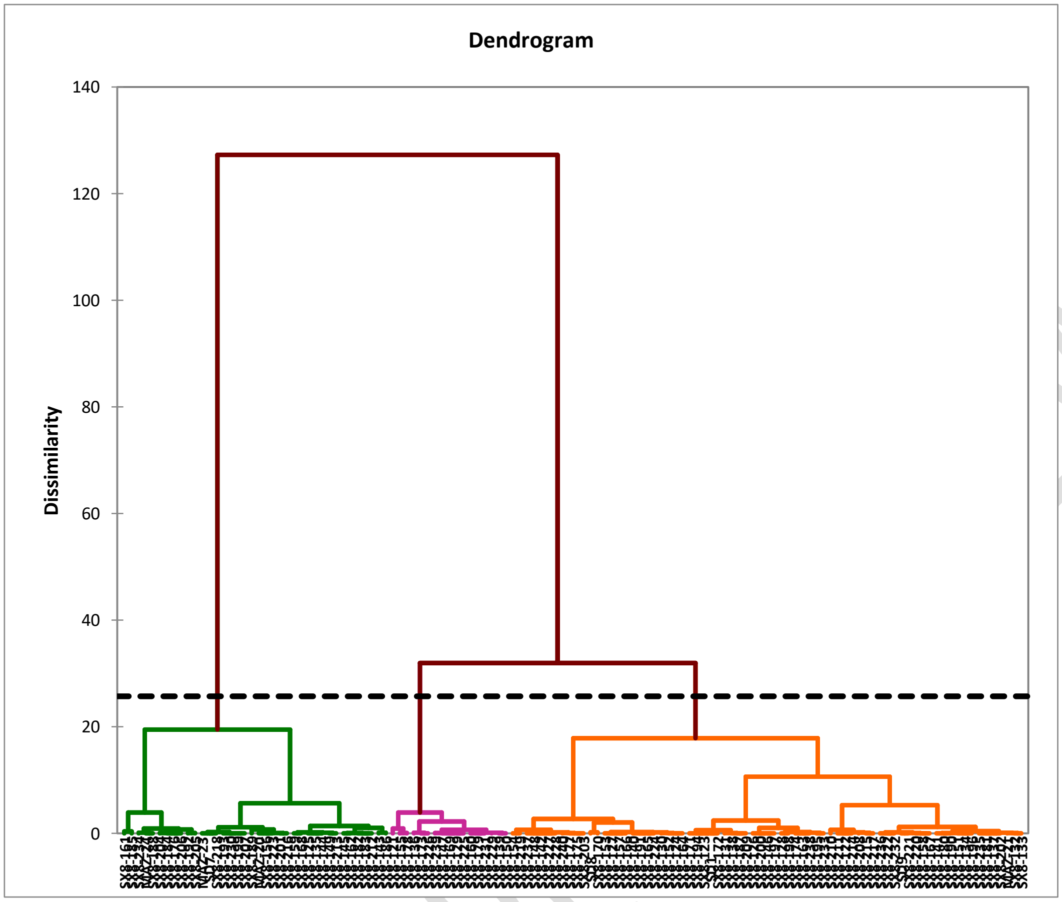

Figure 1: Dendrogram of the 128 maize hybrids revealed by cluster analysis based on plant height, days to tasseling and grain yield

3.4. Hybrids performance within cluster

Hybrids performance within clusters were obtained by comparison with checks (SR21, Bondofa and Komsaya). Best hybrids were considered to yield 25% more than checks. within the cluster I, four hybrids [SX8-186=5.9 t/ha, SX8-213=5.5 t/ha, SX8-149=5.5 t/ha and SX8-143=5.3 t/ha) yielded 43%, 33%, 32% and 29% more than SR21 and 40%, 31%, 30% and 26% more than Bondofa (Figure 3). In the cluster II, most hybrids (SX8-198, SX8-233, SX8-128, SX8-195, SX8-210, SX8-238, SX8-171, SX8-163, SX8-131, SX8-172, SX8-174, SD1, SX8-194, SX8-123, SX8-126, SX8-138, SX8-211, SX8-209, SX8-146, SX8-200, SX8-122, SX8-187 and SX8-197) were better than tested checks (SR1 21, Bondofa and Komsaya) except SX8-151 (6.4 t/ha) and MAZ-21 (6.4 t/ha) whose yields were lower (Figure 3). In the cluster III, yield ranged from 6.4 to 8.7 t/ha and all hybrids performed better than the three checks in the trial. Overall, tested hybrids yield ranged from 4 to 8.7 t/ha within which interval is found the potential yield of SR21 (5.10 t/ha) and Bondofa (6.5 t/ha), but still below the potential yield of Komsaya (8-9 t/ha). For multi-location trial needs, the best hybrids were chosen in the cluster II and cluster III and their yield ranged from 7.3 to 8.7 t/ha. (Table 4).

Table 4: Characteristic of cluster obtained from hierarchical analysis

Variables	Cluster I	Cluster II	Cluster III	Pr > F	Significant
Ger	87.3% a	90.2% b	92.1% b	0.023	Yes
PH	1.3 a	1.5 b	1.8 c	0.000	Yes
EH	0.7 a	0.8 b	0.9 c	0.000	Yes
Lg	4.7% a	6.2% a	6.3% a	0.498	No
LgM	2.2% a	2% a	2.2% a	0.915	No
GY	4.2 a	6.2 b	7.5 c	0.000	Yes
DT	56.3b	55.7 ab	54.7 a	0.028	Yes
DS	59.9 b	58.8 a	57.8 a	0.001	Yes
Mat	105.7 b	105.2 ab	104.7 a	0.078	No

3.5. Analysis of variance across environments

The results of the combined ANOVA across environments for the 20 hybrids showed that genotype main effect (G), environment main effect (E) and G × E were all highly significant ($p < 0.0001$) for grain yield (Table 5). Only replication effect was not significant at 1%.

Table 5: Combined analysis of variance for grain yield of 20 hybrids across five environments

Source of Variables	DF	SS	MS	F value	Pr > F
Env	4	276.336158	276.336158	140.25	<.0001
Rep	3	5.864633	5.864633	2.98	0.0319
Genotype	19	9.606059	9.606059	4.88	<.0001
Env*Genotype	76	9.390329	9.390329	4.77	<.0001
Error	297	585.168949	1.970266		
Mean	6.732381				
CV	20.84941				
R^2	0.775306				

Env = Environment; Rep= Replication; CV = Coefficient of variation; SS=Sum of Squares; MS= Mean Square; Pr = probability

3.6. Twenty best hybrids across five environments.

Yield performance of these 20 hybrids across five environments is presented in Table 6. The overall mean across the five (5) environments for the 20 selected hybrids ranged from 5.774 t ha−1 to 8.692 t ha−1. The highest yielding hybrid across environments was obtained at Kamboinsé by SX8-121 with a yield of

12.975 t ha−1 and the lowest yield was obtained at Saria by SX8-233 with a yield of 2.203 t ha−1. Overall, the hybrids yielded better at Kamboinsé than remaining sites. The bold and underlined mean yields are for those hybrids pointed out for higher or lower yield in the comments.

Table 6: Mean grain yield (t/ha) of 20 hybrids across five environments in 2019

Geno	Environnent					
	Di	Fada	Farako-Ba	Kamboinse	Saria	Mean
SEMA-1	11.000	5.725	7.012	4.250	3.103	6.218
SEMA-2	8.225	5.400	7.309	9.350	3.920	6.841
SEMA-3	5.350	6.600	8.855	8.675	4.618	6.820
SEMA-4	8.125	6.800	6.930	10.100	4.198	7.230
SEMA-5	6.675	6.425	8.566	9.300	4.520	7.097
SX8-121	9.975	6.350	9.395	**12.975**	4.765	**8.692**
SX8-128	10.650	5.775	4.734	10.050	2.973	6.836
SX8-129	7.075	6.250	8.059	7.925	4.968	6.855
SX8-131	8.900	4.850	6.488	5.525	3.940	5.941
SX8-136	6.925	5.975	8.266	9.925	4.375	7.093
SX8-155	8.775	5.575	5.813	5.150	3.555	**5.774**
SX8-173	4.150	5.675	7.145	9.500	4.745	6.243
SX8-178	6.500	6.175	6.516	8.325	4.828	6.469
SX8-195	5.925	6.325	8.426	7.675	3.355	6.341
SX8-198	10.350	6.100	6.746	12.900	3.410	7.901
SX8-225	7.775	7.100	7.855	7.575	4.150	6.891
SX8-226	9.725	6.225	7.168	8.250	2.813	6.836
SX8-231	6.350	5.975	6.230	9.850	3.615	6.404
SX8-233	9.475	4.250	9.188	4.450	**2.203**	5.913
SX8-239	6.225	5.575	6.574	9.125	3.553	6.210
Mean	7.907	5.956	7.364	8.544	3.880	

Geno= genotypes; Env= environment

3.7. Identification of high yielding and stable genotypes across sites

Figure 2 displays the average environment coordination (AEC) view of the GGE biplot showing stability and performance ranking of the hybrids across five environments. Stability as well as high performance of the tested hybrids were revealed. This was achieved by drawing an AEC on the genotype-focused biplot. The arrow headed line points to higher performing hybrids across environments while the crossing lines point to greater stability (poor variability) according to the direction. So, the biplot revealed that high yielding hybrids were SX8-121, SEMA-4, SX8-198, SEMA-5 and SEMA-3. On the contrary, SX8-233, SEMA-1, SX8-131 and SX8-155 exhibited poorest yields. Regarding hybrid stability across the testing environments, hybrids SX8-121, SEMA-2, SX8-131 and SX8-239 showed high stability. On the other hand, the unstable hybrids were SX8-233, SEMA-3, SX8-198 and SX8-128. Both high yield and high stability were displayed by hybrid SX8-121. In GGE biplot, the best genotype is also the one with large PC1 scores (high mean yield) and near zero PC2 scores (high stability). The analysis revealed that PC1 and PC2 accounted respectively for 44.91% and 21.79% of the total GGE (genotype and genotype by environment interaction) and a total of 66.70%, and through figure 2, it is clearly shown that SX8-121 is the genotype with the high PC1 score with PC2 score near zero (among the stable one).

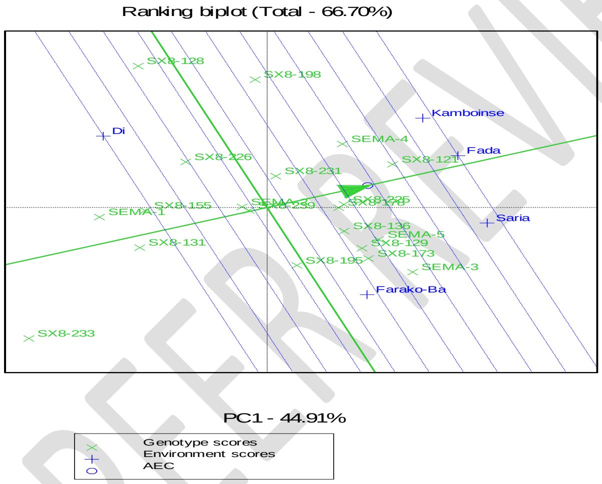

Figure 2: Biplot of the average environment coordination (AEC) view showing mean performance and stability of 20 hybrids

3.8. Identification of mega environments

GGE biplot has the ability to show the which-won-where pattern and mega environment differentiation from the genotype by environment interaction and reveal a precise summary of the G × E pattern on a multi environment trial. Mega environment is a group of environments sharing almost the same and best genotypes. The polygon in Figure 3 is formed by the connection of hybrids that are fur away from the biplot origin such that all the remaining genotypes are contained in the polygon. Consequently, five sectors were drawn with the best or poorest hybrids (SX8-128, SX8-198, SX8-121, SEMA-3 and SX8-233) located on the vertices of the polygon, and where environments fell into four sectors representing mega-environments. The environments were grouped as follows: three environments (Kamboinse, Fada and Di) appeared in their own sectors individually and two environments (Farako-Ba and Saria) appeared in one sector. The vertex genotype for the mega-environment composed of two environments (Farako-Ba and Saria) was the genotype SEMA-3. The remaining vertex genotypes (SX8-128, SX8-198, SX8-121 and SX8-233) were displayed out of all the mega-environments and consequently did not fit in any of them, but genotypes SEMA-4 and SX8-121 were respectively close to Fada and Kamboinse environments.

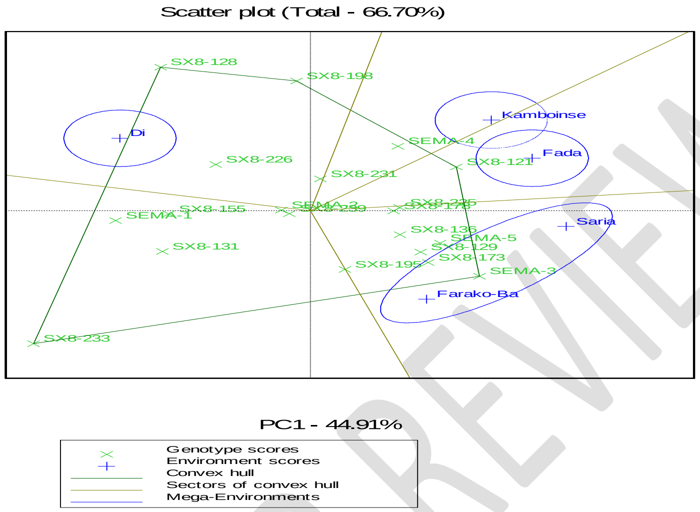

Figure 3: polygon view of the GGE-biplot showing the mega-environment based on grain yield of 20 hybrids

3.9. Identification of ideal environment and genotypes

The GGE biplot is useful to identify ideal environment through PC1 and PC2 scores. The ideal testing locations or environments is determined by small (absolute) PC2 score and a large PC1 score. Small PC2 score refers to the representativeness of all environments while large PC1 score indicate power to discriminate genotypes in terms of genotype main effect. In addition to PC score, environment that are located in the center of the concentric circles are the ideal (stable). Consequently, Fada was the most ideal environment as identified from GGE biplot (Figure 4). The AMMI analysis also indicates that environment of Fada had the best IPCA2 value of 0.55 and Figure 4 clearly shows that environment of Fada is located almost on first concentric circles. Among testing environment, the nearest environment of Fada is Kamboinse and Saria which are located respectively on the third and the fourth concentric cercles.

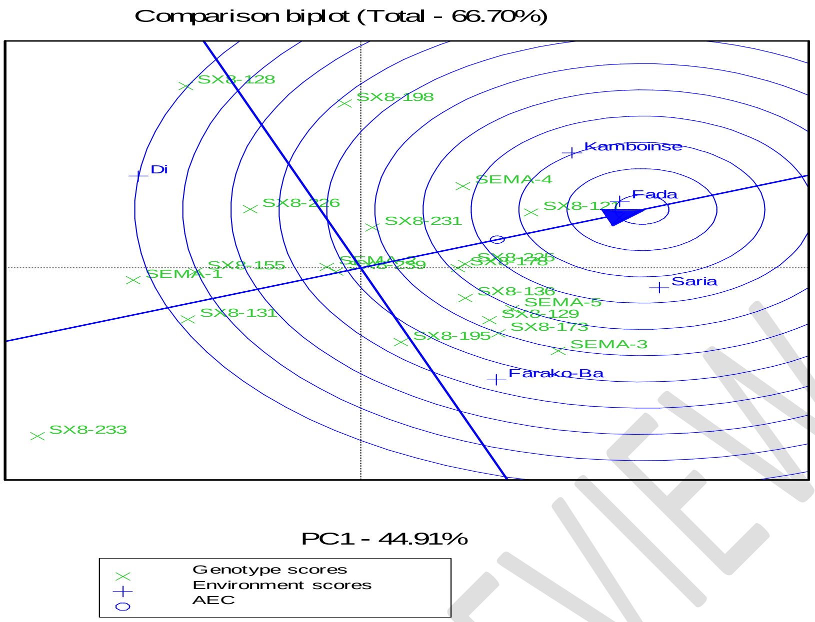

Figure 4: Comparison view of 20 hybrids with ideal environment

The study revealed an important environmental variation with three environments which had positive IPCA1 score [Fada (0.009), Saria (0.236) and Kamboinse (2.205)] and the two others with negative IPCA1 score [Farako-Ba (-0.231) and Di (-2.219)]. The AMMI analysis also indicated that genotype's reaction was different according to environmental variation and the best AMMI model allows for selection of the best hybrids that suit specific environments. The four best hybrids selected by AMMI model for each environment are presented in Table 7. Accordingly, hybrids SX8-121 performed well in two stable environments (Fada and Saria) and ranked as second and fourth best performing hybrids at Kamboinse and Di. SEMA-3 was selected as the best performing hybrid at Farako-Ba and ranked as second and third high yielding hybrid at Saria and Fada. SX8-198 performed well at Kamboinse in a stable condition and ranked fourth at Di in an unstable farming condition. Some hybrids such as SEMA-1, SX8-225, SEMA-4, SX8-129, SX8-136, SX8-128 performed specifically to a given environment (Table 7).

Table 7: Environments ranked on IPCA scores including the first four recommended genotypes for each environment based on AMMI the estimates

NE	Environment	Mean	IPCA1 score	1st	2nd	3rd	4th
1	Di	7.911	-2.2199	SEMA-1	SX8-128	SX8-198	SX8-121
2	Farako-Ba	7.364	-0.2306	SEMA-3	SX8-129	SEMA-5	SX8-225
3	Fada	5.959	0.0090	SX8-121	SEMA-5	SEMA-3	SX8-136
4	Saria	3.880	0.2361	SX8-121	SEMA-3	SEMA-5	SX8-129
5	Kamboinse	8.548	2.2055	SX8-198	SX8-121	SX8-128	SEMA-4

4. DISCUSSION

The wide dispersal of data around the mean along with quite large value of coefficient of variation for most of studied traits including germination rate, lodging parameters, plant cycle and grain yield indicated that hybrids reacted differently from each other. Concerning the germination rate, the results obtain in our study were a bit beyond result reported by Nyembo *et al,* (2014) [9] whose found a germination rate ranging from 22% à 66%. In our case, the rate was higher and increased 100% for some hybrids. For plant cycle, some hybrids had days to tasseling and silking around 50 days after planting, meaning they could reach phycological maturity at 85 days after planting and could be considered as early maturing varieties. However, some hybrids were recorded with days to tasseling and silking around 66 to 69 days after planting, meaning they could reach physiological maturity around 100 days after planting and could be considered as intermediate maturing group. For the remaining agro-morphological parameters which are routinely used to characterize local maize varieties, improved varieties including hybrids, studies conducted by authors such as Moussa *et al,* (2018) [10] and Zoma (2010) [11] revealed important variation.

The principal components result identified the main variables responsible for high discrimination among hybrids. PC1 explained most of the variation observed in the germination (Ger), plant height (PH), plant cycle parameters such as days to tasseling, silking and maturity (DT, DS & Mat) and the grain yield (GY) whereas PC2 was linked to morphological traits related to ear height (EH) and PC3 was linked to lodging parameters (Lg and LgM). This indicates that major variables allowing differentiation among genotypes were associated with PC1 (31,1%) and within variables associated to PC1, grain yield (0,8) and plant cycle parameter [DT (-0,74) DS (-0,8)] contributed more to the variation. The PC2 and PC3 explained less variation among tested hybrids and accounted respectively for 17,56 and 12,7 for the observed variation.

The results suggest that focus should be directed toward yield and plant cycle parameters while selecting directly for performance and adaptability for Sudan and Sudano-Sahelian areas for Burkina Faso. Vaisi and Golparvar (2013) [12], in their investigation to improve grain yield and seed weight in oats, found that selection of panicle and grain number per panicle was relevant. Ibrahim et al. (2014) [13] found that grain yield exhibited strong and positive phenotypic and genotypic correlation with its components.

The result of principal components analysis gave a hierarchical classification by using variables associated with the major components (PC1). The 128 hybrids were grouped into different clusters according to plant height, plant cycle and grain yield. Low yielding, short hybrids with intermediate maturity time characterized the first cluster. The cluster II was composed of medium yield, medium height hybrids with intermediate maturity while the cluster III was composed of tall hybrids, quite early with the highest yield potential. Concerning grain yield comparison with checks within clusters, the majority of hybrids performed better than checks in all clusters. In fact, SR21 is an opened pollinated variety while Bondofa and Komsaya are top crosses hybrids compared to tested hybrids which are three-way hybrids. Three-ways hybrids tended to be uniform and more productive than other type of hybrids and opened pollinated varieties (Le Conte, 1950) [14] and according to Dzido (1984) [15] only classic hybrids are the more interesting in terms of yield.

The combined ANOVA analysis showed significant effects for genotypes, environments and genotypes by environment interaction. This indicated that environments were highly variable and revealed also that hybrids react differently according to environment. The highly significant mean squares of environments for grain yield revealed that the environments were diverse, which is in agreement with the previous results reported by Gezahegn *et al*, (2017) [16] on Napier grass. According to the cumulative rainfall data, the tested locations were divided into three; Farako-Ba representing the wettest location following by Di, Saria and Kamboinse with medium rainfall level and lastly, Fada representing the less wet site. In fact, Farako-Ba is located in the Sudanian climatic zone with high rainfall level while Di, Saria, Kamboinse and Fada are located in Sudano-sahelian with lower rainfall. Geographical coordinates (longitude, latitude and altitude) also displayed diversity within studied sites. The high significance of genotypes by environment (sites) interaction (< 0.001) for grain yield indicated that genotypes interacted differently across environments.

This result justifies the need to identify the most stable and productive hybrids across environments and also to identify suitable hybrids for specific environments. According to Yan and Tinker (2005) [17], genotypes displaying both high yield and stability across environments are considered as ideal genotypes. Consequently, from this investigation, hybrids SX8-121 exhibited high mean yield and high stability. High yield was identified by using the single-arrowed line which is the AEC abscissa pointing to higher mean yield across environments while high stability was defined using the crossing lines in either direction (the shorter was the crossing line for a genotype, the higher was the stability of that genotype). This indicates that SX8-121 was broadly adapted, had high consistent ranking across environments and may therefore be cultivated across sudan and Sudano-Sahelian agro-climatic zone of the country. In this particular case, similar studies reported that broad adaptation is important than narrow one [Kayaga, 2017 [18]; Gauch and Zobel, (1997) [19]].

The GGE biplot has also the ability to show the which-won-where pattern and mega environment differentiation from the genotype by environment interaction and revealed a precise summary of the G × E pattern on a multi environment trial. According to Yan and Rajcan (2002) [20], mega environment is a group of environments that shared almost the same and best genotypes. In this study, the GGE biplot analysis of grain yield response and stability of 20 hybrids showed that PC1explained 44.91% of total variation while PC2 explained 21.79% and together, the two axes accounted for 66.70%. This implies that the biplot of PC1 and PC2 adequately approximated the environment centered data. The biplot for 20 hybrids was divided into five sectors and four mega-environments within which different genotypes could be selected and deployed to similar environments as reported by Yan and Tinker (2006) [21]. The relationship among environments and which won were pattern showed that Saria and Farako-Ba were similar while Fada, Kamboinse and Di were different from first mega-environment (Saria and Farako-Ba) and also from each other.

Fada was the high yielding and stable environment while Kamboinse was the most discriminating environment among tested hybrids (high yielding environment) but less stable than Fada. In opposite Di was the low yielding and unstable environment. Saria and Farako-Ba were in the same environment with medium yield hybrids. The result clearly exhibited different mega-environment which were associated to either high, medium or low yielding hybrids. This is in agreement with explanation provided by Badu-

Apraku *et al*, (2011) [3] about mega-environment. In fact, in 2011, Badu-Apraku *et al,* (2011) [3] reported that the ability of a test environment to represent the mega-environment is referred to as the representativeness.

As mentioned earlier, an ideal test environment is the one representative of other environments and the most discriminating for genotypes (Tonk *et al*., 2011 [22]; Yan and Kang, 2003 [23]). From the PC scores, the most discriminating test location was Kamboinse because of its large PC1 score but was less representative due to their large angles with the AEC abscissa as compared to Fada that seemed to be the most representative location because of its small PC 2 and its position which was almost in the first concentric cercles. The result is in agreement with statement reported by Yan and Rajcan (2002) [20] whom confirmed that ideal testing locations or environments is determined by small (absolute) PC2 score while large PC1 score indicate power to discriminate genotypes in terms of genotype main effect.

After identifying the best genotype (SX8-121) and the ideal environment (Fada), it was important to identify other superior hybrids suited to specific environments. The four best hybrids selected by AMMI model for each environment were: SEMA-1, SX8-128, SX8-198 and SX8-121 were the first four high yielding in the unstable environment of Di; SEMA-3, SX8-129, SEMA-5 and SX8-225 were the four best at Farako-Ba (medium yield and unstable environment; SX8-121, SEMA-5, SEMA-3 and SX8-136 were the four best in the ideal environment (Fada); SX8-121, SEMA-3, SEMA-5 and SX8-129 were the four best hybrids in the low yielding and stable environment of Saria; SX8-198, SX8-121, SX8-128 and SEMA-4 were identified as the best performing hybrids in high yielding and stable environment of Kamboinse.

5. CONCLUSION

This study revealed that genotypes, environments and genotype × environment interaction were significant for grain yield. The hybrids therefore performed differently with respect to yield in each of the five test environments and their relative performance varied from one environment to another. The AMMI biplot showed large variability among the environments and among tested hybrids for yields. The GGE biplot discriminated the study area into four mega-environments which seemed to be linked to the yielding potential of tested hybrids. High yielding hybrids were identified for each mega-environment and could be proposed for release for production. These hybrids are SEMA-1 for mega-environment of Di, which is related to the low yielding environment and SEMA-3 for the of Farako-Ba (medium yield and unstable environment),

SX8-121 for Fada (stable and high yielding environment) and Saria (low yielding and stable environment) and lastly SX8-198 was identified as the best performing hybrid in high yielding and stable environment of Kamboinse. However, the most outstanding hybrid was SX8-121 which had the potential for production across environments and be released and commercialized. The highest yielding hybrid per environment could be recommended for the specific environments where they performed well. The results of this study should be confirmed through further evaluation of hybrids at different locations of the Bimodal Humid Forest Zone during both minor and major seasons for several years.

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