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Seed yield stability and analysis of genotype x environment interaction of sesame genotypes in central south of Niger

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1 ABSTRACT

The experiment was conducted in the central south of Niger in 2015 and 2016 under rainfed conditions across ten environments. The objective of the study was to evaluate the adaptability and stability of ten sesame genotypes across locations and years. The experimental design was a completely randomized block design with 5 replicates in each environment. Genotypes grain yields (averaged across environments) ranged from 722 kg ha^{-1} for 38-1-7 to 1095 kg ha^{-1} for SN403 and Environment grain yields (averaged across genotypes) ranged from 473 kg ha^{-1} at Bandé 2016 (Ban16) to 1414 kg ha^{-1} at Gounaka 2015 (Gou15). The combined ANOVA for grain yield showed significant effects of the genotypes, environments and genotype x environment interaction. According to the Genotype x Environment interaction biplot (GGE bi-plot), genotypes 10 (SN403), 6 (SN-01-06) and 1 (38-1-7) were highly stable while the unstable genotype was 4 (HB168). Furthermore, the Genotype main effects and GGE bi-plot showed Gou16 as the most discriminating and representative environment. Three different mega-environments (ME) were identified, the first ME containing Gou15, Haw15, Maï15and Dad15 with DS01 as wining genotype; the second ME concern Maï16, Band16, Haw16, Band15 and Gou16 with GK01 as the best genotype and the third ME encompassing Dad16 with HB168 as wining genotype.

2 INTRODUCTION

Sesame (*Sesamum indicum* L.) (Photo 1) is an ancient oil seed crop known and used by man. Nowadays, world demand for its seeds is increasing owing to its good quality oil (50 %), protein (25 %) and for content of antioxidants (Arslan *et al.* 2007; Uzun *et al.* 2008; Erbas *et al.* 2009; Boureima *et al.* 2016). Beside these nutritional benefits, sesame cropping has many agricultural advantages: it grows well in tropical to temperate climates, it can grow on stored soil moisture without the need for rainfall or irrigation, and be grown in pure stands with low input, or else in mixed stands with diverse crops. Despite its multifaceted importance, less attention is dedicated to the crop by research centres so that genetic and breeding improvement efforts in sesame have been limited making the results of such efforts slow to emerge. The productivity of the crop is very low (434 kg ha^{-1}) in the studied area (central south of Niger) compared with the potential of the crop (2 000 kg ha^{-1}) and the world average yields, specially countries like Mozambique which produce up to 1500 kg ha^{-1} (Buss 2007). The main driving forces of this less productivity are the lake of adapted cultivars in the growing areas and the large intra and inter-seasons climate variability.

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Photo 1: Sesame plant at reproductive phase

Furthermore, the crop is known to be highly variable when grown across locations (Boureima *et al.* 2016; Baraki *et al.* 2016). When genotypes are tested for performance at several environments by crop producers and breeders, the rankings usually differ as specified difference in environment may produce different effect on specific genotypes. Such inconsistent performance of genotypes across environments is called genotype x environment interaction (GEI) (Asfaw *et al.* 2009). According to Samonte *et al.* (2005), GEI is commonly observed as the differential ranking of cultivars yields among locations or years at the same locations and is expected when environments are highly diverse. Consequently, in selection of superior genotypes, it is not only the average performance that is important, but also the magnitude of the interaction matters (Gauch and Zobel 1997; Ebdon and Gauch 2002). The presence and importance of GEI has long been recognized in the testing and recommendation of plant varieties, and no sensible producer would grow a plant variety based on information from a single environment (Yan and Tinker 2005). Therefore, plant breeders conduct multi-environment trial (MET) primarily to identify the superior cultivar for a target region and secondarily to determine if the target region can be subdivided into different mega-environments (Yan *et al.* 2000) allowing to select for specific adaptation. Sesame is a short day plant and sensitive to photoperiod, moisture stress and different management practices and its yield and yield components are not stable and vary widely over different environments. Hence, this experiment was undertaken to identify stable and high yielding genotype(s) and to recommend best sesame genotype(s) for the different sesame growing areas to boost sesame production in the central south of Niger. When GEI is present and significant, several statistical methods had been developed to analyze and identify stable and high yielding genotypes. Additive main effect and multiplicative interaction (AMMI) is important to analyze multi-environment trials (METs) data and it interprets the effect of the genotype (G) and environments (E) as additive effects and the GEI as a multiplicative component (which are sources of variation) and submits it to principal component analysis (Zobel *et al.* 1988). Another multivariate stability measure called Genotype main effects and Genotype x Environment interaction (GGE) effects is important to identify mega-environments, the "which-won-where" pattern, and to evaluate genotypes and test environments (Yan *et al.* 2007).

3 MATERIALS AND METHODS

3.1 Plant material and area description:

Ten sesame genotypes were used in this study. They were SN-01-04; SN-01-06; SN 103; SN 203; SN 303; SN 403; HB 168; GK 01; DS 01; and 38-1-7. The trials were conducted during two main cropping seasons (2015 and 2016) at five locations: Maiguizawa (13°58'N, 8°8' E), Dadin Sarki (13°44'N, 7°56'E), Gounaka (13°40'N, 8°1'E), Hawandawaki (13°21'N, 8°14'E) and Bandé (13° 10' N, 8° 53' E). A

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randomized complete block design with five replications was used in all locations and years. The plot had 6 rows of 5 m length, 60 cm between rows and 20 cm between plants within the row. Sowing was done by hand drilling in rows and two weeks after sowing, plants were thinned to two per hole giving a total density of 166 667 plants per hectare. Management practices such as insect, pest, disease and weed control were uniformly applied at all locations per years as per the recommendation for sesame growing. A composite N-P-K fertilizer (15-15-15) was applied at a rate of 80 kg ha^{-1} before sowing and 50 kg ha^{-1} of Urea before flowering at each location. In both seasons, data were recorded for plant height (PH), height to the first capsule on the main stem (PHFC), number of branches per plant (NB), number of capsules per plant (NCP) and seed yield. For seed yield evaluation, the four central rows were harvested. Prior to harvesting, the first two plants at the borders of each row were discarded. Before sowing, soil samples were taken at each location at 0-40 cm depth to determine some chemicals characteristics (Table 1).

Table 1. Chemical properties of soils of the locations.

Location	Depth (cm)	N *mg/kg*	P *mg/kg*	CEC *cmol⁺/kg*	K *mg/kg*	pH *UI*
Dadin Sarki	0-20	57.6	2.77	4	632 .3	6.9
	20-40	32.8	1.62	4.1	738.0	6.5
Gounaka	0-20	33.4	2.08	3.8	388.5	6.6
	20-40	21.6	traces	3.6	495.0	6.3
Hawan Dawaki	0-20	36.0	0.97	3.3	276.8	6.0
	20-40	28.2	traces	3.6	324.0	6.0
Maiguizawa	0-20	41.9	1.16	3.7	477.8	6.3
	20-40	26.9	traces	1.3	504.0	6.2
Bandé	0-20	110.7	3.79	3.7	326.3	6.1
	20-40	59.0	1.48	3.6	277.5	6.1

3.2 Statistical analysis: A combined analysis of variance was performed from the mean data of all environments to detect the presence of GEI and to partition the variation due to genotype, environment and genotype x environment interaction. In the analysis, each combination between the five location and 2 years was considered as an environment, making a total of 10 environments. The additive main effects and multiplicative interaction (AMMI) model analysis of grain yield was performed separately as a unique multivariate model using GEA-R (Version 4.0, Cimmyt, Mexico). Moreover, AMMI biplot and sites regression (SREG) model analyses were carried out. A GGE biplot was also executed using GGEBiplotGUI, an R package. This methodology uses a bi-plot to show the factors (G and GE) that are important in genotype evaluation and that are the sources of variation in GEI analysis of Multi-environment trial (MET) data (Yan 2001). The GGE biplot was used to visually analyze the results of SREG analysis of MET data (Samonte *et al.* 2005). This methodology uses a biplot to show the two factors (G plus GE) that are important in cultivar evaluation and that are also the source of variation in SREG model analysis (Yan *et al.* 2001). In this study, GGE biplot was used to compare the performance of different sesame genotypes at an environment, compare the genotype performance in different environments, identify and select genotypes that are consistent and highly productive across different environments.

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4 RESULTS AND DISCUSSION

4.1 Combined ANOVA: The combined analysis of variance for all agronomics traits studied revealed that there were significant variation among the genotypes, environments (year, location, year x location) and genotype by environment interaction (Genotype x Location, Genotype x Year, and Genotype x Location x Year) (Table 2). These significant variations confirm that the difference of the traits was due to both the main and interaction effects (Baraki *et al.* 2016). The ANOVA also revealed that the response of the genotypes was unstable across years at the same location and across years and locations for a given genotype. Table 2 showed that the variation from year to year at the same location was 36-fold greater than that of one location to another. This trend confirms the existence of a Genotype X Environment Interaction (GEI) and indicates greater influence of temporal variation on seed yield performance of sesame genotypes. Combined ANOVA determines if GEI is a significant source of variation or not and estimates it, but does not provide insight into the patterns of genotypes or environments that give rise to the interaction (Samonte *et al.* 2005).

Table 2. Mean squares for different agronomical traits recorded on sesame genotypes across locations and years

Source of variation	DF	PHFC (cm)	P H(cm)	NB	NCP	FL50	Yield (kg ha^{-1})
Rep	4	11.9	343.2	1.7	209.9	9.6	74313
Gen	9	3912.5**	2593.8**	55.7**	1025.6**	423.5**	460923**
Loc	4	1015.6**	4574.1**	82.9**	4335.3**	1628.6**	460923**
Year	1	866.7**	25634.1**	96.0**	48282.3**	139.4**	16797738**
Gen*loc	36	92.6	241.5	4.4**	415.1**	5.5*	82203
Gen*Year	9	530.6**	928.7**	17.6**	951.9**	19.5	176074**
Loc*Year	4	18345.7**	7233.5**	10.7**	5130.6**	889.1**	2573782**
Gen*Loc*Year	36	143.8	214.9	2.8**	202.4	5.7**	84015*
Residual	368	122.2	294.3	2.8	236.3	3.3	58462

PHFC- Plant height to the first capsule, PH- plant height, NB-number of branches, NCP-number of capsules per plant, FL50- date of 50 % flowering

4.2 AMMI model analysis: The ANOVA from the AMMI model for grain yield also detected significant variation ($p<0.001$) for both the main and interaction effects for genotypes (G) and environments (E) (location/year).The environment effect explained 81.09 % of the G+E+GE variation followed by the GEI (12.30 %) and the genotypes effects (6.60 %) (Table 3). Environment grain yields (averaged across genotypes) ranged from 473 kg ha^{-1} at Bandé 2016 (Ban16) to 1414 kg ha^{-1} at Gounaka 2015 (Gou15). Genotypes grain yields (averaged across environments) ranged from 722 kg ha^{-1} for 38-1-7 to 1095 kg ha^{-1} for SN403. The AMMI model analysis had partitioned the GEI into the first two significant interaction principal component axis (IPCAs) with contributions of IPCA1 (29.27%) and IPCA2 (26.84 %) to GE sum of squares (SS). Together, they accounted for 56.11 % of GE interaction SS. The third IPCA explained 16.98 % of GE SS but this was not significant. Gauch and Zobel (1996) reported that in normal multi-environmental trials, E accounts for 80 % of

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the total yield variation, while G and GE each account for about 10 %.

Table 3. Analysis of variance for the AMMI model of the genotypes in the test environments for grain yield (kg ha^{-1})

Source	DF		SS	Explained (%)	MS	P value
ENV	9		47022544	81.09	5224727.11	0
GEN	9		3828752.29	6.60	425416.92	0
ENV*GEN	81		7134629.07	12.30	88081.84	0.00644
IPCA1	17		1801101.73	29.27	105947.16	0.02506
IPCA2	15		1651344.7	26.84	110089.65	0.02359
IPCA3	13		1044611.04	16.98	80354.69	0.16897
Residuals	372		21794196.1		58586.55	

4.3 GGE biplot analysis

4.3.1 Similarity/dissimilarity among environments and mega-environment classification: A GGE biplot based on environment-focused singular value partitioning is most appropriate for visualizing the similarity/dissimilarity among environments (Yan and Tinker 2005). The distance between two environments determined by both the length of the vectors and the angle between them, measures their dissimilarities. The angles between genotype, environment, or between genotype and environment vectors determine the nature of GEI. The interaction is positive for acute angles, zero for right angles, and negative for obtuse angles (Kandus *et al.* 2010). Accordingly, in figure 1, two groups of environments are apparent: Gou15, Haw15, Maï15, Dad15, Ban15, Maï16, Ban16, Haw16 and Gou16 vs Dad16. Environments within each group are similar with small angles but the two groups appear to be independent of each other (close to a right or obtuse angle and therefore a near-zero or negative correlation). Therefore, Figure 1 suggests two different mega-environments. Mega-environment 1 consists of Gou15, Haw15, Maï15, Dad15, Ban15, Maï16, Ban16, Haw16 and Gou16, and mega-environment 2 consists of Dad16. The near right angle between the two mega-environments implies that cultivar selection in one mega-environment is largely independent of performance in the other. Therefore, different selection strategies are required for each mega-environment.

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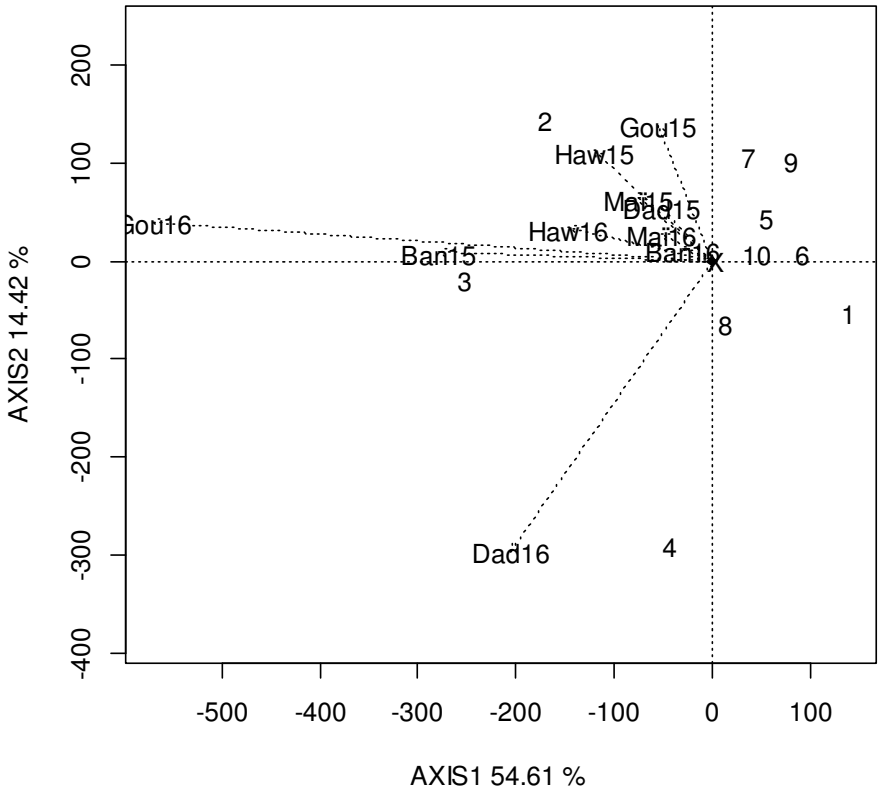

Figure 1. Environment focusing scaled vector view of GGE biplot. Gou-Gounaka, Haw-Hawandawaki, Maï-Maïguizaoua, Dad-Dadin Sarki, Ban-Bandé, 15-2015, 16-2016, 1 to 10: genotypes numbers

4.3.2 Identification of best genotypes for each environment: The figure 2 is based on a "Tester-centred (G+ GE)" table, without any scaling and it is row metric preserving. The polygon is formed by connecting the markers of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. Figure 2 also contains a set of lines perpendicular to each side of the polygon. These perpendicular lines divide the biplot into several sectors. The winning genotype for each sector is the one located at the respective vertex. Genotypes located at the vertices of the polygon reveal the best or the poorest in one or other environment (Frutos *et al.* 2013). There are 5 sectors with cultivars 2 (DS01), 3 (GK01), 4 (HB168), 1 (38-1-7) and 9 (SN303) as the corner or vertex cultivars. Environments Gou15, Haw15, Maï15and Dad15 fell in the sector in which 'DS01' was the vertex cultivar meaning that 'DS01' is the best genotype for these environments. The environments Maï16, Band16, Haw16, Band15 and Gou16 fell in the sector where genotype 3 (GK01) is the vertex cultivar, meaning that GK01 is the best cultivar for these 5 environments. Genotype 4 (HB168) was the highest yielding genotype at the mega-environment that consisted of Dad16. No environment fell into sectors with 38-1-7 and SN303 as the vertices, indicating that these genotypes were low yielding at all

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environments. Multilocation trials conducted across years are necessary to verify the pattern of locations grouped into mega-environments and genotypes identified as highest grain yielders for each mega-environment (Yan *et al.*, 2000; Yan and Rajcan 2002). The figure 3 is the average-environment coordination (AEC) view of the GGE biplot, which has the following interpretation (Yan and Tinker 2006):

• The single-arrowed line is the AEC abscissa (or AEA) and points to higher mean yield across environments. Thus, the genotype 3 (GK01) had the highest mean yield, followed by genotype 2 (DS01), genotype 4 (HB168), etc., whereas genotype 1 (38-1-7) had the lowest mean seed yield.

• The AEC ordinate passes the plot origin and is perpendicular to the AEC abscissa and points to greater variability (poorer stability) in either direction. Thus, genotype 4 (HB168) was highly unstable, whereas genotypes 10 (SN403), 6 (SN-01-06) and 1 (38-1-7) were highly stable. However, these later genotypes are low yielding in all environments.

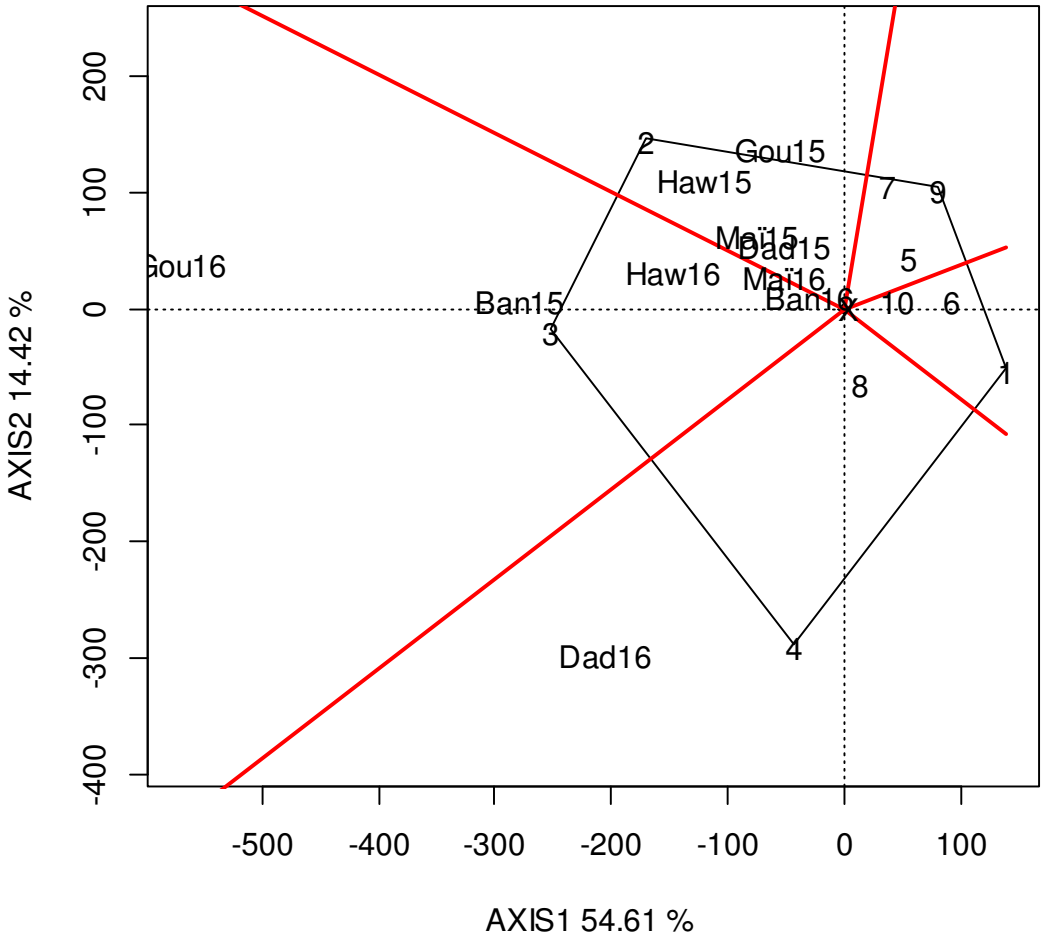

Figure 2. Genotype plus genotype x environment (GGE) biplot showing the mega-environments and their respective highest yielding genotypes. Gou-Gounaka, Haw-Hawandawaki, Maï-Maïguizaoua, Dad-Dadin Sarki, Ban-Bandé, 15-2015, 16-2016, 1 to 10: genotypes numbers

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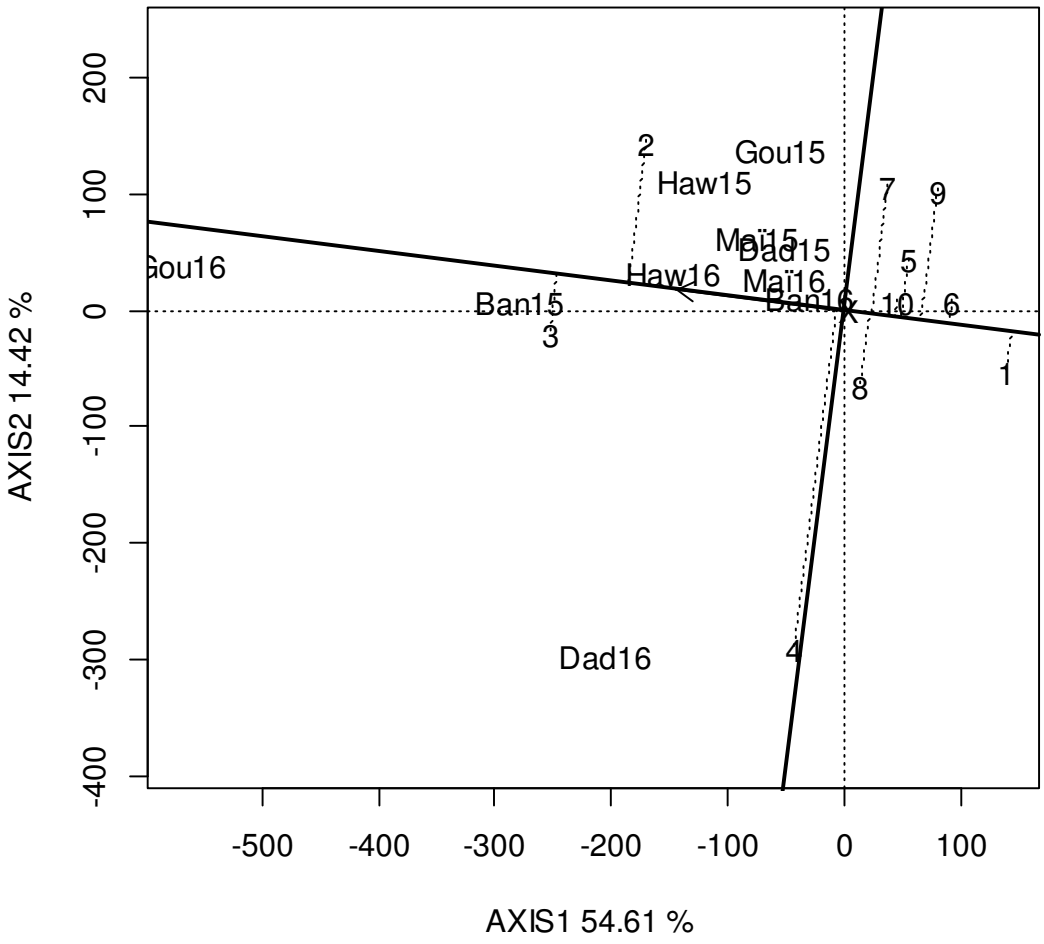

Figure 3: Genotype plus genotype x environment (GGE) biplot showing the yielding ability and stability of ten sesame genotypes. Gou-Gounaka, Haw-Hawandawaki, Maï-Maïguizaoua, Dad-Dadin Sarki, Ban-Bandé, 15-2015, 16-2016, 1 to 10: genotypes numbers.

In Figure 4, the arrow is where an ideal cultivar should be. Its projection on the AEA was designed to be equal to the longest vector of all cultivars, and its projection on the AEC ordinate was obviously zero, meaning that it is absolutely stable (Frutos *et al.* 2013). Therefore, genotypes located closer to the ideal genotype are more desirable than others. Thus, genotype 3 (GK01) was more desirable than genotype 2 (DS01). Figure 5 shows the representativeness and discriminating ability of environments and is based on a "Tester- centred (G + GE)" table, without any scaling and it is column metric preserving (GH biplot). The vector length, that is the absolute distance between the marker of an environment and the plot origin, is a measure of the discriminating ability: as the longer vector, the discrimination of the environment increases (Frutos *et al.* 2013). Therefore, among the ten environments studied, Gou16 and Dad16 were most informative while Ban16 and Maï16 were least discriminating. The average environment (represented by the small circle at the end of

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the arrow) has the average coordinates of all test environments. AEA is the line that passes through the average environment and the biplot origin. A test environment that has a smaller angle with the AEA is more representative of other test environments (Yan and Tinker 2006). Thus, Gou16 is most representative whereas Dad16 and Gou15 are least representative.

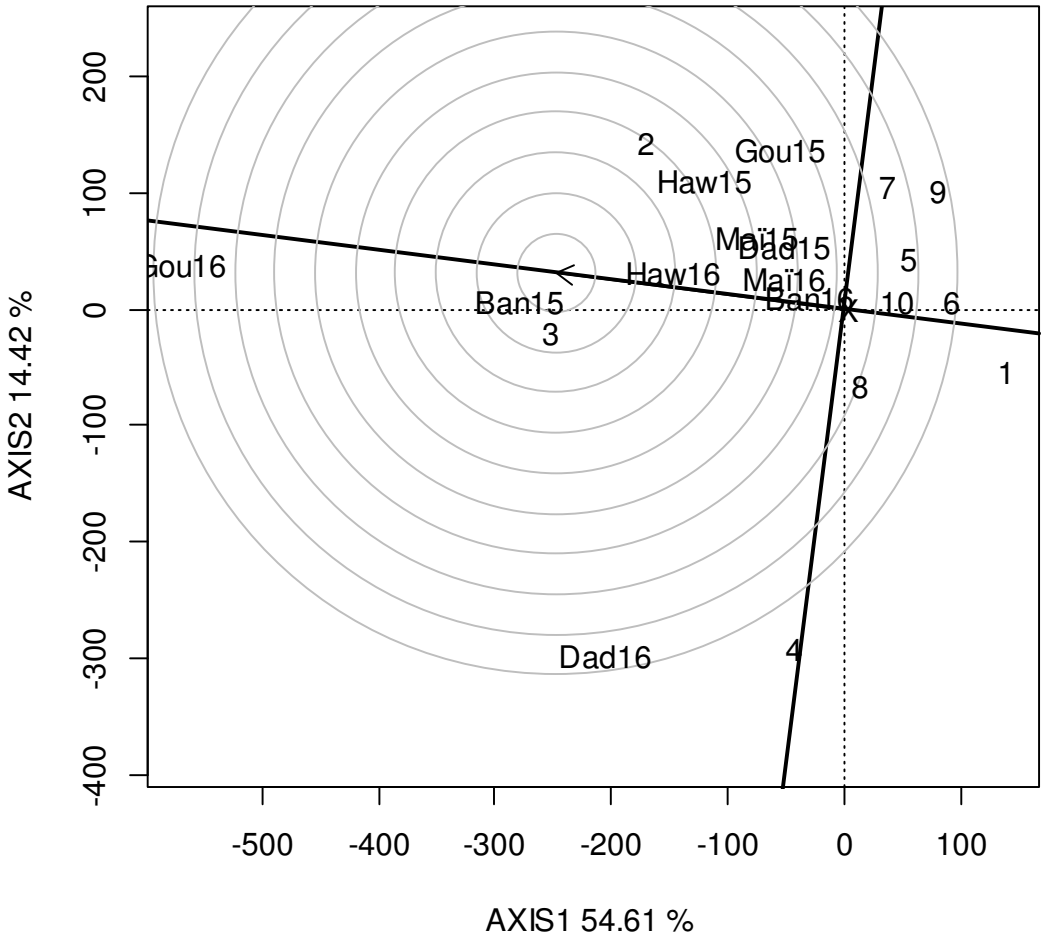

Figure 4. Ranking genotypes based on both mean performance and stability. Gou-Gounaka, Haw-Hawandawaki, Maï-Maïguizaoua, Dad-Dadin Sarki, Ban-Bandé, 15-2015, 16-2016, 1 to 10: genotypes numbers

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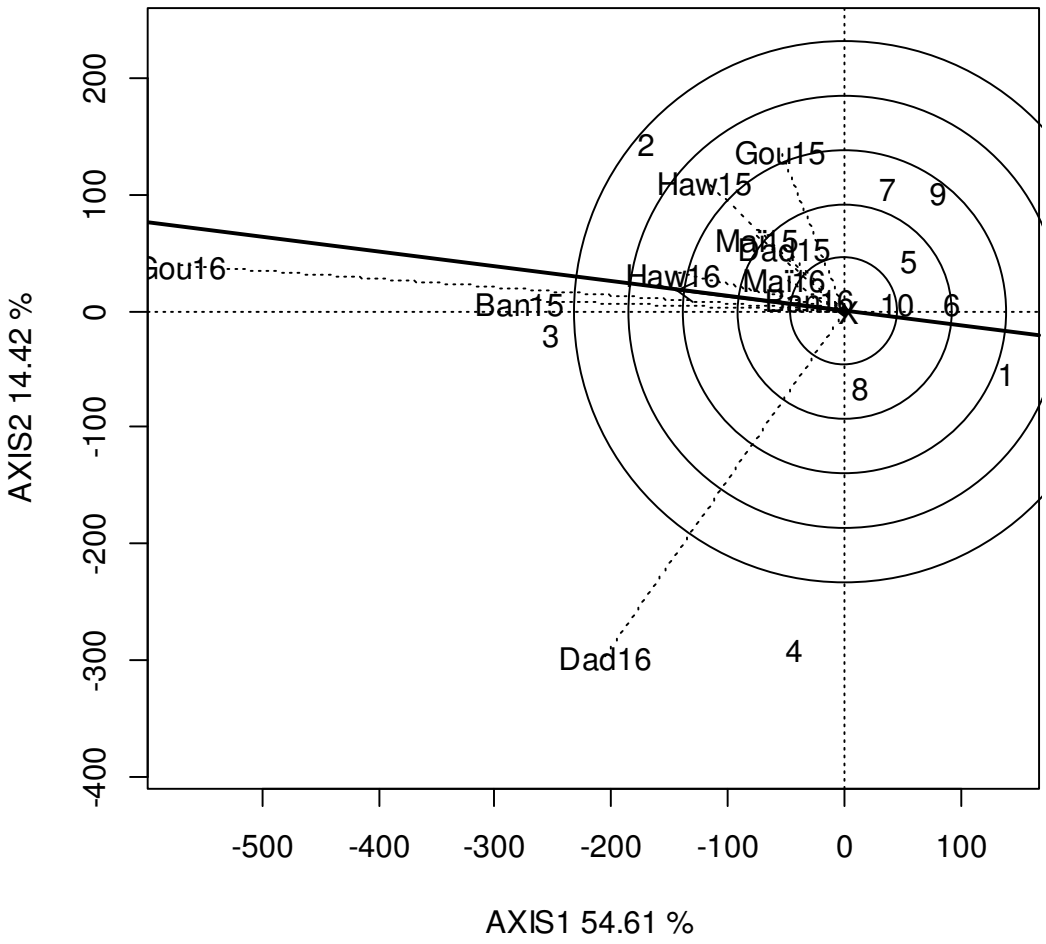

Figure 5. Discriminativeness against representativeness of test environments. Gou-Gounaka, Haw-Hawandawaki, Maï-Maïguizaoua, Dad-Dadin Sarki, Ban-Bandé, 15-2015, 16-2016, 1 to 10: genotypes numbers

The ideal test environment should be most discriminating (informative) and most representative of the target environment. Figure 6 defines an ideal test environment, which is the centre of the concentric circles. Here Gou16 represents the most discriminating environment.

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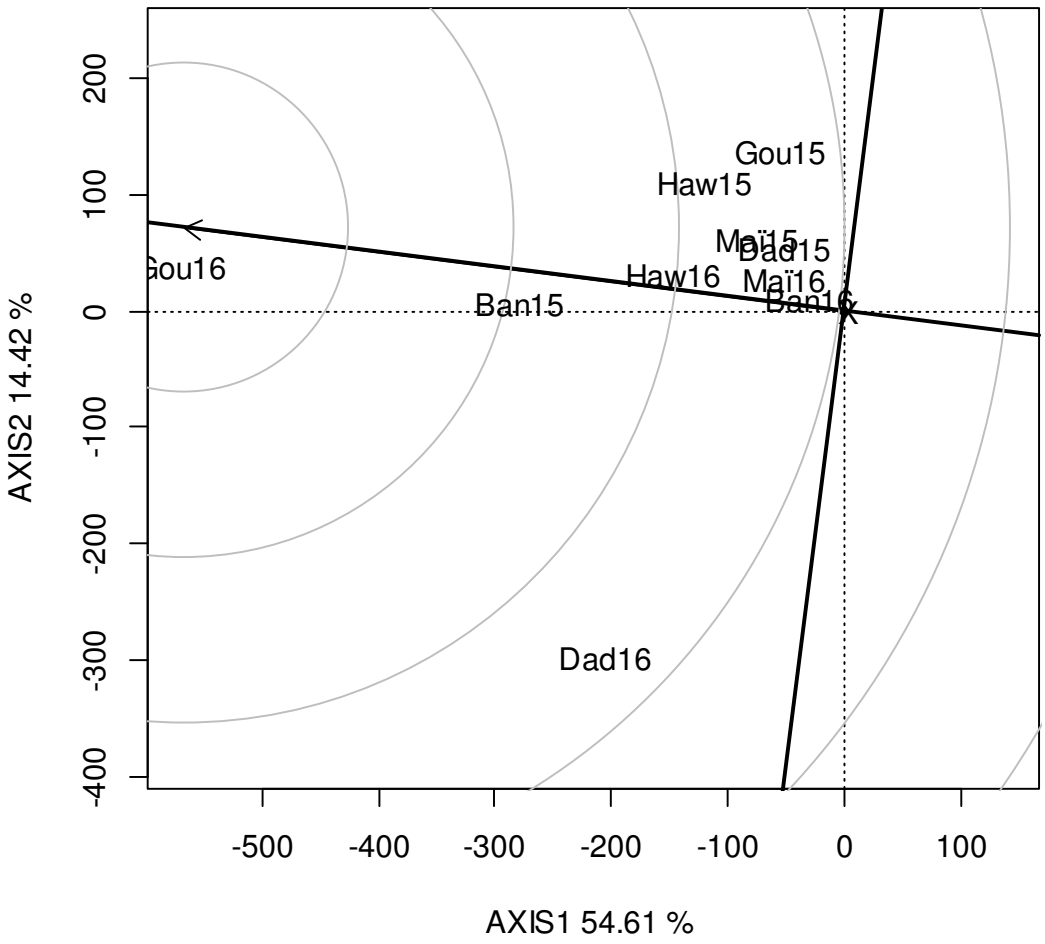

Figure 6. Ranking environments based on discriminating ability and representativeness. Gou-Gounaka, Haw-Hawandawaki, Maï-Maïguizaoua, Dad-Dadin Sarki, Ban-Bandé, 15-2015, 16-2016.

5 CONCLUSION

In this study, combined ANOVA showed significant differences among sesame genotypes for grain yield across environments. The results also showed that the environments were highly variable and that the temporal (year) variation was more profound than spatial (location) variation in exerting effects on genotypes seed yield performance. GGE-biplot enabled the identification of the best (Gou16) and the less discriminating (Ban16 and Maï16) environments for sesame genotypes evaluation for seed yield performance. The genotype GK01 was the best cultivar for 5 environments (Maï16, Band16, Haw16, Band15 and Gou16) while HB168 was the highest yielding genotype at the mega-environment that consisted of Dad16. The genotypes 38-1-7 and SN303 were low yielding at all environments.

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