



Genotype \times environment interaction and stability analysis for seed yield and yield components in sesame (*Sesamum indicum* L.) in Benin Republic using AMMI, GGE biplot and MTSI

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ABSTRACT

Increasing production requires the development of high yielding cultivars adapted to various environments. Multi-environment trials (MET) remains the best approach to assess the performance of accessions across environments. The objective of this study was to select the best performing and stable accessions of sesame across different environments in Benin Republic. Nineteen sesame accessions were evaluated across eight environments using a randomized complete block design with four replicates. The accessions were evaluated for three traits: days to 50% flowering (D50F), thousand-seed weight (TSW), and seed yield (SY) during 2020 growing season. The stable and top-performing accessions across environments were determined using AMMI (Additive main effects and multiplicative interaction), GGE (Genotype main effect and genotype \times environment interaction), and MTSI (Multi-trait stability index). AMMI analysis of variance showed a significant difference across environments for the three traits. The accessions were affected by environmental conditions for the three traits. The broad-sense heritability estimates were high (>0.60) for all the traits, indicating the improvement is achievable through selection. AMMI1 and AMMI2 biplots identified G10 and G13 as high seed yielding accessions adapted to environments E1, E2. The GGE biplot showed two mega-environments for TSW and three mega-environments for D50F and SY. For SY, G11 and G13 were the best accessions in the first mega-environment, G10 the best accession in the second mega-environment; G3 and G8 were the best accessions in the third mega-environment. AMMI and GGE analyses identified G10, G5, G12 as high seed yielding and stable accessions across environments. GGE biplot revealed that E1

Abbreviations: AMMI, Additive main effects and multiplicative interaction; Df, Degree of freedom; D50F, Days to 50% flowering; E, Environment; EnvMean, mean per environment; G, Genotypes; G \times E, Genotypes by environment interactions; GGE, Genotype main effect and genotype \times environment interaction; MET, Multi-environment trials; MS, Mean square; MTSI, Multi-trait stability index; PC, Principal Component; SS, sum of squares; SY, seed yield; TAHMO, Trans-African Hydro-Meteorological Observatory; TSW, Thousand-seed weight.

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and E2 were the most suitable environments for multi-location trials based on their discriminating ability and representativeness. MTSI indicated G10, G13, G19 as promising germplasm to be recommended for breeding program.

1. Introduction

Sesame (*Sesamum indicum* L.) is an important oil seed crop mainly grown for its edible seeds used to make cake, flour, sauce, confectionery and oil [1,2]. The seed contains 50–60% of oil which is a good source of antioxidants such as sesamol, sesamol and tocopherol. The oil seed has also cosmetic, pharmaceutical, and nutraceutical uses [3]. Due to its importance, sesame is widely cultivated with an increasing production volume around the world followed by high competition on the market among producing countries for domestic and international trade [4]. Worldwide, sesame production was estimated to 6,549,725 tons in 2019. In Africa, the total production was estimated to 1,332,369 tons in 2009 compared to 3,998,148 tons in 2019 [5]. Such increase in sesame production in Africa by more than 50% in one decade shows the growing interest for sesame cultivation. However, the overall observed trends in the increase in sesame production volume in Africa is due to efforts of few countries. In Burkina-Faso, sesame is the second most exported crop after cotton [6]. The main importers of sesame from Burkina-Faso are Japan, Switzerland, Egypt, the Netherlands, France, Germany, China, Spain, United Kingdom, and Dubai [7]. Benin is lagging behind in terms of sesame production (10,000 tons) compared to neighboring countries like Burkina-Faso (374,703 tons) and Nigeria (480,000 tons) [5]. The highest sesame yields in Africa were recorded in Cameroon (1293.6 kg ha⁻¹) and Egypt (1248.9 kg ha⁻¹) [8]. The yields recorded in Nigeria and Burkina-Faso in 2018 were 1063 kg ha⁻¹ and 603 kg ha⁻¹ [4,8] while low yields (449.91 kg ha⁻¹) were reported in Benin [9]. Based on sesame performance in neighboring countries with similar agroecological conditions and the growing interest for the crop, there is a great potential in sesame to become priority cash crop in Benin. Tapping into the potential of the crop requires the availability of the high-performing varieties across environments [10]. However, there has not been any effort in introducing and disseminating top performing and market preferred sesame varieties in Benin yet. The few research conducted on the crop to date focused on socio-economic incidences analysis and genetic diversity analysis of the crop [9,11,12]. The extension of sesame production into various agroecological zones in Benin can help boost its production.

The fact that crop yield and other quantitative traits are influenced by environmental factors represents a challenge for sesame production upscaling. In addition, the variation of yield across accessions under the same or different conditions are attributed to the effect of the genotype by environment interaction ($G \times E$) [13]. To successfully select the best accessions for a given environment, it is essential to carry out multi-environment trials (MET). MET are appropriate to evaluate the performance of cultivars across locations and years, predict the yield as well as examine the stability of high-performing accessions for target location [14]. Selection of well performing accessions in MET requires the assessment of genotypebyenvironment interactions accessions which interpretation can be complex [15,16]. The main statistical methods that have been proposed to improve MET accuracy were the Additive main effects and multiplicative interaction (AMMI) developed by Gauch et al. [17] and the Genotype main effect and genotype \times environment interaction (GGE biplot) developed by Gabriel et al. [18] and Kempton [19]. The two methods are complementary and were used simultaneously by several authors to analyze MET data [20]. The AMMI model includes both additive (ANOVA) and multiplicative (PCA) components and account for the underlying interaction patterns [21,22]. The GGE biplot, more recent than AMMI model, shows simultaneously mean performance and stability, optimized environments for specific accessions, and help to identify mega-environments [23]. The two methods are used for both multi-year and single year trials. A single year trial may have limited value because of the year-to-year variation but Yan [24]asserted that biplot analysis of single year multi-location trial data is worthwhile.

Our present study targets selection of accessions based on key traits such as days to 50% flowering, thousand-seed weight and seed yield. However, breeding based on gathering multiple traits together in one new genotype requires appropriate statistical tool such as Smith-Hazel index, multi-trait genotype-ideotype distance index, multi-trait index and based on ideotype design, and multi-trait stability index (MTSI) [25].

In this paper, we evaluated the stability and adaptability of nineteen sesame accessions across eight environments in Benin Republic to select the best performing and stable accessions for sesame cultivars development program.

Specifically, we:

- (a) assessed the interaction between accessions and environments for days to 50% flowering (D50F), thousand-seed weight (TSW) and seed yield (SY) using AMMI and GGE biplot models;
- (b) selected the best performing accessions across environments for targeted traits through multi-trait stability index.

We hypothesized that:

- (a) all the sesame accessions used are performant and stable across environments for D50F, TSW, SY and,
- (b) the best performing accessions identified through multi-trait stability index give seed yield beyond 500 kg ha⁻¹ with maximum 50% flowering date of 30 days.

2. Materials and methods

2.1. Experimental sites

The experiments were carried out during 2020 cropping season from April to December in eight environments namely Abomey-Calavi (E1), Sékou (E2), Tchaourou (E3), Djougou (E4), Boukoumbé (E5), Matéri (E6), Kérou (E7) and Kandi (E8), distributed across different agroecological zones of Benin. Abomey-Calavi (E1) and Sékou (E2) are located in Bar land zone, Tchaourou (E3) in the Central Cotton Zone, Djougou (E4), Boukoumbé (E5), Matéri (E6) are located in the Northern Cotton Zone, Kérou (E7) and Kandi (E8) are located in the Western Atacora Zone (Fig. S1). The Bar land zone is located in the southern part of the country where sesame cultivation is currently marginal. The northern cotton zone and the Western Atacora Zone are located in the northern part of the country in sesame production zone. The climatic conditions during the trials and characteristics of different environments were presented in Supplementary Table S1.

2.2. Plant materials, experimental design and field management

Nineteen (19) accessions including thirteen local accessions and six introduced lines from China (Supplementary Table S2) were evaluated. The local accessions were assembled during a germplasm collection mission in the northern part of Benin in 2019 and stored in the Genebank of the Genetics, Biotechnology and Seed Sciences Unit (GBioS) of the University of Abomey-Calavi (Republic of Benin). The introduced varieties were obtained from the Oil Crops Research Institute of Agricultural Sciences of China.

A randomized complete block design with four replications was used in each location. Each replication consisted of nineteen plots. On each plot, twenty-six plants were arranged in two ridges of thirteen plants with a distance of 0.3 m between plants and 0.5 m between ridges. A distance of 1.5 m separates each replication. Weeds were controlled manually. No fertilizer was applied and chemical treatment with insecticides and fungicides was done when needed.

2.3. Data collection

Data were recorded on five central plants of each ridge making a total of ten plants per plot except for D50F where the data were collected considering the total plant per plot. Collected data were on traits such as days to 50% flowering (D50F), thousand-seed weight (TSW) and seed yield (SY).

To get the thousand-seed weight values, the coefficient of variation of 8–10 samples of 100 seeds were calculated. Thousand-seed weight value was approved when the coefficient was less than 5%. The value obtained was multiplied by 10 to obtain the thousand-seed weight [1].

The seed yield was calculated using the following formula (Eq. 1) by Nadeem et al. [26].

$$SY = \frac{\text{Seed weight per plot (kg)}}{\text{Plot size (m}^2\text{)}} * 10000 \quad 1$$

SY: Seed yield (kg ha⁻¹)

2.4. Statistical analysis

2.4.1. Descriptive statistics and variance components estimation

The descriptive statistics (means, coefficient of variation) for each trait and per accession were computed per environment and across environments. Combined analysis of variance across environments was performed to assess trait variation across and within environments using the following statistical method (Eq. 2):

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{kj} + \varepsilon_{ijk} \quad 2$$

Where Y_{ijk} = observed value of genotype i in block k of environment (location) j , μ = grand mean, G_i = effect of genotype i , E_j = environment or location effect, GE_{ij} = the interaction effect of genotype i with environment j , B_{kj} = the effect of block k in location (environment) j , ε_{ijk} = error (residual) effect of genotype i in block k of environment j .

Genetic parameters were estimated and broad-sense heritability H^2 was computed following the formula (Eq. 3) used by Alvarado et al. [27].

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{ge}^2}{e} + \frac{\sigma_e^2}{r}} \quad 3$$

σ_g^2 = genotypic variance, σ_{ge}^2 = genotype by environment interaction variance, σ_e^2 = variance due to error, e = the number of environments, r = number of replicates.

2.4.2. AMMI model and GGE biplot analysis

The AMMI model combining the standard analysis of variance with principal component analysis suggested by Zobel et al. [28] was

used to determine the effect of genotype (G), environment (E) and G × E effects on the traits.

The following model (Eq. 4) was used:

$$Y_{ger} = \mu + \gamma_g + \beta_e + \sum_{n=1}^N p_n \gamma_{gn} z_{en} + \theta_{ge} + \varepsilon_{ger} \quad 4$$

where Y_{ger} = trait value of genotype g in environment e for replicate r , μ = grand mean, γ_g = genotype mean deviations, β_e = environment mean deviations, p_n = eigenvalue of principal components analysis (PCA) axis n , γ_{gn} and z_{en} = genotype and environment PCA scores for PCA axis n , θ_{ge} = residual, ε_{ger} = difference between the Y_{ger} mean and the single observation for replicate r .

The GGE biplot, was used to detect the genotype by environment interaction pattern, classification in mega-environment (which-won-where pattern), selection of genotypes based on stability and mean yield, and characterization of testing environments based on their discriminating ability and representativeness.

The following model (Eq. 5) for GGE biplot as described by Yan [24] was used to display the G and GE interaction patterns in the data in a biplot:

$$Y_{ij} - \bar{Y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad 5$$

where: Y_{ij} = average value of the trait of genotype i in the environment j , \bar{Y}_j = average of the trait over all accessions in environment j environment's mean effect; λ_1, λ_2 = singular values associated with PC1 and PC2; ξ_{i1}, ξ_{i2} = eigen values of genotype i for PC1 and PC2 respectively, η_{j1} and η_{j2} = eigen values of environment j for PC1 and PC2 respectively, ε_{ij} = residual associated with genotype i in environment j .

2.4.3. Multi-trait stability index

The multi-trait stability index (MTSI) was determined following the formula (Eq. 6) used by Olivoto et al. [29] to select the stable accessions for the studied traits. The accessions with lowest MTSI were considered as superior accessions [25].

$$MTSI_i = \left[\sum_{j=1}^f (F_{ij} - F_j)^2 \right]^{0.5} \quad 6$$

MTSI_{*i*} = multi-trait stability index for the i -th genotype, F_{ij} = j -th score of the i -th genotype, F_j = j -th score of ideal genotypes. The different analysis were performed with package "metan" in software R 4.0.5 RCore Team [30].

3. Results

3.1. Mean values and combined analysis of variance for days to 50% flowering, thousand-seed weight and seed yield across environments

The average values of the nineteen (19) accessions for the days to 50% flowering (D50F), thousand-seeds weight (TSW) and seed yield (SY) were computed per environment and across environments (Supplementary Table S3). Overall, D50F ranged from 31 to 92.25 days. The early and late flowering accessions were recorded in Abomey-Calavi (E1). In this environment, the accessions G14, G17, G18, G19 (Chinese accessions) reached 50% of flowering 31 days after sowing (DAS) whereas G7 reached 50% flowering 92.25 DAS. The TSW values ranged from 1.62 g to 3.55 g. The lowest value was recorded in Boukoumbé (E5) for the accession G3 while the highest value was recorded in Abomey-Calavi (E1) for the accession G12. The minimum and maximum average values for thousand-seed weight across environments were 2.38 (recorded in Kérou (E7)) and 2.98 g (recorded in Abomey-Calavi (E1)).

Overall, average SY varied between 92.90 kg ha⁻¹ and 2275.09 kg ha⁻¹. G18 (92.90 kg. ha⁻¹) in Matéri and G10 (2275.09 kg ha⁻¹) in Sékou had the lowest and highest yields respectively. The highest average yields were recorded in Sékou (E2, 1270.56 kg ha⁻¹) and Abomey-Calavi (E1, 1223.59 kg ha⁻¹) whereas the lowest yields were recorded in Materi (E6, 161.20 kg ha⁻¹) and Tchaourou (E3, 212.13 kg ha⁻¹).

There was a high significant variation ($p < 0.001$) across environments, accessions and G × E for all the traits (Supplementary Table S4)

Table 1

Genetic parameters for the variables D50F, TSW, SY.

Genetic parameters	Code	D50F	TSW	SY
Genotypic variance	σ_g^2	0.49	0.70	0.22
Phenotypic variance	σ_{phen}^2	0.55	0.74	0.30
Genotype × Environment	σ_{ge}^2	0.05	0.001	0.04
Broad-sense heritability	h_g^2	0.88	0.94	0.74
Accuracy of selection	AS	0.93	0.96	0.86

D50F: Days to 50% flowering, TSW: Thousand-seed weight, SY: Seed yield

Table 2
AMMI model for D50F, TSW, and SY.

SOV	Days to 50% flowering (D50F)				Thousand-seed weight (TSW)			Seed Yield (SY)		
	DF	SS	MS	%variation	SS	MS	% variation	SS	MS	%variation
ENV	7	12130***	1732.8***	11.37	29.50***	4.2139***	21.17	1.04e+08***	14810063***	43.33
REP(ENV)	24	1299***	54.1***		1.52***	0.0634***		5.83e+06***	242769***	
GEN	18	32068***	1781.6***	30.07	46.19***	2.5661***	33.15	1.73e+07***	961606***	7.2
GEN: ENV	126.0	25562***	202.9***	23.97	17.94***	0.1424***	12.87	3.12e+07***	247753***	13
PC1		20056.8		18.80	5.265		3.7	1.82e+07		7.58
PC2		3094.3		2.9	4.578		3.2	6.75e+06		
PC3		1096.0		1	3.413		2.4	4.85e+06		
PC4		621.3		0.5	2.150		1.5	9.32e+05		
PC5		430.8		0.4	1.610		1.1	2.28e+05		
PC6		180.3		0.1	0.508		0.3	1.39e+05		
PC7		82.2		0.07	0.415		0.29	8.42e+04		
Residuals		10013			26.24			5.10e+07		
Total		106633.8			139.332			2.40e+08		

*** significant difference at $pp < 0.001$.

ENV: environment, REP: replication, GEN: genotypes/accessions, PC: principal component, DF: degree of freedom, SS: sum of squares, MS: mean square.

3.2. Estimation of genetic parameters of studied traits

Genotypic variances were higher than Genotype × Environment variances for all traits. The broad-sense heritability was high for the variables studied (Table 1). The highest value (0.94) was recorded for TSW and the lowest value (0.74) was recorded for SY. The accuracy of selection was high (>0.80) for all the traits.

3.3. AMMI and principal component analysis (PCA) for D50F, TSW, SY

There was a high significant ($p < 0.001$) variation among sesame accessions across environments for D50F, TSW, and SY (Table 2). Environment contributed to 11.37% of the total variation of the sum of squares of D50F, while 30.07% and 23.97% of variation of the sum of squares of this trait were attributable to accessions and G × E interaction, respectively. Regarding the TSW, the contribution of the environment, genotypes and G × E interaction, to the total variation of the sum squares was 21.17%, 33.15% and 23.97%, respectively.

Environment contributed to almost a half (43.33%) of the total variation of the sum of squares for the variable SY whereas genotypes, and G × E contributed to 7.2% and 13% respectively, to the variation of the sum of squares.

3.3.1. AMMI1 biplot analysis for D50F, TSW, SY

The AMMI1 biplot (Fig. 1) showed the main effect and interaction (IPCA) of both accessions and environments on D50F, TSW and SY. The x-axis showed the values of the traits D50F, TSW, SY and the y-axis showed the PC1 scores of both accessions as well as the environments. The horizontal lines that cross the IPCA-1 indicated the point where IPCA-1 = 0.

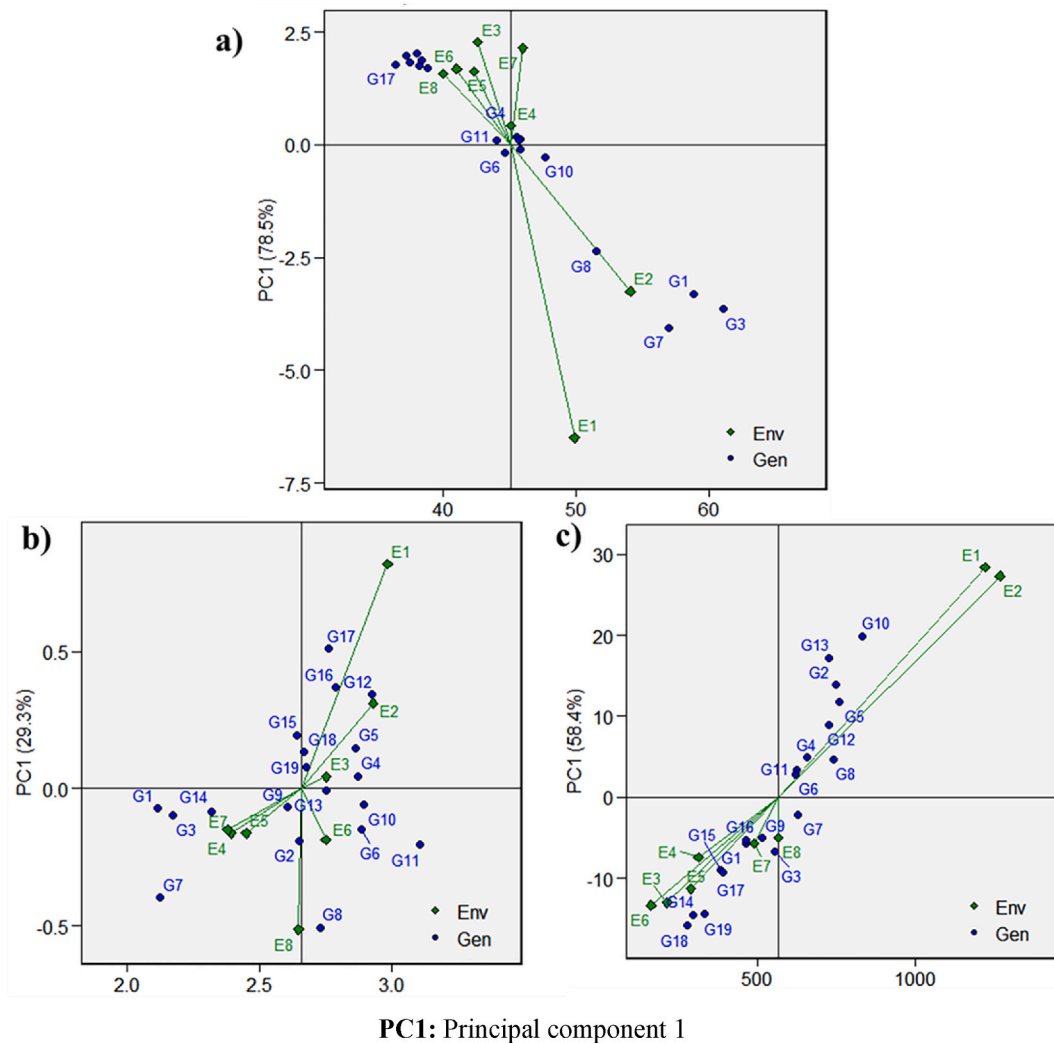


Fig. 1. AMMI 1 biplot for days to 50% flowering (a) thousand-seed weight (b) and seed yield (c).

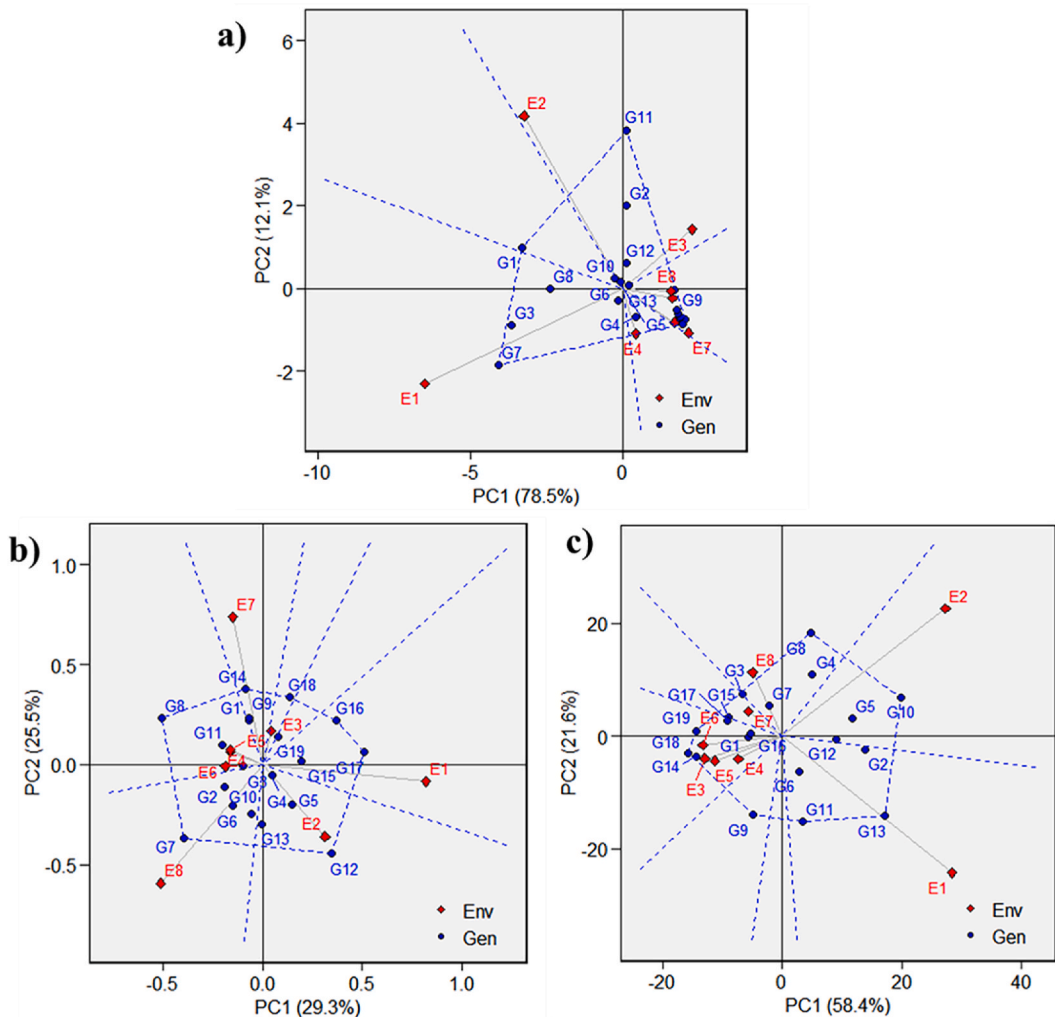
For the trait D50F, the early flowering accessions were G17, G18, G14, whereas the late flowering accessions were G3, G1, G7, G8. Early flowering was observed in the environments E3, E4, E5, E6, E8 while late flowering was observed in E1, E2 and E7. The late flowering accessions G1, G3, G7 were most fitted to the environments E1 and E2 (Fig. 1a).

The mean value of TSW on the x-axis was beyond 2.5 (Fig. 1b). The accessions G11, G6, G10, and G12 had the highest TSW values while the lowest values for this trait were recorded in G1, G3, G7, and G14. Bigger seeds were recorded in the environments E1, E2, E3, and E6 while smaller seeds were observed in the environments E4, E5, E7, and E8.

The x-axis of Fig. 1c showed a mean value of seed yield which was about 500 kg ha⁻¹. Therefore, the high yielding accessions were G10, G13, and G02 and were adapted to E1 and E2 whereas the least performing accessions were G14, G18, G19, and G17 and adapted to E3, E4, E5, E6, and E7. The highest seed yields were recorded in E1 (Abomey-Calavi) and E2 (Sékou) while the lowest seed yields were recorded in E3, E4, E5, E6, and E7.

3.3.2. AMMI2 biplot analysis for D50F, TSW, SY

The AMMI2 biplot model (Fig. 2) contains two PC1 (Principal component 1) versus PC2 (Principal component 2) and indicates the stability information of the accessions. The first two principal component (PC) axis explained 90.6% of total variation of the sum of squares of the G × E interaction for D50F (Fig. 2a). The accessions or environments close to the origin are the most stables and accessions close to certain environments perform better in those environments than accessions distant from those environments. Therefore, E5 and E8 were the most stable environments while the most stable accessions across environments were G8, G10, G5, G13, G9, G6 and G19. The accession G9 was adapted to E8 and the accessions G18, G14, G15 and G16 were adapted to E5, E6 and E7.



PC1: Principal Component 1, PC2: Principal Component 2

Fig. 2. AMMI 2 biplot for days to 50% flowering (a) thousand-seed weight (b) and seed yield (c).

The two principal components of Fig. 2b explained 54.8% of the total variation of the sum of squares for TSW. The accessions G3, G4, G19, G15, G17, G11 and G2 were the most stable across environments. The stable environments were E4, E5 and E6. Regarding adaptability of accessions to environment, G3 is adapted to E4 and E6, G11 adapted to E5.

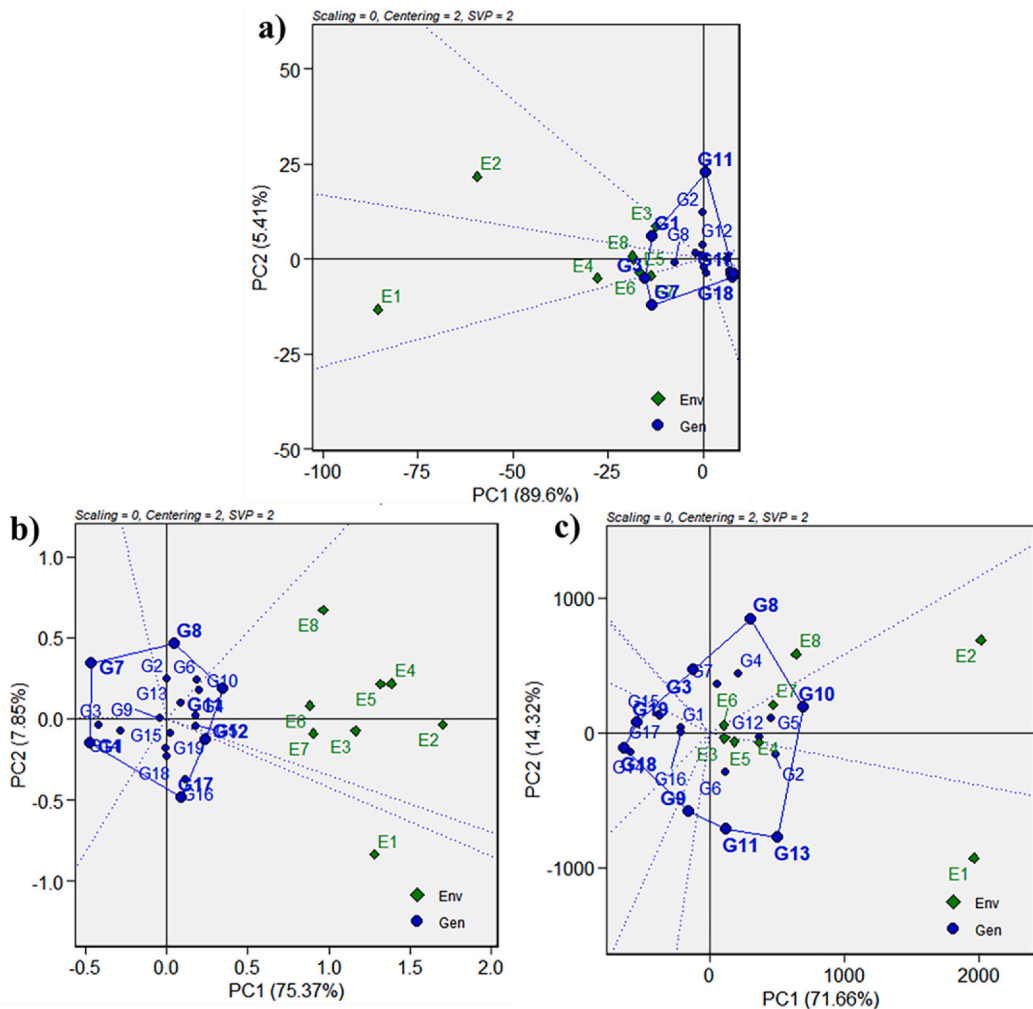
For seed yield (SY), the two principal components explained 80% of total of variation of the sum of squares. The stable accessions were G2, G12, G1, G16, G19 and G5. For the adaptability, the high seed yielding accessions G10 and G13 were adapted to E2 and E1 respectively, while the low yielding accessions G14 and G18 were adapted to E3 and E6 (Fig. 2c).

3.4. GGE biplots analysis for D50F, TSW, SY

The GGE biplot analysis performed in this study included partitioning the environment in mega environments (Which-won-where), mean performance and stability of accessions, and test environment evaluation.

3.4.1. Which-won-where (mega-environment investigation in sesame in Benin)

Based on D50F, the 8 environments were gathered in three mega-environments (Fig. 3a). The first mega-environment included E2 and E3, the second mega-environment included E1, E4, E5, E6, E8 and the last mega-environment included E7. The polygon vertices included G1, G3, G7, G11, G18. The vertex of the first mega-environment was G1 while the one of the third mega-environments were G3 and G7. G1, G7 and G3 had high values in their mega-environment for D50F, but low values for principal component (PC) suggesting those were late flowering accessions. Thus, G1 was the late flowering accessions in the first mega-environment and G3 with G7 were the late flowering accessions in the third mega-environment. There is no accession (vertex) belonging to the second mega-



PC1: Principal Component 1, PC2: Principal Component 2

Fig. 3. Which-won-where pattern of days to 50% flowering (a) Thousand-seed weight (b) and seed yield (c).

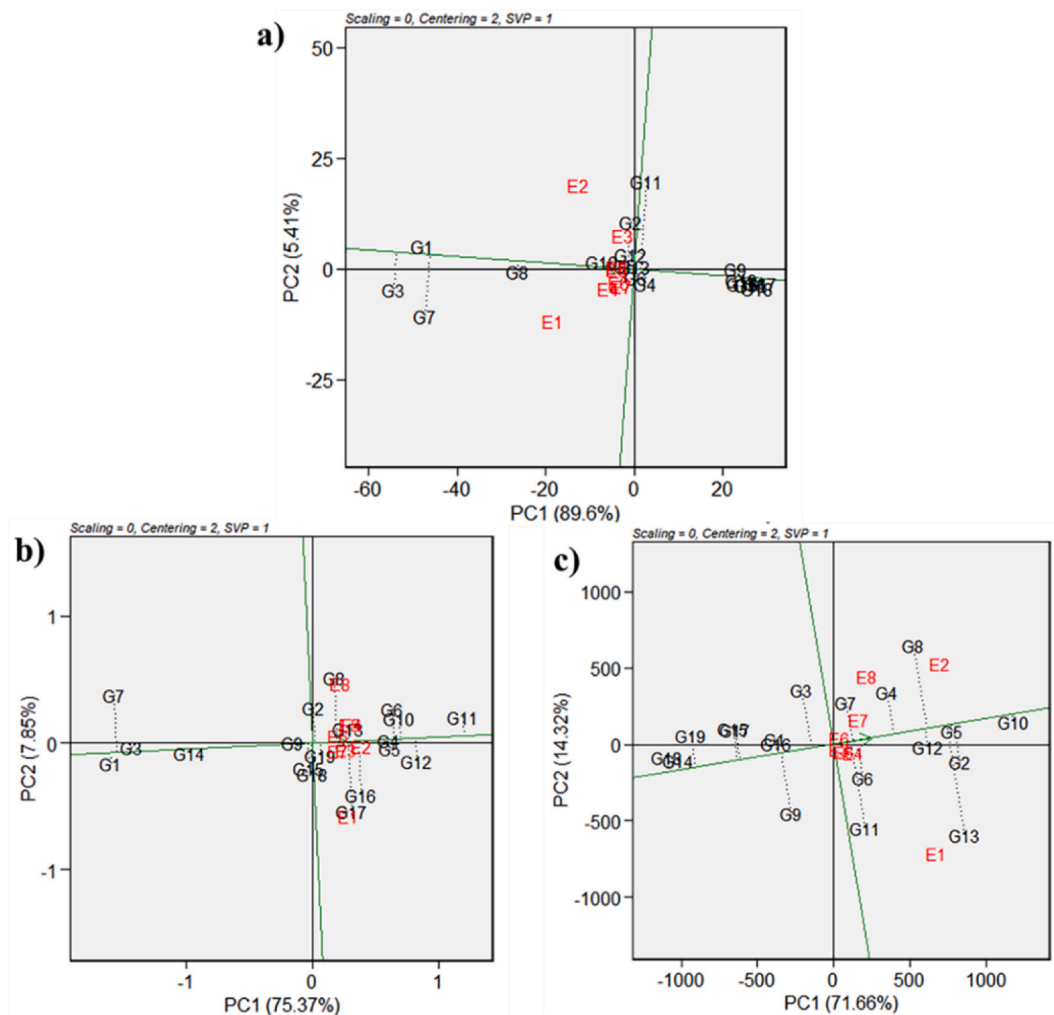
environment. The other accessions which fell in region without environment were the accessions with poor performance whatever the environment so were the early flowering accessions.

The biplot axis of Fig. 3b showed that the environments were combined in two mega-environments for TSW. The first mega-environment was only made of E1 and the second mega-environment included E2, E3, E4, E5, E6, E7 and E8. The accessions with highest values for TSW in the first mega-environment were G17 and G12 whereas G11 had the highest TSW value in the second mega-environment. The other accessions G2, G6, G1 and G7, arranged in region without environment had poor performance for TSW whatever the environments.

Three mega-environments were shown by biplot axis for SY (Fig. 3c). The first mega-environment included E1, E3, E4 and E5 the second mega-environment composed of E2, E6, E7 and the third one of only E8. The polygon's vertices included accessions namely G8, G10, G13, G11, G09, G18, G19 and G3. G11 and G13 were the vertex in the first mega-environment, therefore the high yielding in this mega-environment. G10 had the highest value in the second mega-environment while G3 and G8 showed the highest values in the third mega-environment. The accessions G9, G18, G19, G16 and G1 not appearing in any mega-environments were considered as accessions with poor performance irrespective to the environments.

3.4.2. Means performance and stability analysis for D50F, TSW and SY

The GGE biplot showing the Mean vs Stability (Fig. 4) was used to assess accessions for both mean performance and stability for variables D50F, TSW and SY. Overall, accessions in the direction of the arrow had the highest values. The stability of the accessions is represented by the second axis where the most stable accessions were located very close to the origin. Therefore, considering D50F, the accessions G3, G1, G7, G8 and G10 were the late flowering accessions whereas G18, G17, G16, G19 and G9 were early flowering



PC1: Principal Component 1, PC2: Principal Component 2

Fig. 4. Mean and stability biplot for days to 50% flowering (a) thousand-seed weight (b) seed yield (c).

accessions. In terms of stability represented by the second axis, the most stable accessions were G19, G13, G09 for early flowering accessions and G1, G10, G8 for late flowering accessions (Fig. 4a). E5 and E8 were revealed as stable environments.

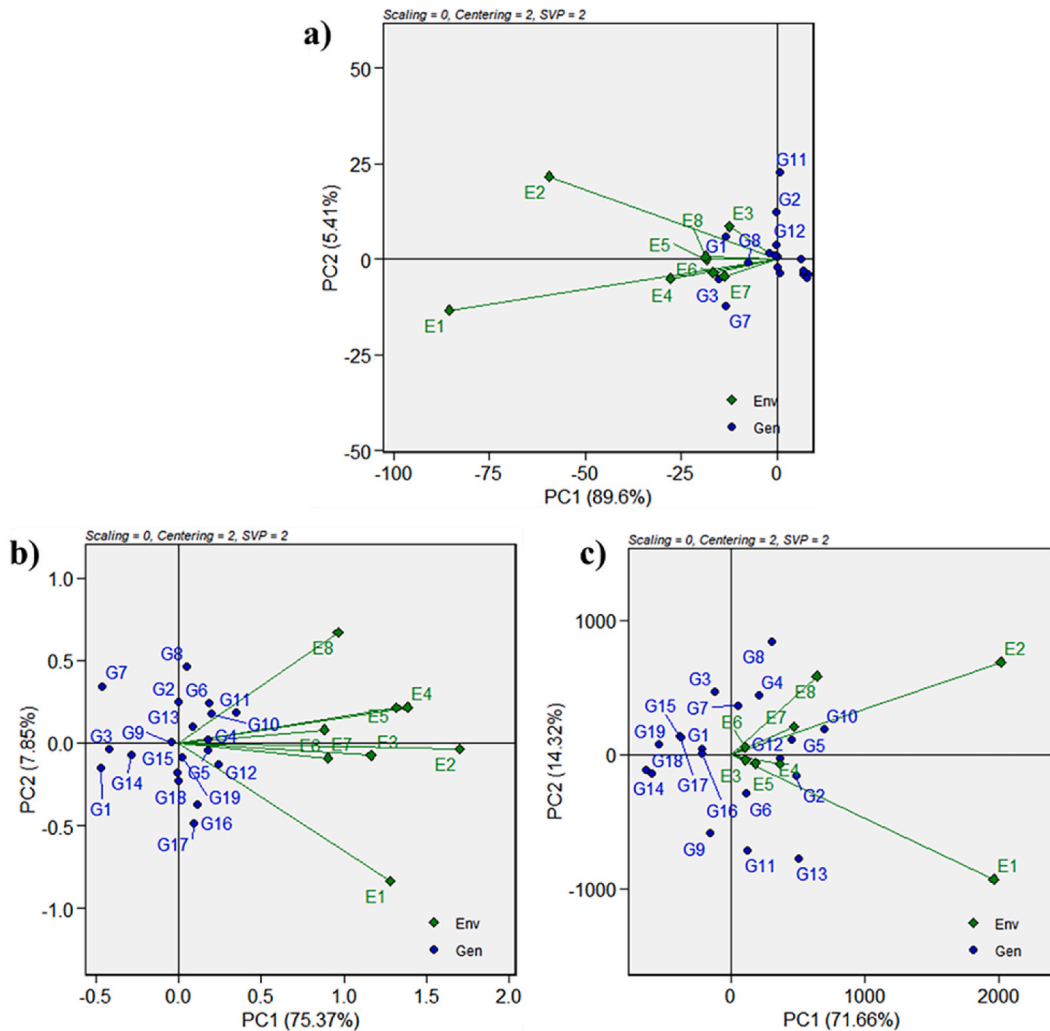
The accessions with high TSW mean values were G11, G12, G10 in the decreasing order. The stable accessions with high TSW values were G4, G5, G13 and G19. G3, G1, G14, G9 had low TSW values. The stable environments for this trait were E2, E3, E4, E5, E6 and E7 (Fig. 4b).

As far as SY is concerned, the classification of accessions was G10 > G02 > G5 > G13 > G08 > G12 > G04 > G06 > G07 > G11 > grand mean > G03 > G09 > G16 > G1 > G15 > G17 > G19 > G14 > G18. Among the high yielding accessions, the most stable accessions were G10, G5, G12. Among the low yielding accessions, the most stable accessions were G1, G16, G18, G14 (Fig. 4c).

3.4.3. GGE biplot analysis in sesame for D50F, TSW, SY

Fig. 5 was plotted to identify the discriminating power and the representativeness of test environments. The environment showing long vector have high discriminativeness for accessions and the environment with high representativeness is showed by the smallest of the angle between environment and mean-environment axis. For D50F, E1 and E2 presented long vectors which means they have high discriminativeness of accessions while E1, E5 and E8 were found more representative of the accessions. E1 had both discriminativeness ability for accessions and representativeness of test environments and was considered as ideal environment to select adapted accessions for D50F (Fig. 5a).

E2 was identified as the most discriminative and representative test environments for TSW (Fig. 5b). Regarding SY, E1 and E2 were the most discriminative environments and E3, E4, E5, E6 were the most representative test environments for the accessions (Fig. 5c).



PC1: Principal Component 1, PC2: Principal Component 2

Fig. 5. GGE biplot of days to 50% flowering (a), thousand-seed weight (b) and seed yield (c).

E1 and E2 were found to be discriminative for the accessions or representative for all the studied variables and therefore can be used as test environments for MET.

3.5. Multi-trait selection for D50F, TSW, SY

Selection of sesame accessions for D50F, TSW and SY simultaneously was performed through multi-trait stability index (MTSI). The selection differential was negative for SY. The selection differential for WAASB (Weighted Average of Absolute Scores) index was 26.9%, 31.3% and 18.7% for SY, TSW and D50F, respectively (Table 3). The three selected accessions with the lowest MTSI values (Supplementary Table S5) were G19, G10, and G13 (Fig. 6).

4. Discussion

The present study assessed the performance of nineteen local and exotic accessions in various agroecological zones in Benin. We aimed at identifying early flowering, high-yielding, and big seed size accessions.

4.1. Mean values, analysis of variance and AMMI model of studied variables across environments

Considering the seed yield (SY), the values obtained in this study for each accession ranged from 92 kg ha⁻¹ to 2275.09 kg ha⁻¹. For the means of the accessions across environments, the highest value for seed yield was 1270.5 kg ha⁻¹ in the environment E2 whereas the lowest value was 161.2 kg ha⁻¹ in the environment E6 (Supplementary Table S3). The maximum seed yield value obtained in this study was higher than that previously reported in the country. In Benin, the average sesame yield recorded from 2003 to 2013 was around 449.91 kg ha⁻¹ [9]. The highest values of seed yield were obtained in the environments E1 (Abomey-Calavi) and E2 (Sékou) located in the southern part of the country where sesame is not currently cultivated. This confirms the assertion that sesame can be grown and performed well in various environments [31]. We suggest promoting interventions to attract farmers in southern part of Benin to start growing sesame. In the northern part of the country where sesame is cultivated, the maximum of average seed yield obtained in this study was around 600 kg ha⁻¹. This value was recorded for a few accessions and the yield of most accessions was under 500 kg ha⁻¹ (Fig. 1). Such difference across environments could be explained by the fact that climatic conditions in the northern is different from the ones in the southern Benin. The replication of this study over the years could confirm this assertion. More breeding actions need to be undertaken to have varieties with high seed yield not only in the northern zone (production zones) but stable across all the agroecological zones of the country.

A highly significant variation ($p < 0.001$) was obtained among accessions for SY (Supplementary Table S4). The genetic diversity of the accessions needs to be assessed to identify the source of variation. The observed variation could be due to the fact that studied environments are distributed across various agroecological zones which therefore present a wide range of climatic characteristics as explained by Mortazavian et al. [32] who mentioned that yield can present considerable variation because of wide range of climatic conditions. In addition, Bozovic et al. [33] pointed out the fact that unpredictable environmental conditions hindered high yielding accessions selection. Despite the variation across environments, the high values obtained for heritability and accuracy of the selection showed strong selection response for those characters. The high heritability for the traits was reported by Hika et al. [34] and Kalaiyarasi et al. [35] in Ethiopia and India respectively. The AMMI model results (Table 2) showed that the environments have high effect on the variation of sesame accessions for seed yield. Similar findings were reported by Belay et al. [36] in Ethiopia and Seyni et al. [37] in Niger on sesame accessions. Conversely to seed yield, the effect of accessions was higher than that of environment and G × E interaction for D50F and TSW suggesting that environment did not have much effect on these traits. This was confirmed by the high estimated genotypic variance for D50F and TSW compared with SY. The same results were obtained by Baraki and Berhe [38] who showed that TSW did not significantly vary across year, confirming that environment has little effect on this trait. For D50F, the Chinese accessions were found to be early flowering accessions across environments and based on the result of AMMI 1 and GGE biplot for flowering, the northern environments are more favorable for early flowering accessions production.

The accessions from China were found to be more adapted to the known sesame production zones (Fig. 1) where the local accessions used in this study were collected. This was not expected since it is well known that local accessions show most of the time good results compared to “imported” varieties in the local accessions environment. We can conclude that the Chinese accessions may have a good genetic potential than the local accessions. However, the stability of the performance of the Chinese accessions requires several years trials to confirm this finding. Furthermore, the genetic relationship among all accessions is required to guide improvement of the

Table 3
Selection differential of the WAASB index for D50F, TSW, SY in sesame accessions.

Traits	Factor	Xo	Xs	SD	SD%
SY	FA 1	55.40	40.50	-14.9	-26.9
TSW	FA 1	58.60	76.90	18.3	31.3
D50F	FA 1	65.50	77.70	12.3	18.7
Mean		59.82	65.03	5.23	7.7

(Xo) = original mean, (Xs) = mean of the selected accessions, SD = selection differential, SY: Seed yield (kg ha⁻¹), TSW = Thousand-seed weight (g), D50F = Days to 50% flowering.

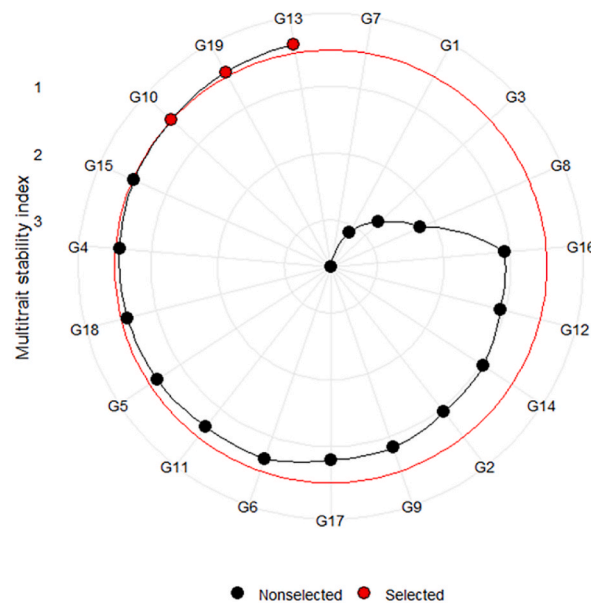


Fig. 6. Accessions of sesame selected by multi-trait stability index on days to 50% flowering (D50F), thousand-seed weight (TSW), and seed yield (SY).

local cultivars as they might have others breeding traits. The acceptability or willingness of farmers to adopt these Chinese varieties by local farmers should be investigated.

4.2. Assessing AMMI and GGE models across environments

Based on our results, AMMI model explained 90.6%, 54.8% and 76.4% of variation for D50F, TSW and SY respectively. GGE biplot explained 95.01%, 82.72% and 85.98% of variation for D50F, TSW and SY, respectively. These results showed that the GGE biplot provided more information on the variability than AMMI model.

The AMMI and GGE biplot models identified the same accessions as high-performing and stable accessions for the three traits. For example, for SY, accessions such as G10, G2, G5, G13, G8, were the high yielding accessions with G10, G5, G12 the most stable accessions. In addition, the two models identified environments E3, E4, E5, E6 as the most stable environments. The consistency between the two models in identifying superior and stable accessions and stable environments was also reported by other authors on maize [39] and on wheat [40].

SY was affected by environments and the eight studied environments were divided in three mega-environments. We noticed in this study that the environments E1 (Abomey-Calavi), E2 (Sékou) belonging to the same agroecological zone fall in the different mega-environments. As mentioned by Nai-yin et al. [41] this was explained by the fact that mega-environment is a set of locations that consistently share the best set of accessions across years, but are not necessarily geographically continuous. The climatic conditions of the two locations might further explain this observation.

In our study, the representativeness and discriminativeness of the nineteen accessions and eight environments (Fig. 5) showed that E1 and E2 located at the southern part of the country where the cultivation of sesame is currently marginal were the most discriminative and representative of accessions meaning that they provide more information for the selection of the accessions and ideal for selecting the best accessions [42].

The GGE biplot “Mean and stability” (Fig. 4) was used to identify favorable accessions as performed by Oral et al. [43] and Daba et al. [44]. Favorable accessions should have both high mean performance and high stability for the studied traits which means in the interpretation that an ideal genotype should have the highest PC1 score (high yielding ability) and lowest (absolute) PC2 score (high stability) [45]. Regarding the seed yield, the favorable (high seed yielding and stable) accessions were G2, G5, G10, G12 (Fig. 4c) which was the same result obtained with AMMI2 biplot method. These accessions are candidates for dissemination and foundation for breeding program.

4.3. Multi-trait stability index

The results of MTSI (Fig. 6) showed three accessions G10, G13 and G19 with lower MTSI score as ideal accessions which combine the studied traits. Among the best accessions, G19 which provided low performance in seed yield was selected because it was stable across environments, early flowering, and it has high TSW value. The MTSI was used by many authors such as Zuffo et al. [46] on soybean and Hussain et al. [47] on chickpea to select accessions which combine stability and performance for many characters.

Therefore, G10, G13 and G19 could be recommended for breeding programs and for production by farmers across the country.

5. Conclusion

This study evaluated sesame accessions in different environments in Benin Republic for days to 50% flowering (D50F), thousand-seed weight (TSW) and seed yield (SY). The performance of sesame accessions based on the traits of interest varies considerably across environments. Environments have less effect on TSW and D50F than SY. AMMI and GGE biplot indicated G10, G5, G12 as high yielding and stable accessions across environments. E1 (Abomey-Calavi) and E2 (Sékou) located in southern part of the country were high yielding environments. GGE biplot indicated that environments were divided in two mega-environments for TSW and three mega-environments for D50F and SY. E1 and E2 were identified as most discriminating environments whereas E3, E4, E5, E6 identified as the most representative. Three accessions, namely G10, G13, G19 were identified as superior accessions based on the three traits. These results in terms of adaptability and stability are valid for the predictable environmental components of locations. We suggest multi-years trials for the unpredictable factors of the environment of the region where the accessions were evaluated.

Consent for publication

The content of this manuscript has been approved by all authors.

Data availability statement

The data associated with our study is available in a publicly repository and will be shared upon request.

CRedit authorship contribution statement

Christel Ferréol Azon: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Writing – original draft, Writing – review & editing. **Nicodème Fassinou Hotegni:** Conceptualization, Formal analysis, Methodology, Writing – original draft, Writing – review & editing. **Eurydice Olga Deedi Sogbohossou:** Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Lewis Gnangle:** Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Guillaume Bodjrenou:** Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Charlotte O. Adjé:** Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Komivi Dossa:** Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Clément Agbangla:** Conceptualization, Formal analysis, Methodology, Supervision, Writing – review & editing. **Florent J.B. Quenum:** Conceptualization, Formal analysis, Methodology, Supervision, Writing – review & editing. **Enoch G. Achigan-Dako:** Conceptualization, Formal analysis, Methodology, Supervision, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.heliyon.2023.e21656>.

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