

YIELD PERFORMANCE AND STABILITY ANALYSIS OF OKRA
(*ABELMOSCHUS ESCULENTUS* L. MOENCH) ACCESSIONS
USING AMMI AND GGE BILOTS

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Abstract: The identification of adaptable, stable and high yielding genotypes under varying environmental conditions prior to release poses a lot of challenge to plant breeders in selecting the best genotypes of okra. The genotype × environment interaction is a major challenge to plant breeders because a large interaction can reduce selection gain and make the identification of superior cultivars difficult. The objectives of this study were to evaluate the performance of okra accessions in different environments and identify a high yielding and stable accession so as to select a parent for further breeding work. Seventeen accessions of okra were evaluated at Akure during the rainy season of 2018, at Akure and Oye during the rainy season of 2019; and at Akure during the rainy season of 2020, making a total of four environments. The additive main effects and multiplicative interaction and GGE-biplots were employed for the evaluation of the G×E interaction and stability studies in the four environments. The AMMI analysis identified NGB00378a as the most stable accession and high yielder. Also, GGE biplot identified NGB00378a as highly stable and the high yielder while NGB00355 was the highest yielder, but fairly stable. However, NGB00378a combines good performance with stability. Therefore, NGB00378a is an ideal accession that should be recommended for further breeding work.

Key words: environment, genotype, interaction, performance, stability.

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is one of the most important vegetable crops in the world, mainly grown for its tender leaves and pods (Chattopadhyay et al., 2011). It is a nutritious vegetable which provides dietary fiber (Kumar et al., 2010), protein, fats and carbohydrates (Saifullah and Rabbani,

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2009), vitamins, minerals and medically important compounds (Kumar et al., 2010). Okra is highly nutritious and valuable, and as a result, its performances and production across locations and environments all over the continents should be highly encouraged. Okra is widely grown in Nigeria for its edible fresh pod for cooking soups. Several researchers have worked on the production, cultivation, diversity, correlation and heritability studies of okra in Nigeria (Aminu et al., 2016; Komolafe et al., 2021a; AdeOluwa and Kehinde, 2011; Bello et al., 2015). Komolafe et al. (2021b) carried out correlation studies on forty genotypes of okra in Akure, Nigeria and concluded that pod yield per plant had highly significant and positive genotypic and phenotypic correlations with plant height, number of leaves, petiole length, internode length, plant height at flowering, peduncle length, fruit length, fruit diameter, number of seeds and number of pods. Oyetunde and Ariyo (2015) investigated gene action controlling yield and related traits in okra and concluded that both additive and dominant gene actions controlled the expression of characters in okra. Alake and Ariyo (2012) evaluated twenty-five West African okra genotypes from diverse geographical backgrounds in five different environments in Nigeria for the stability of performance using AMMI and GGE biplot analyses and concluded that the GGE biplot explains higher proportions of the sum of squares of the $G \times E$ interaction and it is more informative with regards to environments and cultivar performance than the AMMI analysis. Twenty-nine okra accessions were evaluated for stability and yield performance in four environments in Nigeria and both AMMI and GGE-biplot models identified LD88/1-8-5-2, 47-4 and NH88/1-8-16-2 as the best accessions for cultivation across seasons (Nwangburuka et al., 2011).

Many genotypes or varieties of okra that perform very well as regards yield and component in a particular environment tend to perform poorly or differently in another environment. This results from the interaction between genotype and the environment, which is referred to as genotype \times environment interactions. Kang (2004) defined genotype \times environment interactions as the disparity in the performances of genotypes or cultivars across different environments. This has been a major problem in plant breeding because it leads to inconsistency in the yield performances of genotypes or accessions over different locations and environments, which makes the selection of the best genotype or consistent performing lines difficult (Ariyo and Ayo-Vaughan, 2000). Genotype \times environment interactions retard progress in the crop improvement programme by complicating the breeding processes as a result of the unstable performance of accessions or genotypes across a wide range of locations or environments. As a result, the genotype \times environment interaction study is imperative to plant breeders in order to determine stable and high yielding genotypes across different environments (Olayiwola and Ariyo, 2013), to test cultivar adaptation (Dias and Krzanowski, 2003), to evaluate newly enhanced genotypes across test environments before a specific genotype is released for cultivation (Akter et al., 2015).

Many researchers have demonstrated the effectiveness of the AMMI model in understanding the $G \times E$ interaction in yield, estimating yields more accurately and selecting superior genotypes more reliably (Alake, 2018; Nassir and Ariyo, 2005). The AMMI analysis combines additive components in a single model for the main effects of genotypes and environments as well as multiplicative components for the interaction effect (Edugbo et al., 2015). The AMMI model displays main effects of genotypes and environments and their interactions and also contributes to the improved genotype evaluation, recommendation and selection of test environments (Abay and Bjornstad, 2009). The GGE biplot model provides breeders with a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega-environments (Yan, 2001; Yan and Kang, 2003). The GGE biplot analysis is another method which integrates the genotype and genotype by environment effects in the evaluation of cultivars. The GGE that uses graphic axes identifies superior cultivars in the mega environments (Akcura et al., 2011). Mega environments comprise groups of environments which consistently share the same test genotypes (Abay and Bjornstad, 2009). Miranda et al. (2009) reported that the GGE biplot informatively explains a higher proportion of the sum of squares of the $G \times E$ interaction with regards to environments and cultivar performance and makes visualization more logical and biological for practice than AMMI. The objectives of this study were to (i) evaluate the performance of seventeen (17) okra accessions in different environments using AMMI and GGE biplots and (ii) identify high yielding and stable accessions across environments so as to select a parent for further breeding work.

Material and Methods

Seventeen accessions of okra used for this research were sourced from five agro ecological zones of Nigeria, namely: Sudan savannah, Derived savannah, Southern Guinea savannah, Northern Guinea savannah and humid forest, through the gene bank of the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Oyo State, Nigeria (Table 1). The experiment was carried out in Akure, Ondo State and Oye, Ekiti State, over a three-year period (2018–2020). Seventeen accessions of okra were evaluated at Akure during the rainy season of 2018 (FUTA2018), Akure and Oye during the rainy season of 2019 (FUTA2019 and FUOYE2019); and in Akure during the rainy season of 2020 (FUTA2020), making a total of four environments (Figure 1). The experiments were carried out in a randomized complete block design (RCBD) with three replications. One-row experimental plots of 6-m length were used. The rows were 1 m apart while the plant-to-plant distance in each row was 0.6 m. Three seeds were sown per hole and later thinned to two plants per stand. Weeds were controlled manually at three-week intervals and insect pests were controlled using

Cypermethrin at the rate of 50ml/10 liters of water. Agro-meteorological data at FUTA and FUYOYE experimental sites from January to December 2018–2020 (Table 2) revealed that there were differences in environmental conditions of the different locations from year to year.

Table 1. Okra accessions collected in Nigeria – sources, places of collection, agro-ecological locations and their qualitative traits.

S/N	Accession	Source	Place of collection	Agro-ecological location	Stem pubescence	Pod pubescence	Stem colour	Petal colour	Pod colour	Position of the pod on the main stem
1	NGB00297	NACGRAB	Kebbi State	Sudan savannah	Slightly conspicuous	Prickly	Green	Yellow	Green	Pendulous
2	NGB00298	NACGRAB	Nasarawa State	Derived savannah	Slightly conspicuous	Slightly rough	Green	Yellow	Green	Erect
3	NGB00299	NACGRAB	Oyo State	Derived savannah	Conspicuous	Prickly	Green	Yellow	Green	Erect
4	NGB00302	NACGRAB	Kano State	Sudan savannah	Conspicuous	Prickly	Green	Yellow	Green	Erect
5	NGB00303	NACGRAB	Unknown	Unknown	Glabrous	Downy	Purple-green	Yellow	Purple-green	Erect
6	NGB00304	NACGRAB	Niger State	Southern Guinea savanna	Conspicuous	Prickly	Purple-green	Yellow	Purple-green	Erect
7	NGB00331	NACGRAB	Oyo State	Derived savannah	Slightly conspicuous	Slightly rough	Green	Yellow	Purple-green	Erect
8	NGB00346	NACGRAB	Kebbi State	Sudan savannah	Conspicuous	Prickly	Green	Yellow	Green	Erect
9	NGB00347	NACGRAB	Unknown	Unknown	Slightly conspicuous	Slightly rough	Purple	Yellow	Purple-green	Erect
10	NGB00350	NACGRAB	Unknown	Unknown	Conspicuous	Prickly	Green	Yellow	Green	Erect
11	NGB00355	NACGRAB	Ondo State	Humid forest	Conspicuous	Prickly	Red-green	Yellow	Green	Erect
12	NGB00356	NACGRAB	Edo State	Humid forest	Slightly conspicuous	Downy	Green	Yellow	Green	Erect
13	NGB00369	NACGRAB	Niger State	Southern Guinea savanna	Conspicuous	Prickly	Green	Yellow	Green	Erect
14	NGB00371	NACGRAB	Niger State	Southern Guinea savanna	Slightly conspicuous	Slightly rough	Red-green	Yellow	Green	Erect
15	NGB00378a	NACGRAB	Delta State	Humid forest	Glabrous	Downy	Green	Yellow	Green	Erect
16	NGB00378b	NACGRAB	Delta State	Humid forest	Glabrous	Slightly rough	Green	Yellow	Green	Erect
17	NGB00430	NACGRAB	Unknown	Unknown	Glabrous	Slightly rough	Green	Yellow	Green	Erect

Source: NACGRAB = National Centre for Genetic Resources and Biotechnology.

Data collection

Data were collected from six plants in each row on the following traits:

- (i) Plant height at 50% flowering (cm): This was determined by measuring the plant from the soil level to the tip of the main stem when half of the plants in a plot flowered;
- (ii) Plant height (cm): This was measured from the soil level to the tip of the plant at maturity;
- (iii) Number of seeds per pod: This was determined at maturity by counting the number of seeds in five randomly selected pods and averaging the pods;
- (iv) Pod yield per plant (g/plant): This was determined by averaging and summing the weight of green pods harvested from five sampled plants at all picking times.

Data analysis

Data on the above traits were subjected to a combined analysis of variance to determine the effects of the environment (E), the genotype (G) and the genotype × environment interaction.

The data were subjected to the additive main effects and multiplicative interaction (AMMI) analysis in order to determine the stability of the accessions. The AMMI model first fits the additive effects for the genotypes and the environments and the multiplicative term for interactions of genotypes with the environments. According to Gauch and Zobel (1996), the linear model for AMMI is presented as:

$$Y_{ij} = \mu + B_i + C_j + \sum \lambda_x \cdot \alpha_{ix} \cdot \delta_{jx} + R_{ij} + E \quad (1)$$

where Y_{ij} is the value of the i^{th} genotype in the j^{th} environment; μ is the grand mean; B_i is the deviation of the i^{th} genotype from the grand mean; C_j is the deviation of the j^{th} environment from the grand mean; λ_x is the singular value for PC axis x ; α_{ix} and δ_{jx} are the PC scores for axis x of the i^{th} genotype and j^{th} environment, respectively; R_{ij} is the residual and E is the error (Gauch, 1992).

To measure the value of genotypes and rank based on yield stability, the AMMI stability value (ASV) proposed by Purchase et al. (2000) was calculated.

AMMI stability value (ASV) was calculated using the formula proposed by Purchase et al. (2000) as follows:

$$ASV = \sqrt{\left[\frac{IPCA\ 1SS}{IPCA\ 2SS} (IPCA\ 1_{Scores}) \right]^2 + (IPCA\ 2_{Scores})^2} \quad (2)$$

where $IPCA\ 1\ SS / IPCA\ 2\ SS$ is the weight given to the $IPCA\ 1$ -value.

The GGE biplot model was used according to Yan (2001) as:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad (3)$$

where Y_{ij} is the mean of genotype i in environment j , μ is the grand mean, β_j is the main effect of environment j , λ_1 and λ_2 are the singular values for the first and second principal component (PC1 and PC2), respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively, η_{j1} and η_{j2} are eigenvectors of environment j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j .

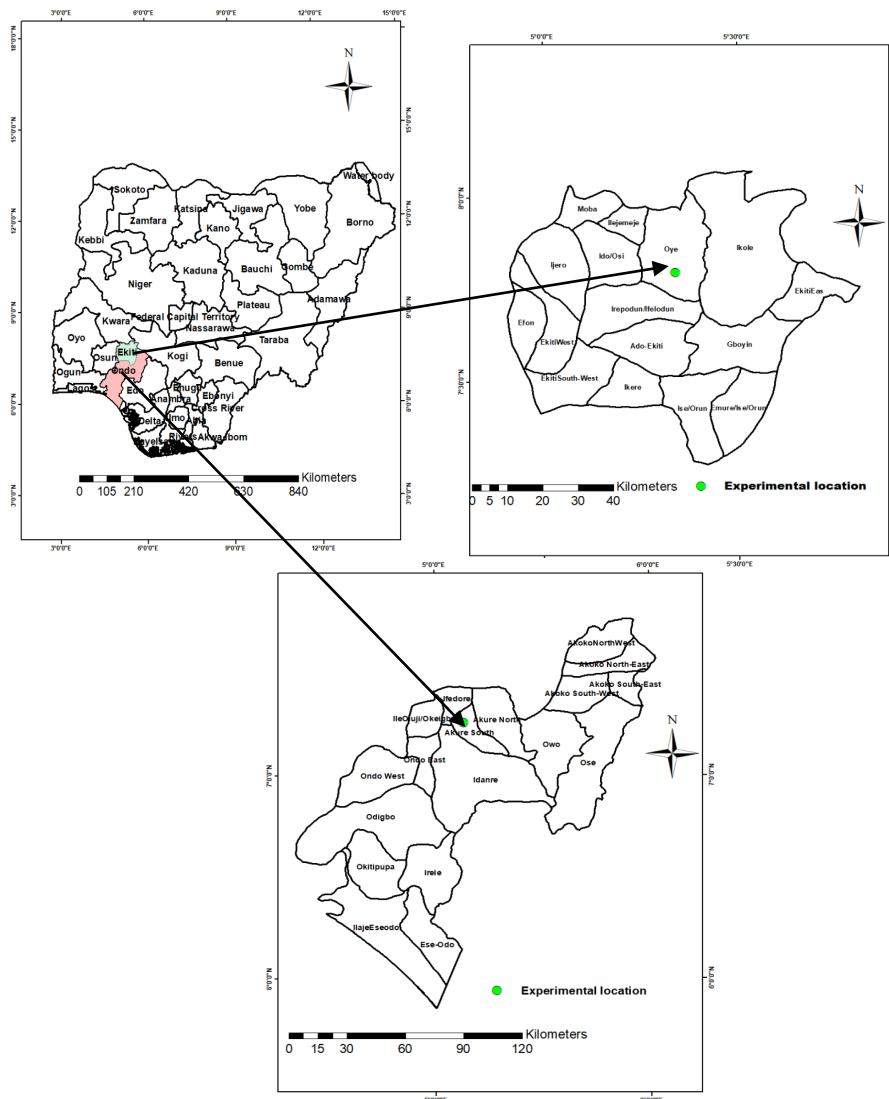


Figure 1. Experimental sites of the study location in Nigeria.

Genotype stability index

A stability index recommended by Farshadfar (2008) was calculated for each accession by summing the overall mean performances and ASV for each trait as given by:

$$GSI_i = RASV_i + RY_i, \quad (4)$$

where: GSI_i = the genotype stability index for the i^{th} genotype across the environment for each trait; $RASV_j$ = the rank of the i^{th} genotype across the environment based on ASV;

RY_i = the rank of the i^{th} genotype based on mean performance across the environment. The genotype with the lowest GSI was considered the best for a particular trait across the environment.

Results and Discussion

Agro-metrological data at FUTA and FUYOYE experimental sites from January to December 2018–2020 (Table 2) revealed that there were differences in environmental conditions of the different locations from year to year.

One of the major goals of every plant breeding programme is the selection and development of high yielding genotypes with wide stability across various agro-ecological environments. Genotypes do not perform exactly the same way in different environments as a result of genotype by environment interaction (GEI), making it difficult for breeders to select the appropriate genotype during cultivar development. Ariyo and Ayo-Vaughan (2000) have reported that in any multi-site evaluation programme where interactions are of practical importance, selection for stability is of prime consideration.

The combined analysis of the variance of the main effects of pod yield per plant and three agronomic traits of 17 accessions of okra grown in four environments are presented in Table 3. The results revealed that accessions, environments and their interactions were highly significant for final plant height, plant height at 50% flowering, number of seeds per pod and pod yield. Results of the combined analysis of variance show that the response of accessions was influenced by the environments. This is in agreement with the reports by Ariyo and Ayo-Vaughan (2000), Javia (2014), Alake (2018), Alake and Ariyo (2012) who reported the high influence of environment on the assessed traits, which makes it difficult to identify stable genotypes among the available genotypes.

The result of the AMMI analysis of variance for pod yield of seventeen accessions of okra grown in four environments is presented in Table 4. This showed that the accession and environment were highly significant as well as the accession x environment interaction. The total sum of squares shows that the environment had a greater proportion of 57.54% of the total variation; interaction had 24.96% while 17.5% was attributed to the accession, indicating that there were

substantial differences among studied environments which advocated the adequacy of running stability analysis. This is in accordance with the findings of several authors like Irfan (2018), Gebremedhin et al. (2014), Munaro et al. (2014). The large variance due to the effect of environment obtained in this present study also agrees with the findings of Rad et al. (2013), who obtained 51.9% of the total variation as the effect due to environment but contrary to the findings of Akter et al. (2015), Alake and Ariyo (2012), who had only 12.49% and 4.6%, respectively, of the total sum of squares attributable to the environmental effect. The magnitude of the G x E interaction sum of squares higher than that for accessions indicated that there were substantial differences in genotypic response across environments. This is in agreement with previous reports (Alam et al., 2015; Vaezi et al., 2017).

Table 2. Average monthly rainfall, maximum and minimum temperatures, relative humidity, and sunshine duration during growing periods of multi-environment trials of okra at the Federal University of Technology, Akure and Federal University Oye Ekiti, Nigeria

Year/Location	Month	Temperature		Relative humidity		Rainfall (mm)	Sunshine (hr)
		Max (°C)	Min (°C)	Max (%)	Min (%)		
2018/FUTA	April	29.8	23.9	95.6	71.2	130.6	8
	May	28.7	23.2	96.3	70.1	187.0	8
	June	26.9	23.2	96.1	82.0	218.6	7
	July	26.3	22.6	95.8	84.2	203.3	7
	August	26.0	22.5	96.5	84.2	227.7	6
	September	26.5	22.0	98.5	83.3	360.8	7
	October	27.6	22.8	98.4	79.2	197.5	8
	November	28.7	23.3	99.1	74.0	30.6	7
	December	29.8	19.8	93.1	50.0	7.2	9
	2019/FUTA	April	29.4	23.8	94.4	72.0	103.4
May		27.8	23.5	95.7	76.2	175.0	7
June		27.1	23.4	96.6	84.3	256.6	7
July		26.0	22.3	95.7	80.9	225.7	6
August		25.8	22.2	96.5	83.9	180.1	6
September		26.4	22.3	97.5	83.2	326.2	6
2019/FUOYE	April	30.8	24.0	91.19	62.69	76.9	3.5
	May	28.1	23.4	93.25	73.05	164.0	3.1
	June	27.5	23.4	92.81	78.65	253.1	2.8
	July	26.3	22.3	94.28	78.66	203.1	2.8
	August	26.0	22.1	95.24	80.78	171.4	2.8
	September	26.6	22.1	96.45	82.40	324.8	2.8
2020/FUTA	March	30.7	24.1	93.6	58.8	47.0	8
	April	29.4	24.0	97.1	68.9	125.3	8
	May	27.7	23.6	96.9	80.8	177.7	7
	June	26.8	22.8	97.0	83.3	205.9	7

The GEI was partitioned into the first two IPCA axes and the residual. The first two interaction principal component axes (IPCA) were highly significant and cumulatively contributed 78% of the total GEI. IPCA 1 and IPCA 2 explained 41.33% and 36.79%, respectively, of the total GEI variance. The mean yield of 17 accessions of okra grown in four environments and the values of the first IPCA scores from the AMMI analysis are presented in Table 5. Pod yield/plant ranged from 120.70g to 299.40g plant⁻¹ for NGB00304 and NGB00355, respectively. The environmental means ranged from 114.50 for FUTA 2019 to 312.90 for FUTA 2020. NGB00304 had the largest IPCA score of 7.58 while NGB00355 had the smallest IPCA score of -8.57. Similarly, FUTA 2018 had the largest IPCA score of 9.72 while FUTA 2020 had the lowest IPCA score of -13.43. Thus, when an accession and environment have the same sign on their respective first IPCA axes, their interaction is positive; if different, their interaction is negative.

Table 3. The analysis of variance for the pod yield (g/plant) and three agronomic traits of 17 okra accessions in four environments.

Source	df	Final plant height	PHAF	NSPP	PYPP
REP	2	20.7	181.7	37.0	11374*
ENV	3	48038.5**	26006.7**	28955.9**	442814**
ACC	16	4796.6**	2291.0**	1818.0**	25261**
ENV*ACC	48	1354.1**	1005.7**	577.3**	12004**
Error	134	323.0	168.3	50.7	1769
Total	203				

*, ** = significant at $P < 0.05$, < 0.01 , respectively. df = degree of freedom; REP = replication, ENV = environment, ACC = accession; PHAF = plant height at flowering, NSPP = number of seeds per pod, PYPP = pod yield per plant.

Table 4. The AMMI analysis of variance for the pod yield of 17 okra accessions tested over four environments.

Source of variation	DF	SS	MS	% Total SS	% Treatment	% interaction (G×E)
Treatments	67	2308810	34460**	89.89		
Accession	16	404175	25261**		17.5	
Environments	3	1328443	442814**		57.54	
Block	2	37803	4725			
Interactions	48	576192	12004**		24.96	
IPCA 1	18	238125	13229**			41.33
IPCA 2	16	211970	13248**			36.79
Residuals	14	126097	9007**			
Error	136	222005	1734	10.11		
Total	203	2568618	12653			

** = significant at $P < 0.01$.

Table 5. Means and the first PCA scores of the AMMI analysis of pod yield of 17 okra accessions evaluated in four environments.

Accession	FUTA18	FUTA19	FUOYE2019	FUTA2020	Mean (g)	IPCA1
NGB00297	102.60	93.30	122.60	268.10	146.60	1.18
NGB00298	116.20	101.10	50.50	223.80	122.90	3.27
NGB00299	155.40	122.00	286.30	320.60	221.10	1.88
NGB00302	124.80	95.50	150.10	245.70	154.00	3.24
NGB00303	111.50	90.70	246.20	308.60	189.20	0.46
NGB00304	135.00	71.50	121.60	154.60	120.70	7.58
NGB00331	164.90	113.60	333.00	306.80	229.60	3.16
NGB00346	131.60	107.30	106.00	238.20	145.80	3.57
NGB00347	150.40	137.70	101.30	272.40	165.50	2.73
NGB00350	100.70	89.30	210.30	307.30	176.90	-0.12
NGB00355	138.40	193.70	323.70	542.00	299.40	-8.57
NGB00356	83.60	142.60	87.90	403.10	179.30	-5.88
NGB00369	107.70	110.30	78.50	276.20	143.20	0.75
NGB00371	62.80	87.20	68.80	301.10	130.00	-2.20
NGB00378a	133.50	139.30	172.50	344.50	197.40	-0.76
NGB00378b	81.20	134.90	116.30	404.10	184.10	-5.84
NGB00430	94.30	117.10	242.20	401.70	213.80	-4.45
Mean (g)	117.30	114.50	165.80	312.90	177.63	
IPCA1	9.72	1.62	2.09	-13.43		

AMMI IPCA 1 and IPCA 2 scores of okra fruit yield, the AMMI stability value (ASV) and the genotype stability index (GSI) for 17 accessions of okra are presented in Table 6. The genotype ranking based on GSI, which combines both ASV and mean pod yield performance rankings revealed that NGB-00378a, NGB-00350, NGB-00299 and NGB-00297 were the most desirable accessions as they combine high yield with stability. Considering the ASV ranking values alone, NGB00378a and NGB00297 with the lowest values would be the most stable accessions even with low mean pod yield while NGB-00355, NGB-00331, NGB-00304, NGB-00356 and NGB-00378b would be unstable accessions. Unfortunately, NGB00331 and NGB00355 ranked the first and second best, respectively, in yield but the most unstable accessions according to ASV ranking. However, they were found to be fairly stable according to GSI ranking scores. Accession NGB-00378a was found to be the most stable accession according to ASV and GSI rankings and as a result, the best accession to be selected.

The AMMI I biplot for okra pod yield grown in four environments is presented in Figure 2. The Y-axis represents the first IPCA while the X-axis is the main effect, the yield of okra pods. The accessions NGB-00356, NGB-00378b, NGB-00378a, NGB-00350, NGB-00430, NGB-00303, NGB-00299, NGB-00355 and NGB-00331 yielded above average while FUTA 2020 was the most favourable

environment since AMMI placed them on the right-hand side of the midpoint while NGB-00298, NGB-00347, NGB-00369, NGB-00371, NGB-00346, NGB-00297, NGB-00304 and NGB-00302 were low yielding because they were placed on the left side of the midpoint of the biplot. Results showed that NGB-00350, NGB-00303, NGB-00378a, NGB-00302 and NGB-00297 were very close to the equator of the IPCA1 and so the most stable accessions. On the other hand, NGB-00355, NGB-00331, NGB-00304, NGB-00356 and NGB-00378b though high yielding were the most unstable accessions because they were located far from the IPCA1.

Table 6. The ranking of 17 accessions of okra by mean performance, AMMI stability value (ASV) and genotype selection index (GSI) for pod yield evaluated in four environments.

Accession	Mean yield (g)	Yield rank (YR)	ASV	ASV rank (RASV)	GSI	GSI rank
NGB00297	146.60	12	1.65	2	14	4
NGB00298	122.90	16	6.01	12	28	16
NGB00299	221.10	3	5.69	10	13	3
NGB00302	154.00	11	3.44	4	15	6
NGB00303	189.20	6	4.96	8	14	4
NGB00304	120.70	17	8.04	15	32	17
NGB00331	229.60	1	8.60	16	17	8
NGB00346	145.80	13	4.57	7	20	11
NGB00347	165.50	10	5.12	9	19	9
NGB00350	176.90	9	3.31	3	12	2
NGB00355	299.40	2	9.90	17	19	9
NGB00356	179.30	8	7.93	14	22	15
NGB00369	143.20	14	4.04	6	20	11
NGB00371	130.00	15	4.00	5	20	11
NGB00378a	197.40	5	1.16	1	6	1
NGB00378b	184.10	7	6.96	13	20	11
NGB00430	213.80	4	5.94	11	15	6

The finding that the AMMI plot accounted for a substantial part of the total sum of squares suggested that the model was more appropriate in explaining the G×E interaction. The variability in the amount of rainfall in different locations was probably responsible for the differences in the performance of the accessions. This is in agreement with the report of Ariyo and Ayo-Vaughan (2000), who also reported significant interaction.

NGB00298 and NGB00304 had similar low yields but a different large positive interaction. NGB00355, NGB00356, NGB00378a, NGB00378b and NGB00430 had high mean yield and a different high negative interaction. Based on the magnitude of the interaction score, only NGB00303 and NGB00350 could be

considered fairly stable. This is in agreement with Ariyo and Ayo-Vaughan (2000), who reported only G13 and G9 to be fairly stable. FUTA 2018 had the largest interaction, while FUTA 2020 had the least. NGB00303 was favoured by FUTA 2020 and FUYOYE 2019, but it was not favoured by FUTA 2019.

NGB00350 and NGB00302 were located close to the origin and proved highly stable, but they had low mean yields. This is similar to the findings of Irfan (2018), Singh et al. (2019), Mohammadi and Amri (2013) and Oral et al. (2018), who also reported the stability of genotypes with low IPCA 1 values.

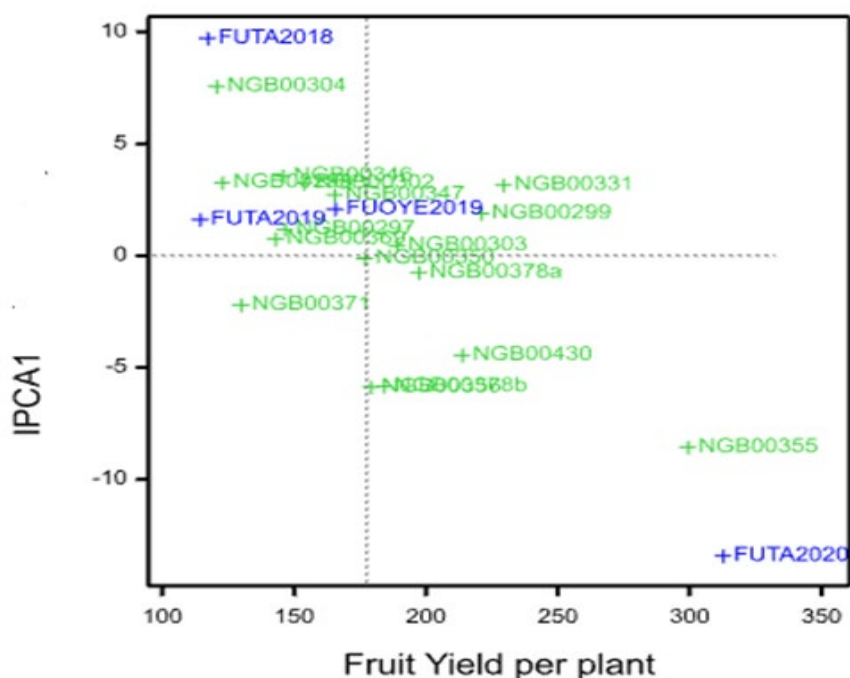


Figure 2. The biplot analysis of GEI based on the AMMI 1 model for the PCA1 scores and fruit yield/plant.

FUTA2018=environment 1, FUTA2019=environment 2, FUYOYE2019=environment 3, FUTA2020=environment 4.

The polygon view of the GGE biplot which shows the which-won-where pattern of the seventeen accessions of okra evaluated in four environments with respect to pod yield per plant is presented in Figure 3. The quadrilateral is divided into six sectors by six projecting lines from the origin and the four environments fell into only two of the sectors. Akure 2018 (E1) and Akure 2019 (E2) fell into sector one with NGB00331 (G7) being the vertex accession while Oye 2019 (E3)

and Akure 2020 (E4) fell into the second sector with NGB-00355 (G11) as the vertex accession. NGB-00331 (G7) and NGB-00355 (G11) accessions were, therefore, the highest yielding accessions. No environment was associated with sectors three, four, five and six where NGB-00356 (G12), NGB-00371 (G14), NGB-00298 (G2) and NGB-00304 (G6) were located. NGB-00331 (G7) won in two environments – FUTA 2018 (E1) and FUTA 2019 (E2), while NGB-00355 (G11) won in FUOYE 2019 (E3) and FUTA 2020 (E4). According to Ariyo and Ayo-Vaughan (2000), who have stated that the high influence of the environment on the performance of traits makes it difficult to identify stable ones among the studied genotypes.

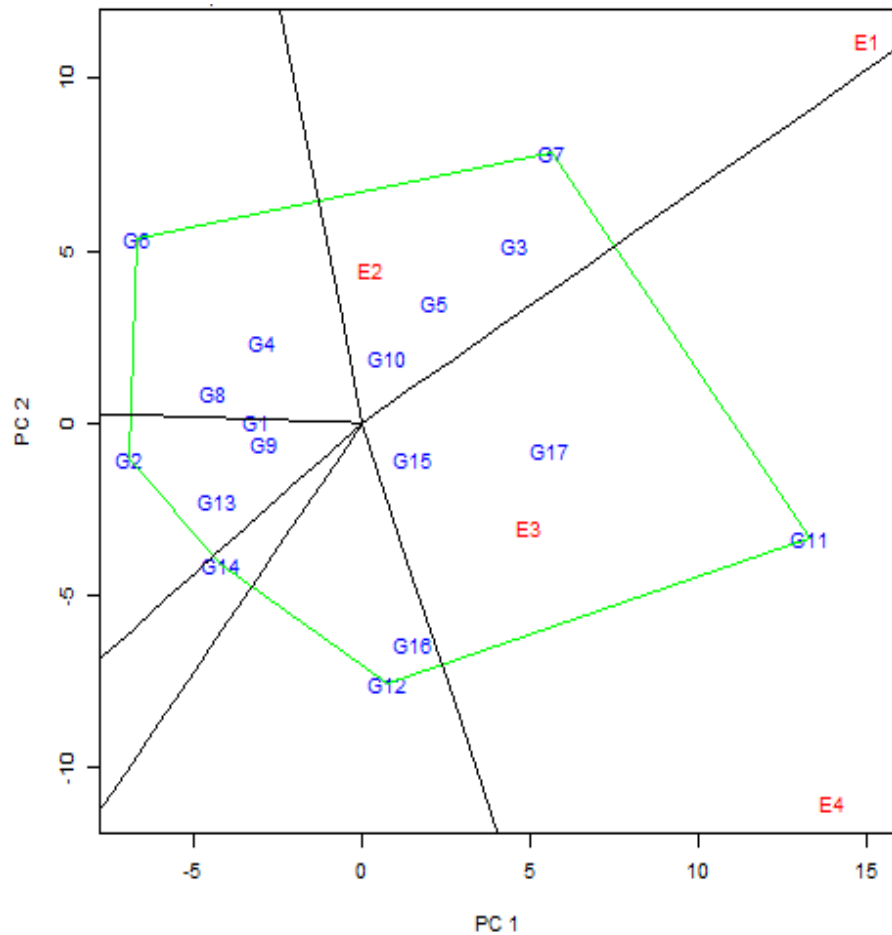


Figure 3. The polygon view of the GGE biplot for pod yield data of 17 okra accessions evaluated across 4 environments between 2018 and 2020.

This means that there is an interaction between genotype and environment. According to GSI ranking, genotypes NGB00378a, NGB00350, NGB00299 and NGB00297 were identified as the stable accessions with high mean yield across the test environment, which makes them the best accessions for selection. According to Yan and Tinker (2006), the genotypes found at the vertex of the sectors had the highest yield than those that are not found at the vertex in all environments (Yan, 2001). NGB00331 (G7) was the best performing accession in Akure 2018 and Akure 2019 while NGB00355 (G11) was the high yielding accession in Oye 2019 and Akure 2020.

The average environment coordinate line (AEC) was used to estimate the yield and stability of accessions in the GGE biplot (Figure 4). The line with a double arrow passing through the biplot origin is referred to as the average environment coordinate (AEC). Proximity to concentric circles indicates a high mean yield while remoteness to it shows a low mean yield. Projections from the biplot origin in either direction on the axis indicate greater instability. Also, the accessions with yield performance greater than the mean yield are those on the right side of the AEC line, while those with a yield lower than the mean yield are on the left side of the line. NGB-00355 (G11) was the highest yielding accession, followed by NGB-00331 (G7), NGB-00430 (G17) and NGB-00299 (G3). Those with mean yield below average include NGB-00304 (G6), NGB-00298 (G2), NGB-00371 (G14), NGB-00369 (G13), NGB-00346 (G8), NGB-00297 (G1), NGB-00302 (G4) and NGB-00347 (G9). The projection from the origin to the AEC indicates the stability of the genotypes. A greater projection into the AEC line regardless of the direction indicates greater instability. Therefore, accessions NGB00331 (G7), NGB00304 (G6), NGB00356 (G12) and NGB00378b were highly unstable while NGB00297 (G1), NGB00347 (G9), NGB00298 (G2), NGB00378a (G15) and NGB00430 (G17) with shorter projections were relatively stable over environments. The accession that combines good performance with stability is NGB00378a (G15) and, therefore, the most desirable accession. The estimation of the yield and stability of genotypes showed that NGB00304 and NGB00298 were the least stable; while NGB00378a (G15) proved to be the most stable and high yielder across the environments. For selection, the desirable accessions are those with both high mean yield and stability. In this study, the accession that combines good performance with high stability is NGB00378a (G15). Therefore, it should be selected. This result is in agreement with the findings of Akter et al. (2015) and Nahief and Mohammad (2013).

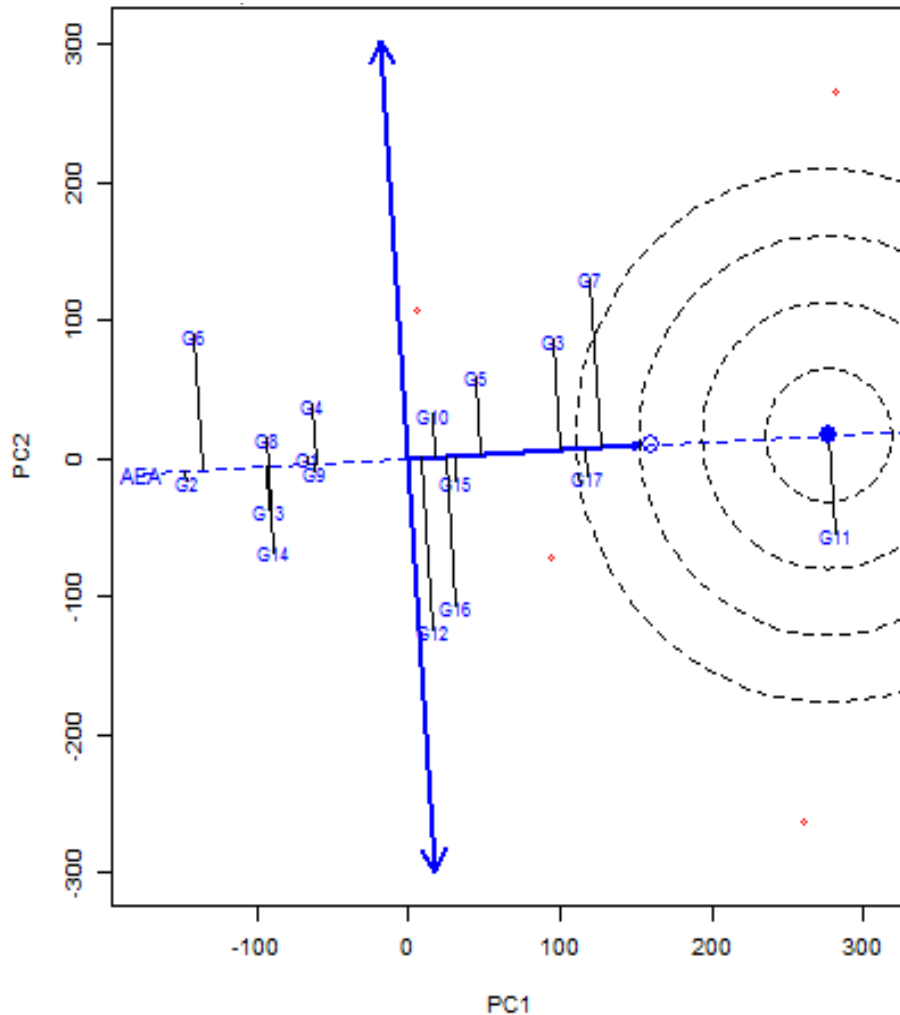


Figure 4. The GGE biplot showing the ranking of accessions for both pod yield and stability performance of 17 accessions of okra evaluated across 4 environments between 2018 and 2020.

The discriminatory power and representativeness of the test environments among the four environments are displayed in Figure 5. A small circle with an arrow pointing to it depicts an ideal environment. From the vector view of the biplot, the length of the environment vectors is a measure of their discriminating ability. In this study, Akure 2020 was the most discriminatory environment. The second most important aspect of test environment evaluation is its representativeness of the mega environments. The smaller the angle, the more

representative the test environment would be. The important properties of an ideal environment are its discriminatory ability and representativeness (Yan, 2001). An ideal environment should be highly discriminating for the tested genotype as well as a representative of the target environments (Yan and Kang, 2003). Hence, FUYOYE 2019 (E3) was the most representative of other varieties in this study.

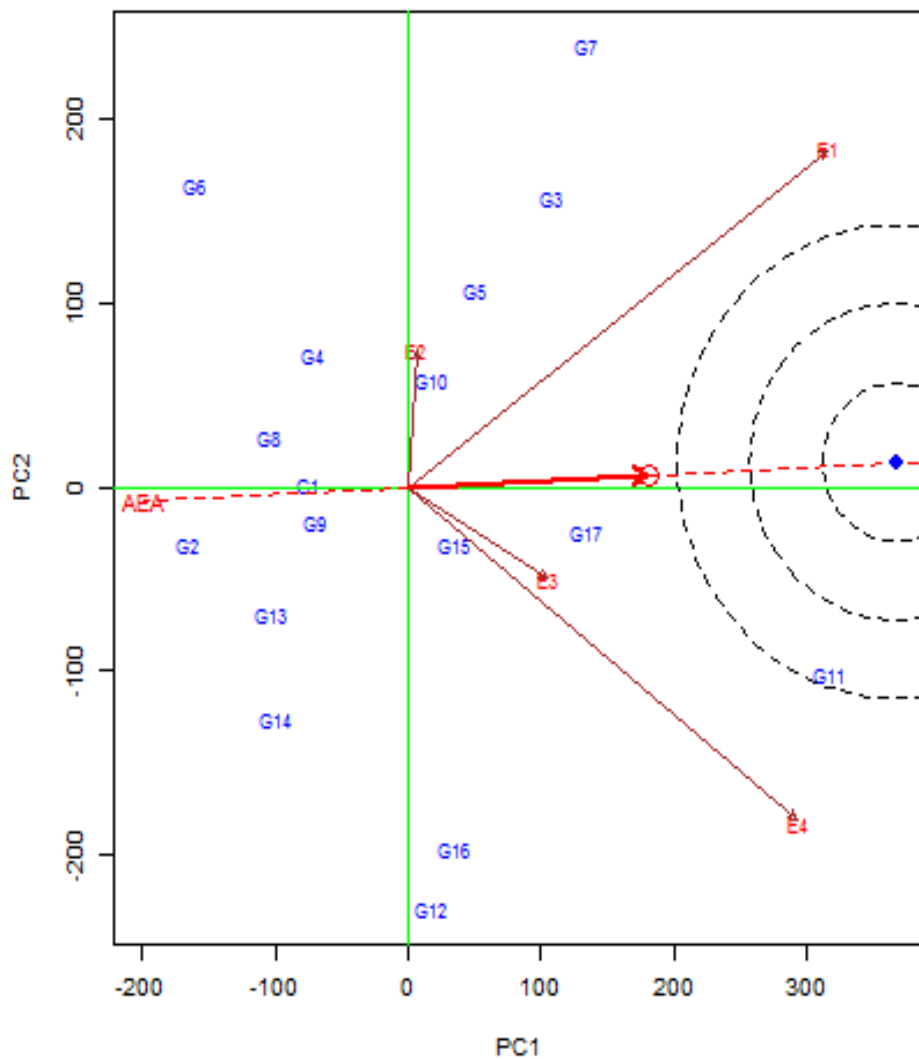


Figure 5. The biplot showing discriminativeness and representativeness based on genotype by environment yield data of 17 accessions of okra evaluated across 4 environments between 2018 and 2020.

The ranking of other environments based on the ideal nature of environments showed that Akure 2020 (E4) was the most discriminatory. Environment E3 has a large PC1 score and a low PC2 score, so this environment is more stable and suitable for all genotypes. This is in accordance with the result of Akter et al. (2015), who reported that environment E3 had a large PC1 score and a small PC2 score, and, as a result, the environment is more stable and suitable for all accessions and that E4 was a discriminating environment due to its large PC2 score.

Conclusion

The AMMI analysis identified NGB00378a to be the most stable accession and high yielder, whereas NGB00331 and NGB00355 also identified as high yielders were highly unstable. Similarly, the GGE biplot identified NGB00378a as a highly stable and high yielder, whereas NGB00355 was the highest yielder, but fairly stable. On the other hand, NGB00378a combines good performance with stability. Therefore, NGB00378a is the ideal accession and should be recommended. The GGE biplot method gave a superior and more thorough description of the stability of the seventeen accessions in identifying the ideal accession and the environment, and reduced the four environments into two mega environments.

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ANALIZA VISINE I STABILNOSTI PRINOSA GENOTIPOVA BAMIJE
(*ABELMOSCHUS ESCULENTUS* L. MOENCH) KORIŠĆENJEM
AMMI I GGE BIPLOTA

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R e z i m e

Identifikacija prilagodljivih, stabilnih i visokoprinosnih genotipova u različitim uslovima spoljne sredine pre puštanja u promet, predstavlja veliki izazov za oplemenjivače biljaka pri odabiru najboljih genotipova bamije. Interakcija genotip \times sredina je veliki izazov za oplemenjivače biljaka, jer velika interakcija može smanjiti selekcionu dobit i otežati identifikaciju superiornih sorti. Ciljevi ovog istraživanja bili su da se proceni vrednost genotipova bamije u različitim spoljnim sredinama i da se identifikuju visokoprinosni i stabilni genotipovi, kako bi se izabrao roditelj za dalji selekcionu rad. Sedamnaest genotipova bamije je ocenjeno na lokalitetu Akure tokom kišne sezone 2018. godine, zatim na lokalitetima Akure i Oje tokom kišne sezone 2019. godine i na lokalitetu Akure tokom kišne sezone 2020. godine, što čini ukupno četiri spoljne sredine. AMMI i GGE biplotovi korišćeni su za procenu interakcije $G \times E$ i proučavanje stabilnosti u četiri spoljne sredine. AMMI analiza je identifikovala, NGB00378a kao najstabilniji genotip i genotip sa visokim prinosom. Takođe, GGE biplot je identifikovao, NGB00378a kao visoko stabilan genotip sa visokim prinosom, dok je NGB00355 bio identifikovan kao najprinosniji genotip, ali umerene stabilnosti. Ipak, u slučaju genotipa NGB00378a, dobar učinak se kombinuje sa stabilnošću. S tim u vezi, NGB00378a predstavlja idealan genotip, koji treba preporučiti za dalji oplemenjivački rad.

Ključne reči: spoljna sredina, genotip, interakcija, prinos, stabilnost.

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