Genotype sensitivity and adaptability for fruit yield in red and green okra on environmental change

SHAHRIZAL M. ABDILLAH[1,♥], MUHAMAD SYUKUR[2,♥♥], WILLY B. SUWARNO[2], ARYA W. RITONGA[2], ANUNG WAHYUDI[3]

[1]Plant Breeding and Biotechnology Graduate Program, Department of Agronomy and Horticulture, Faculty of Agriculture, Institut Pertanian Bogor. Jl. Meranti, Kampus IPB Darmaga, Bogor 16680, West Java, Indonesia. Tel.: +62-251-8629354, Fax.: +62-251-8629352, ♥email: shahrizalmuhabdillah@gmail.com
[2]Department of Agronomy and Horticulture, Faculty of Agriculture, Institut Pertanian Bogor. Jl. Meranti, Kampus IPB Darmaga, Bogor 16680, West Java, Indonesia. Tel.: +62-251-8629354, Fax.: +62-251-8629352, ♥♥email: muhsyukur@apps.ipb.ac.id
[3]Seed Technology Study Program, Food Plant Cultivation, Politeknik Negeri Lampung. Jl. Soekarno Hatta No. 10, Rajabasa Raya, Bandar Lampung 35144, Lampung, Indonesia

Manuscript received: 30 May 2023. Revision accepted: 10 August 2023.

Abstract. *Abdillah SM, Syukur M, Suwarno WB, Ritonga AW, Wahyudi A. 2023. Genotype sensitivity and adaptability for fruit yield in red and green okra on environmental change. Biodiversitas 24: 4289-4298.* Okra is a vegetable plant consumed in immature and beneficial plants of various health. For breeders, this crop had a big chance to develop a high-yield genotype in various conditions. To develop a new variety must be known adaptability and stability in environment tests. This research aimed to evaluate the fruit yield response, sensitivity, and adaptability of okra genotypes in four environment trials. A randomized complete block design with three replications was used in each environment, with ten okra genotypes as the treatment. The AMMI-1, AMMI-2 and GGE biplot illustrated genotype stability and their adaptability. Genotype by environment interaction significantly affected fruit yield, with the environment having a large contribution, with SWR01 being the highest yield. The rate of rainfall and PC1 were explained as 36.98% and 70.17% to the GEI sum of squares, respectively. 'ZAHIRA' and 'GSO03' showed sensitivities to the rate of rainfall. Genotypes 'SWR01' and 'GSO03' were the most favorable genotypes according to ASV and yield performance across environments The AMMI-1, AMMI-2 and GGE biplot confirmed that both were the most suitable genotypes for developing a recent variety of okra in a wide environment.

Keywords: Adaptability, AMMI, GEI, okra, sensitivity, stability

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is a vegetable crop cultivated for a long time in tropical to subtropical regions, ranging from the Mediterranean to equatorial regions (Gemede et al. 2015). Generally, okra differs from other vegetable crops because its fruits contain a lot of mucilage or sap. Various parts of the okra plant have been widely utilized in everyday life, such as the leaves used for hair oil, okra seeds as an alternative coffee beverage, and stem fibers for the textile industry. Most commonly, the fruit of okra is utilized as a vegetable. There are two types of okra: red okra and green okra. The difference between these two types lies in the color of various plant parts, such as the leaf veins, stem, and fruit. Apart from the color resulting from anthocyanin content, there are no striking differences between red and green okra. The okra fruit contains vitamins, calcium, potassium, proteins, fats, and carbohydrates (Durazzo et al. 2019; Sindu et al. 2016). Furthermore, the okra fruit also contains bioactive compounds such as anti-hyperlipidemic agents (Zhang et al. 2018; Nie et al. 2020) and antioxidants (Yuan et al. 2012; Graham et al. 2017). In China, okra is a traditional medicine to prevent diabetes and obesity (Xia et al. 2015). The fruit and okra seeds contain antioxidants, with a content of 598 mg TEAC kg-1 d.w. (Fabianova et al.

2022). It is known that red okra has higher antioxidant content compared to green okra (Anjani et al. 2018).

During the growth phase, okra requires a long period of moisture and temperature. Okra is a plant sensitive to low temperatures, which hampers its growth during the vegetative phase. The microclimate in the environment is a difficult factor to control in agricultural cultivation, making it a primary consideration. Like other plants, okra exhibits different responses due to variations in the microclimate. Genotype x environment interactions may affect yield performances in each environment. It is also influenced by production characteristics, such as fruit weight, a complex trait resulting from the additive effects of genotype, environment, and interactions. The presence of genotype x environment interactions in okra productivity allows for the achievement of maximum yield potential by planting in different environmental conditions.

Climate change in Indonesia recently became a limiting factor that has an impact on the process of agricultural cultivation. Moreover, threats to food, energy, and water security are of great concern in Indonesia (Purwanto et al. 2021). In addition, the climate is an environmental factor that is relatively difficult to control in agricultural cultivation, so it is a major consideration. On the other hand, yield is the complex traits with the accumulation of genotype, environment, and genotype by environment

interaction effect (GEI). Also, different conditions and environments will affect the performance of genotypes (Rubilar et al. 2020). Due to the influence of GEI on okra yield, the maximum yield potential is achieved by planting in various environments with different climatic conditions.

Genotype x environment interactions result in different genotype responses in various environmental conditions, as Olanrewaju et al. (2021) reported in peanuts, affecting stability and yield potential. To evaluate the genotype x environment interactions, several methods can be employed. Currently, the AMMI method is an excellent approach to explain the structure and pattern of genotype x environment interactions in various crops, such as maize (Katsenios et al. 2021), wheat (Gupta et al. 2022), rice (Siddi et al. 2022), chili (Anilkumar et al. 2018), peanuts (Esan et al. 2023), and okra (Sanwal et al. 2020). Furthermore, the AMMI biplot provides visualization regarding the adaptability of specific and broad genotypes. Apart from the AMMI model, factorial regression is another method that can be used to assess the contribution of microclimate factors in genotype x environment interactions. This model allows the inclusion of multiple microclimate factors in the analysis of genotype x environment interactions, enabling the estimation of genotype sensitivity to microclimate factors. Using both of these analytical models makes it possible to comprehensively study the patterns, structure, and contribution of climate factors to genotype x environment interactions. Therefore, this study aims to evaluate the performance of red and green okra genotypes across different environments, estimate genotype x environment interactions and genotype sensitivity to microclimate, and determine genotypes that are stable and broadly or specifically adapted to the environment.

MATERIALS AND METHODS

Plant materials and experimental design

This study used ten okra genotypes (Table 1), consisting of four red okra and green okra genotypes, along with two varieties, red and green okra (Figures 1 and 2). This experiment was conducted in 4 environments (Table 2), including Leuwikopo Experimental Garden IPB, Dramaga Subdistrict, Bogor West Java on March 2022 (ENV1) and Augustus 2022 (ENV2), farmer field in Jenggawah Subdistrict, Jember, East Java on October 2022 (ENV3) and Polinela Experimental Garden, Rajabasa Subdistrict, Bandar Lampung, Lampung (ENV4). Seed harvested from 'ENV1' was used to material in 'ENV2', 'ENV3' and 'ENV4'.

Each trial used a randomized complete block design with three replications. The seedling with 3-5 perfect leaves was planted after ± 21 days of sowing. Plants were watered every day in the morning and afternoon. Every once a week, plants were fertilized with NPK solution (16: 16: 16) 10 g l^{-1}. Insecticide Prefenophos and fungicide with Mancozeb 80% were used to prevent pests and diseases of the plant. The fruit was harvested when still tender and bright color, once a week harvested two times. The trait observation was fruit yield (ton ha-1) in each environment. The meteorology data were collected from the database center of BMKG online on each trial.

Statistical analysis

A combined analysis of variance (ANOVA) was used as a base model to study the GEI on fruit yield (ton ha^{-1}). The significance of mean square GEI was tested using F-test, followed by Tukey test 5% when significance resulted. The study of GEI used three models: the base model, the factorial regression model, and the AMMI model. A factorial regression evaluated the essential environmental factor driving the most GEI fruit yield and genotypic sensitivity to different environmental covariable. This model uses the mathematical formula described by Malosetti et al. (2013) and as follows:

$$E(Y_{ij}) = \mu + \alpha_i + \beta_j + \sum_{k=1}^{K} \varsigma_{ik} z_{jk}$$

Where: α_i represents the genotype; z_{jk} refers to the value of any environmental covariable k for environment j; and ς_{ik} estimates the sensitivity of genotype i to the environmental covariable k. The sum of multiplicative $\sum_{k=1}^{K} \varsigma_{ik} z_{jk}$ approaches the GEI sum of squares. The data were analyzed using SAS on Demand for Academics (https://welcome.oda.sas.com/) by PROC MIXED procedures.

Table 1. List of ten red and green okra genotypes used in this study

Code	Source	Type	Code	Source	Type
SWR01	Line	Red okra	GSO03	line	Green okra
SWR02	Line	Red okra	GSO04	Line	Green okra
SWR03	Line	Red okra	SWR04	Line	Red okra
GSO01	Line	Green okra	NAILA	Variety	Green okra
GSO02	Line	Green okra	ZAHIRA	Variety	Red okra

Table 2. Description of environments used in this study

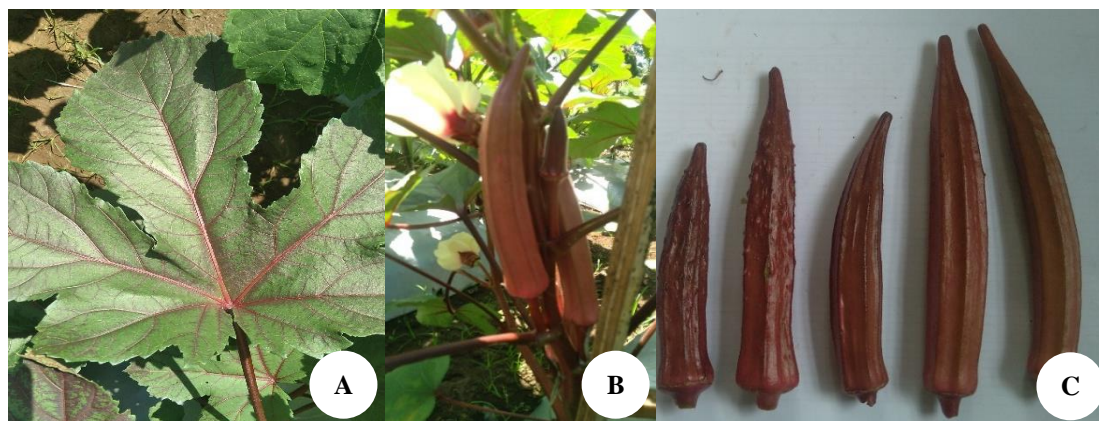| Code	Location	Altitude	Planting
ENV1	Leuwikopo Teaching Farm IPB University, Bogor West Java	200	March 2022
ENV2	Leuwikopo Teaching Farm IPB University, Bogor West Java	200	September 2022
ENV3	Farm field, Jenggawah Subdistrict, Jember East Java	20	September 2022
ENV4	Polinela Teaching Farm, Lampung	112	September 2022

Figure 1. Morphological of red okra: A. Leaf shapes. B. Stem colors. C. Fruit shapes and colors (from left to right: ZAHIRA, SWR01, SWR02, SWR03 and SWR04)
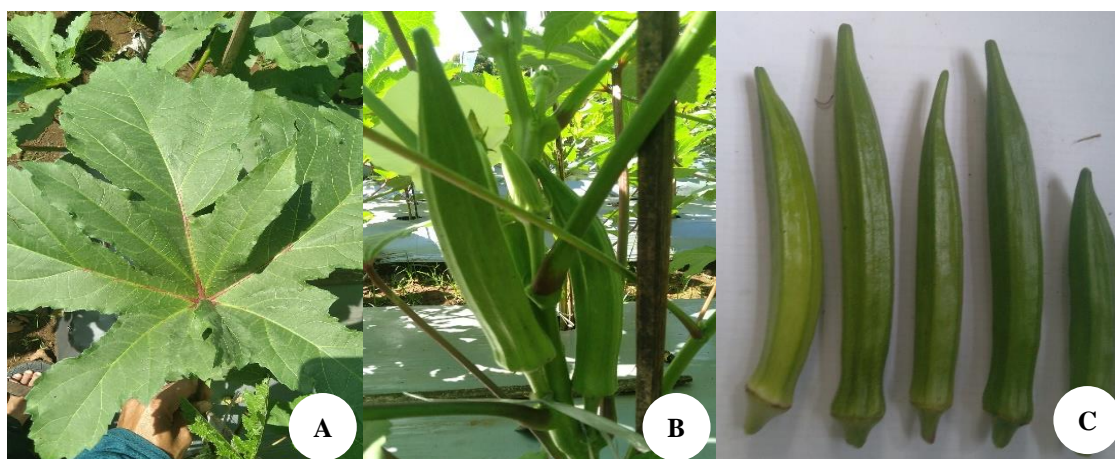

Figure 2. Morphological of green okra: A. Leaf shapes. B. Stem colors. C. Fruit shapes and colors (from left to right NAILA, GSO01, GSO02, GSO03, and GSO04)

The AMMI model was used to decompose the multiplicative GEI effect built upon the base model. It allows by subset of interaction principal components (PCs). A linear model can be formed as follows:

$$(\alpha\beta)_{ij} = \sum_{n=1}^{N} \lambda_n \Upsilon_{in} \delta_{jn}$$

Where: λ_n represents singular value associated with PC n, N is the number of PC. Υ_{in} represents genotype eigenvector i pada PC n, δ_{jn} represents environment eigenvector j for PC n, with all eigenvectors scaled as unit vectors. Genotype stability can be described by distance, as proposed by Jędzura et al. (2023). It helps to identify stable genotypes across environments based on AMMI stability value (ASV). AMMI-1, AMMI-2 and GGE biplots (the which-won where and ranking genotypes) were used to illustrate the stability and adaptability of genotypes across environments. The AMMI and GGE biplot were supported by the 'metan' packages in R (https://cran.r-project.org/web/packages/metan/index.html).

RESULTS AND DISCUSSION

Microclimates conditions in the environment

The microclimate in each environment was recorded during okra cultivation, starting from land preparation to the final harvest. Fruit harvesting began in May in 'ENV1,' while the initial harvest took place in other environments in November. All tested environments showed a tendency for microclimate variability during the growing period (Figure 3). Rainfall in each environment fluctuated throughout the periods, with the highest peak in April II in 'ENV1,' while the highest peaks in October I, November III, and October III were observed in 'ENV2,' 'ENV3,' and 'ENV4,' respectively. The highest relative humidity was found in 'ENV1' and 'ENV2.' The average temperature in 'ENV1' and 'ENV2' ranged from 21°C to 25°C. On the other hand, the highest average temperature in 'ENV3' and 'ENV4' ranged from 25°C to 33°C. 'ENV3' and 'ENV4' represent lowland areas.
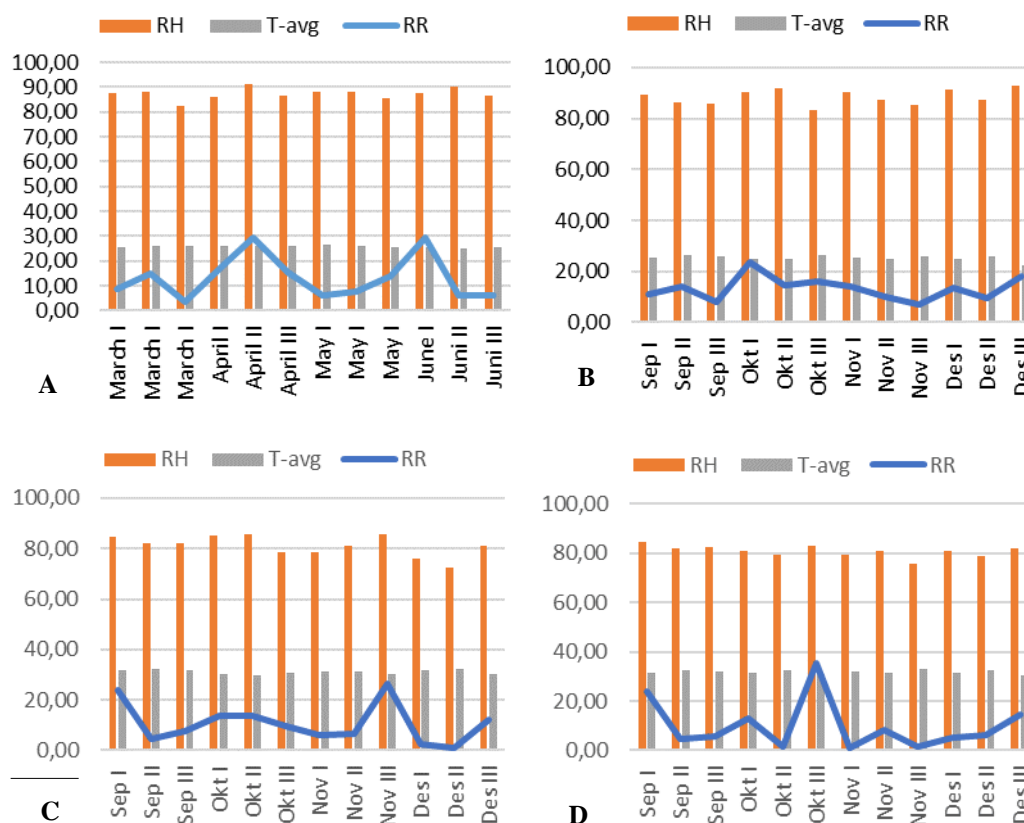
Figure 3. Variability climatic conditions for the four examined environments during the cultivation in: A. ENV1 (Bogor 1); B. ENV2 (Bogor 2); C. ENV3 (Jember); and D. ENV4 (Lampung). RH (average relative humidity), T-avg (average temperature), RR (average rainfall). Source: BMKG online

Genotype by environment interaction

The analysis of variance results is presented in Table 3, where all components of variation show highly significant differences, except for the main genotype factor. The main environmental factor in the general model has the highest proportion of the total sum of squares explained (47.20%), followed by the genotype x environment interaction factor (22.54%). These indicate that environmental factors and interactions are more dominant in influencing the variability of fruit weight response in okra genotypes. The high proportion of the environmental factor indicates that the fruit weight response varies across the tested environments. The genotype x environment interaction factor implies adaptability to each environment and varying sensitivity to microclimate.

Microclimate factors in the environment, hereafter referred to as covariates, can be included in the analysis model through factorial regression. This model can estimate the contribution of microclimate factors to the variability of genotype x environment interactions in fruit weight response. Table 3 shows that the average temperature, relative humidity and rainfall have a highly significant influence. The most considerable contribution of microclimate factors to GxE interaction is rainfall at 35.95%, followed by average temperature at 33.68%. The significance interaction between genotype and microclimate factors indicating that there are okra genotypes that are

sensitive to the microclimate of the environment.

The AMMI model shows the variation of genotype x environment interaction effects on fruit weight, resulting in three main interaction components (Table 3), with PC1 and PC2 showing highly significant and significant differences, respectively. These results indicate that these two main components can explain the variation of genotype x environment interaction. PC1 has the most significant proportion at 68.00%, followed by PC2 at 29.30%, with a cumulative proportion of 97.30%. PC3 represents the residual decomposition of interaction effects with a proportion of 2.70%. Based on the AMMI analysis, it is evident that the main environmental influence, which includes microclimate variations, can cause differences in the fruit weight response of okra. Similar findings were reported by Bishwas et al. (2021), showing that high environmental variability contributes more to the variation of genotype x environment interactions.

Genotype performance

The performance of genotypes across environments for fruit weight can be presented in Table 4. Genotype 'SWR01' (23.43 ton ha-1) exhibited the highest average response compared to the two okra varieties, 'ZAHIRA' and 'NAILA,' in the 'ENV1' environment, followed by genotype 'GSO03' (20.16 ton ha-1). Thus, genotype 'SWR01' has an ideal fruit yield for cultivation in 'ENV1'. The highest average fruit yield response of okra genotypes in 'ENV2'

was shown by genotype 'GSO04,' although it was not significantly different from other genotypes. In 'ENV3,' the highest yield response of okra genotypes was exhibited by 'ZAHIRA,' 'SWR03,' and 'SWR04'. Furthermore, genotype' NAILA' showed the highest fruit yield in 'ENV4' (13.41 ton ha-1). Therefore, the okra lines tested in 'ENV3' and 'ENV4' did not perform better than their commercial varieties, namely 'ZAHIRA' and 'NAILA'. Genotypes' fruit yield response across environments ranged from 12.49 to 15.29 ton ha-1. Genotypes 'SWR01' and 'GSO02' were considered ideal genotypes across environments as they had better fruit yield responses than other genotypes, although they were not significantly different. The highest environmental response for okra fruit yield was observed in the 'ENV1' environment, with 14.48 ton ha-1, while the lowest response was shown in 'ENV3' at 8.78 ton ha-1. Thus, 'ENV3' provided a low response for the tested okra genotypes but not significantly different to the others.

Genotype sensitivity

Genotype sensitivity to changes in microclimate can be assessed using factorial regression by incorporating environmental covariates. Each genotype can exhibit a positive or negative response to changes in microclimate. Genotype sensitivity can be interpreted as how a one-unit change in microclimate can increase or decrease the fruit yield response. Based on Table 5, genotype 'ZAHIRA' shows a significant and positive sensitivity to relative humidity (2.47) but a significant and negative sensitivity to average rainfall (-3.73), indicating that genotype 'ZAHIRA' is highly dependent on high humidity to produce increased fruit weight. However, an increase in rainfall can decrease the fruit weight production of this genotype, also 'NAILA' showed significant and negative sensitivity to rainfall change in environments (-2.40). In contrast, genotype 'GSO03' and 'SWR04' exhibits a significant and negative sensitivity to temperature (-2.06 and -2.34, respectively), indicating that an increasing temperature in the environment tested will enhance the fruit weight production of this genotype. On the other hand, an increase in temperature in the environment causes an increasing in fruit yield for genotypes 'GSO02' (-2.52). However, genotype 'GSO02' shows significant and positive sensitivity to changes in temperature (2.12), indicating that this genotype exhibits optimal fruit weight production with increasing temperatures in the environment. Overall, the analysis of genotype sensitivity to microclimate change showed that no genotype was simultaneously sensitive to all microclimate factors. However, some genotypes showed sensitivity to one or two specific microclimate factors.

Table 3. Combined analysis of variance for fruit yield (kg per-plot) using the base, factorial regression, and AMMI models

Model	Source	DF	MS	F-value	% TSS	% SS to GxE
	Environment (E)	3	432.84	21.37 **	47.20	-
	Replication / E	8	20.25	2.55 **	5.88	-
Base model	Genotype (G)	9	11.08	1.40	3.63	-
	GxE	27	22.96	2.90 **	22.54	-
	Error	72	7.93		20.74	-
Factorial regression	G x Tavg	9	23.20	2.93 **	7.59	33.68
	G x RH	9	20.93	2.64 **	6.85	30.37
	G x RR	9	24.77	3.12 **	8.10	35.95
	PC1	11	38.35	4.84 **	15.33	68.00
AMMI	PC2	9	20.18	2.54 *	6.60	29.30
	PC3	7	2.36	0.30	0.06	2.70

Note: ** significant at 1%, * significant at 5%, degree of freedom (DF), sum of squares (SS), mean square (MS) the percentage of SS each factor explained to total SS (% TSS), and the percentage of SS each variable explained to GxE SS (SS to GxE), RH: average relative humidity (%), RR: averege rainfall (mm), T-avg: average temperature (ºC)

Table 4. Fruit yield (ton ha-1) response in okra genotypes in each environment

Genotypes	Environments				Genotype means (ton.ha-1)
	ENV1	ENV2	ENV3	ENV4	
SWR01	23.43 a	13.78 a	11.73 a	12.21 a	15.29
SWR02	19.13 abc	10.44 a	6.57 ab	14.26 a	12.60
SWR03	19.41 abc	12.65 a	13.75 a	9.70 a	13.88
SWR04	20.94 ab	12.54 a	3.42 b	13.05 a	13.08
GSO01	19.62 abc	12.18 a	6.15 ab	13.05 a	12.49
GSO02	20.96 ab	14.25 a	11.43 a	12.29 a	12.75
GSO03	20.16 abc	14.04 a	8.37 ab	13.51 a	14.73
GSO04	16.68 abc	11.80 a	13.20 a	10.66 a	14.02
NAILA	14.56 bc	12.84 a	9.20 ab	14.90 a	12.87
ZAHIRA	12.96 c	12.22 a	13.76 a	13.13 a	13.02
Environment means (ton.ha-1)	14.48 A	9.36 B	8.78 B	11.41 B	13.47

Note: the numbers followed by the same letter in the same column and the number followed by the same capital in the same line are not significantly different according to 5% Tukey test

AMMI stability and biplot analysis

Genotype stability can be measured using the AMMI stability value (ASV) or AMMI stability value (Table 5). The ASV values of genotypes range from 0.67 to 4.29, with the lowest ASV value indicating the most stable genotype. Genotype 'GSO03' has the lowest ASV value (0.69), making it the most stable genotype across different environmental conditions. It was followed by genotypes 'NAILA' and 'SWR01' with the ASV values (1.42 and 1.45, respectively). Furthermore, genotypes 'SWR01' and 'GSO03' have the highest average response in fruit weight across all environments (15.29 and 14.02 ton ha-1, respectively), making them genotypes with high and stable fruit yield responses in all environments.

The results from the AMMI1 biplot analysis (Figure 4) showed the average fruit yield response of genotypes and environments on the X-axis. At the same time, the respective PC 1 scores were plotted on the Y-axis, explaining 68.0% of the variation. The vertical line dividing the biplot represented the overall fruit yield response and a score of zero for PC 1. Therefore, genotypes located to the right of the biplot center point had fruit yield above grand mean, such as genotypes 'SWR01,' 'GSO03,' 'GSO04,' and 'SWR04.' Furthermore, genotype 'NAILA' was closest to the center point, indicating it was the most stable genotype but with a lower average fruit yield. Based on the AMMI1 biplot, genotypes 'SWR01' and 'GSO03' exhibited high and stable fruit yield across all environments.

The AMMI2 biplot (Figure 5) showed the percentages explained by PC 1 and PC 2, which were 68.0% and 29.3%, respectively, accumulating to 97.3% of the variation in genotype x environment interaction for fruit yield. Genotypes close to the center point of the biplot were the most stable across all environments. Therefore, genotypes 'GSO03' and 'GSO04' were relatively close to the center point of biplot, indicating that the most stable genotypes. Genotypes close to specific environments represent specific adaptability, such as genotype 'SWR04' were able for 'ENV3,' while genotype 'SWR01' were able for 'ENV1.'

Table 5. Genotype sensitivity to environment covariate based on factorial regression and fruit yield (kg per-plot)

Genotype	Average humidity (%)	Average rainfall (%)	Average temperature (ºC)	AMMI Stability Value (ASV)
SWR01	-1.03	3.33 **	0.85	1.45 +
SWR02	-0.58	1.95	0.61	2.06
SWR03	-0.31	-0.40	-1.02	2.62
SWR04	-0.36	-2.01	-2.34 *	2.97
ZAHIRA	2.47 *	-3.73 **	1.20	4.47
GSO01	-0.01	-0.75	0.42	4.29
GSO02	2.05	-1.14	2.52 **	2.31
GSO03	-1.65	0.86	-2.06 *	0.67 +
GSO04	-1.11	2.80 *	0.85	1.42 +
NAILA	0.53	-2.40 *	-1.03	1.88

Note: * significantly different at 5%; ** significantly different at 1%; + favorable genotype
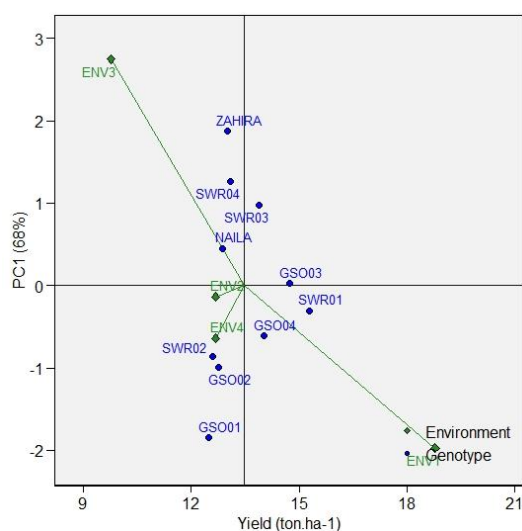

Figure 4. The AMMI-1 biplot for stability and high yield okra fruit across environments
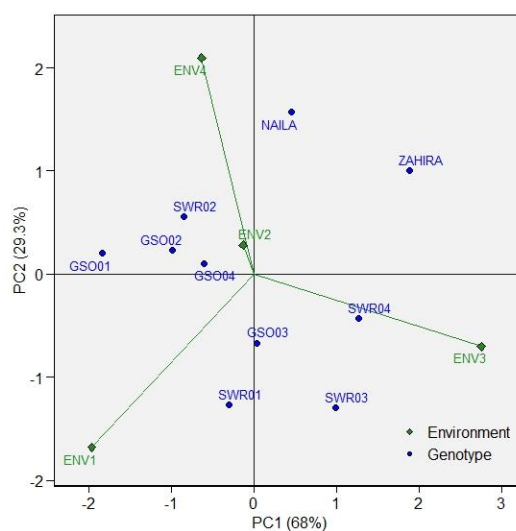

Figure 5. AMMI-2 biplot for genotype by environment interaction for yield
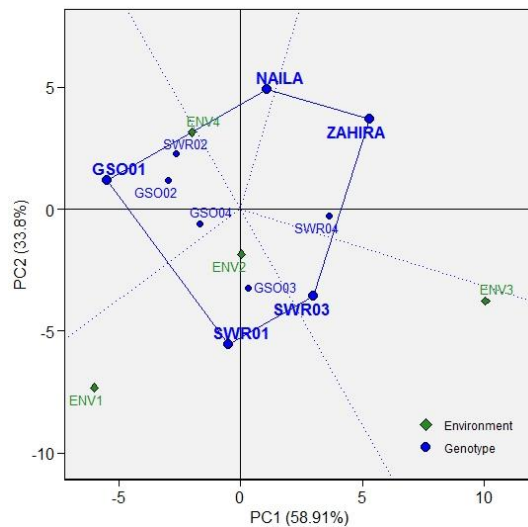
Figure 6. The which-won-where pattern GGE biplot on genotype by environment interaction for fruit yield

Figure 7. The ideal-okra genotype based on ranking genotypes pattern in GGE biplot on for fruit yield and stable

The AMMI analysis of PC scores obtained from the singular value decomposition can be used to detect crossover genotype interactions. The genotype PC 1 scores range from -1.84 to 1.87, while the PC 2 scores range from -1.29 to 1.57 (Figure 5). These scores can determine the interaction patterns of genotypes. Opposite scores on PC 1 and PC 2 (positive-negative or vice versa) indicate crossover interactions. Thus, genotypes 'SWR02,' 'SWR03', 'SWR04', 'GSO01', 'GSO02', and 'GSO03' exhibited crossover interaction patterns. These indicate that the yield performance of okra genotypes in each environment various. Crossover interactions are related to the level of genotype adaptation to the environment.

Figure 6 showed the GGE biplot pattern of which-won-where adaptation specificity of genotypes to environments. The percentages explained by PC 1 and PC 2, represented the genotype x environment interaction, were 58.91% and 33.80%, respectively. The dotted lines dividing the five genotype sectors, namely 'SWR01,' 'SWR03,' 'ZAHIRA,' 'NAILA,' and 'GSO01,' served as the vertices. These genotypes exhibited good responses in specific environments but had poorer responses when planted in other environments. The mega-environment sectors formed in this biplot pattern also represented three environmental sectors. 'ENV1' and 'ENV2' were within one mega-environment sector, while 'ENV3' and 'ENV4' were separated on the biplot. Thus, genotype grouping based on specific environmental adaptability could be easily explained. Genotype 'SWR01' exhibits high yield when planted in 'ENV1' and 'ENV2.' In 'ENV3,' genotype 'SWR03' showed better response when planted in that specific environment. Similarly, genotype 'GSO01' showed good fruit weight response when planted in 'ENV4'.

Based on Figure 7 showed the ideal genotype across environments based on ranking genotypes in GGE biplot analysis. The ideal genotypes were defined by their position are closest on the concentric circle. According to this, genotypes 'SWR01', 'GSO03' and 'SWR03' were
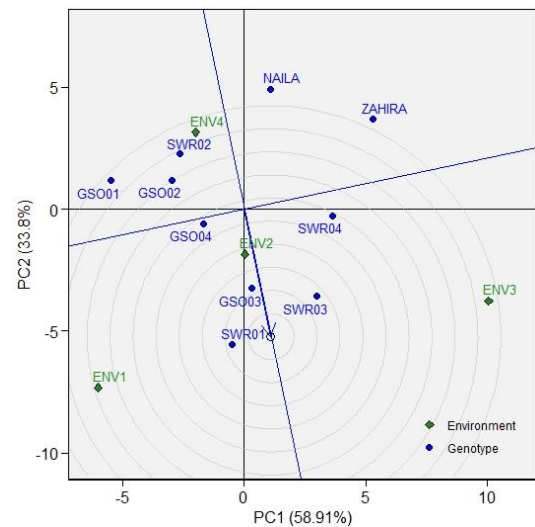
ideal genotype based on this biplot. Also, these genotypes had the high-yield compared with these two varieties. This biplot found that genotype 'NAILA' and 'ZAHIRA' located farthest from the concentric circle, so both genotypes are worst genotypes across environments.

Discussion

This study showed considerable variability in microclimate within the environment, leading to variations in fruit weight production in each environment. It reinforces the notion that the characteristics of the microclimate influence the fruit production of each okra genotype. Increases in temperature, high rainfall, and humidity can result in different responses in terms of production. The four environments tested in this study are lowland areas (< 400 m above sea level) with relatively high temperatures ranging from 20 to 30°C. Additionally, okra is a plant that can adapt well to tropical and subtropical regions. According to Khulluq et al. (2022), temperatures in tropical regions are relatively higher compared to sub-tropical regions due to differences in received radiation on the average surface of 700 W/m². The average temperature in the 'ENV1' environment throughout the period is relatively lower compared to other environments, yet it has higher average fruit weight production compared to other environments. Therefore, other microclimate factors also contribute significantly to the performance of the tested okra genotypes. During the growth period, okra requires a minimum temperature of 18 to 30°C (Makinde et al. 2022).

The environmental effect (47.20%) was larger than genotype effect (3.63%) on the proportion of the total sum of squares (Table 3). It leads to variations in fruit yield on each tested environment. Genotype evaluation in each environment indicated varying responses in fruit yieled among the tested genotypes, signifying the presence of genotype x environment interaction effects. Similar findings have been reported by Olanrewaju et al. (2021),

where genotype x environment interaction effects significantly contribute to peanut pod yield. The heterogeneity of the microclimate in each environment also contributes significantly to the response. It can be observed from the interaction between genotype and microclimate in the regression factorial model. The contribution of microclimate factors (RH, RR, and Tavg) to the variation in genotype x environment interaction results in genotype sensitivity to changes in microclimate, thereby affecting fruit yield positively or negatively. In this study, four genotypes tested were sensitive to changes in rainfall within the environment. It can be inferred that the differential rainfall in all environments tested may influence these genotype responses. Also, the temperature in environment tested contributed to the variation of genotype x environment interaction on fruit yield. According to Aliku et al. (2022), temperature is the dominant factor affecting evapotranspiration as it is constantly changing and varies across different environments. The analysis of variance with the factorial regression model allowed for the inclusion of microclimate factors that play a role in genotype x environment interaction. In this study found that the rainfall rate had a key role to the variation of fruit yield genotype response across environments.

The presence of genotype x environment interaction led the adaptability of each genotype to different environments. Moreover, yield-related traits (such as fruit yield) result from genetic and plant responses to growing conditions (Sabaghnia et al. 2015). Therefore, understanding genotype x environment interaction is crucial as it helps determine genotypes that have specific or broad adaptability (Ummiyah et al. 2021; Singh and Shukla 2022). The AMMI model enabled the analysis of genotype adaptability and stability through the PC1 and PC2 scores of genotypes and graphical visualization using biplots. The AMMI analysis has been widely used to evaluate genotype x environment interactions in various crops, including maize (Brankovic-Radojcic et al. 2018), wheat (Bishwas et al. 2021), sugarcane (Da Silveira et al. 2013), barley (Kilic et al. 2014), okra (Sanwal et al. 2020), and potato (Gurmu et al. 2020). This method is highly effective as it can separate the main effects (genotype and environment) from the interaction effects, allowing only the interaction effects to be included in the analysis model (Singh et al. 2019). One stability parameter in the AMMI method is the ASV, which is based on the distance between the PC1 and PC2 scores of genotypes from the biplot center. The PC1 and PC2 scores of genotypes represent the genotype x environment interaction effects. The small PC1 scores indicate smaller ASV values, indicating greater stability of the genotypes across environments. This method effectively measures genotype stability across environments by assessing the magnitude of the interaction effects. Genotypes 'ZAHIRA' and 'GSO01' have high ASV scores, indicating that these genotypes were not favorable for cultivation across all environments. Thus, these genotypes are relatively adapted to specific environments.

The visualization of AMMI through biplots effectively explained the stability and adaptability of genotypes across environments. According to Scavo et al. (2023), biplot visualization could explain the main effects and interactions in a two-dimensional separately. The AMMI1 biplot (Figure 2) illustrated the fruit yield and the genotype x environment interaction effects, revealing genotypes with high yield with low interaction effects was the favorable genotypes. Therefore, genotypes 'SWR01' and 'GSO03' had high and stable fruit yield across all environments. However, the AMMI2 biplot (Figure 3) showed the interaction effects of the genotype x environment, allowing the assessment of genotype stability based on the proximity of genotype vectors to the biplot center (Agahi et al. 2020). Both the AMMI1 and AMMI2 biplots comprehensively and integratively explain the genotype x environment interaction effects. According to the biplot AMMI1 and AMMI2 genotype 'GSO03' was the best performance across environments with high-yield and stable. The stability analysis using the ASV parameter clarified with the AMMI1 and AMMI2 biplots, where genotype 'GSO03' exhibited stability across all environments. It can be observed through the respective PC1 and PC2 scores of the genotype used in the analysis. These findings align with Khan et al. (2021), which may identify stable genotypes with high yield potential in peanuts across four tested environments.

The AMMI biplot indicated the stability and adaptability of genotypes across environments, it cannot specifically identify the optimal growing environments for all tested genotypes. The GGE biplot can be used for this purpose as its effective and elegant visualization allows for the interpretation of genotype x environment interactions (Esan et al. 2023). The "which-won-where" biplot demonstrates the adaptability of target genotypes to specific growing environments (Hashim et al. 2021). This biplot generates three mega-environments representing the suitability of growing environments for the fruit weight outcomes of the tested okra genotypes. Genotypes at the polygon vertices exhibit good fruit weight response in particular environments. Thus, the vertex genotypes represent the performance and adaptability of genotypes within the mega-environments, making them suitable for those environments (Khan et al. 2021). On the other hand, genotypes located outside the sector lines without any environment sector indicate that these genotypes are not selected due to their poor performance across all tested environments. To summarize the performance of genotype across environments, with stable and high yield may used the 'ranking genotypes' GGE biplot pattern (Figure 7). This biplot can be integrated by AMMI1 and AMMI2 biplot to select genotype with high-yield and stable.

This study demonstrated that the ten tested okra genotypes across four environments exhibit varying responses due to genotype x environment interaction. The environmental factor contributes significantly to the genotype x environment interaction, indicating that the variation in microclimate also affects the interaction. The rainfall factor showed the largest contribution of a microclimate throughout the genotype x environment interaction. Genotype 'ZAHIRA' is the most sensitive to changes in rainfall and humidity. Genotypes GSO03

exhibited the highest fruit yield across all environments. This genotype. Also, this genotype had stability and adaptability across all environments compared to other genotypes. This study can also identify genotypes that have specific adaptation to certain environments, such as 'SWR01' in 'ENV1' and 'ENV2', 'GSO01' in 'ENV4', and 'SWR03' in 'ENV4'. Genotypes 'GSO03' was potential candidates recommended for developing new candidates with high yield potential and good stability across lowland environments. These findings, resulted the red okra genotypes had specifically adapted environments.

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