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Full Length Research Paper

Genetic Analysis of Fruit Yield and Related Traits in Okra (*Abelmoschus esculentus* L. Moench) Genotypes Using Morphological and SSR Markers

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This study investigated the genetic variation in fruit yield and related traits among eight *Abelmoschus esculentus* genotypes using both morphological traits and Simple Sequence Repeat (SSR) markers. The genotypes were obtained from the National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan, and evaluated at the Teaching and Research Farm, Federal University of Technology, Akure, Nigeria, using a randomized complete block design (RCBD) with three replications. Analysis of variance revealed significant differences among genotypes for most traits. Phenotypic coefficients of variation (PCV) were consistently higher than genotypic coefficients of variation (GCV), indicating environmental influence on trait expression. Heritability estimates ranged from 4.78% to 68.81%, with high genetic advance observed for most traits, particularly plant height at flowering, days to maturity, and fruit length, suggesting additive gene action. Among the eight SSR markers used, four (OKRA104, OKRA105, OKRA108, and OKRA111) were highly polymorphic and informative, indicating their utility in diversity analysis and marker-assisted selection. Genotypes NGB00303, NGB00323, and NGB00324 exhibited superior performance in fruit yield and could serve as promising donor parents in okra breeding programs. Conversely, OKRA112 showed limited polymorphism and is not recommended for diversity studies in okra. These findings contribute to the identification of high-yielding genotypes and effective molecular tools for okra improvement.

Keywords: Okra, Genetic variability, Fruit yield, SSR markers, Morphological traits, Heritability

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is a member of the Malvaceae family and is widely cultivated in tropical and subtropical regions for its edible, nutrient-rich pods (Gemede et al., 2015; Elkhalifa et al., 2021). It serves as a staple vegetable due to its high content of vitamins A and C, folate, calcium, potassium, and dietary fiber, and it also offers health benefits such as antidiabetic, antihypertensive, and digestive properties (Das et al., 2019).

Despite its nutritional and economic significance, okra cultivation is constrained by low productivity, susceptibility to biotic and abiotic stresses, and limited genetic improvement—partly due to its self-pollinating nature and polyploid complexity (Dutta et al., 2024). Therefore, genetic enhancement focused on yield and agronomic traits is vital to improving okra productivity.

Genetic diversity plays a pivotal role in crop improvement programs. Morphological characterization offers initial insights into phenotypic variability, but these traits are often influenced by environmental conditions, which can obscure genetic differences (Govindaraj et al., 2015). Molecular markers, particularly Simple Sequence Repeats (SSRs), complement morphological assessments by revealing polymorphisms at the DNA level that may not be phenotypically evident (Ahmad et al., 2018; Bidyananda et al., 2024). SSRs are preferred due to

their co-dominant inheritance, reproducibility, and capacity to detect variation even among closely related genotypes.

Integrating morphological and molecular analyses can provide a comprehensive understanding of genetic diversity, assist in identifying superior genotypes, and support marker-assisted selection (MAS) in breeding programs (Cobb et al., 2019). This study aimed to:

i) assess the growth and yield performance of selected okra genotypes,

ii) determine the genetic components of yield-related traits, and

iii) evaluate genetic diversity using SSR markers.

MATERIALS AND METHODS

Plant Materials and Experimental Design

Eight okra genotypes—NGB00303, NGB00322, NGB00323, NGB00324, NGB00369, NGB00396, NGB00466, and NGB00429—were sourced from the National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Oyo State, Nigeria. Field evaluation was conducted at the Teaching and Research Farm of the Federal University of Technology, Akure, Ondo State, Nigeria.

The experiment followed a Randomized Complete Block Design (RCBD) with three replications. Each genotype was sown in a single-row plot across all replications, totaling 8 plots per replicate. Ten plants were maintained per plot with spacing of 60 cm between rows and 45 cm within rows. Weeding was carried out manually at three intervals during the growth period.

Fertilizer (Urea) was applied three weeks after planting and continued until maturity. Insect pest control was achieved through biweekly application of cypermethrin at a concentration of 50 mL per 10 liters of water, starting four weeks after planting.

Data Collection

Agronomic data were recorded from five randomly selected competitive plants per plot. The following traits were measured:

Days to 50% flowering
Plant height at flowering (cm)
Plant height at maturity (cm)
Days to maturity
Number of leaves per plant at flowering
Fruit width (cm)
Fruit length (cm)
Number of fruits per plant
Total fruit yield per plant (g)

Molecular Analysis

Genomic DNA Extraction

Fresh okra leaves (2g) were surface-sterilized with ethanol and ground in a mortar with 1,000 µL of freshly prepared modified CTAB extraction buffer (100 mM Tris-HCl, pH 8.0; 20 mM EDTA, pH 8.0; 1.4 M NaCl; 2% CTAB). The homogenate was incubated at 60°C for 30 minutes, followed by centrifugation at 12,000 rpm for 10 minutes. The supernatant was transferred to a sterilized eppendorf tube, and 10 µL of RNase was added. The mixture was incubated at 37°C for 5 minutes, cooled for 7 minutes, and then mixed with 1,000 µL of chloroform: isoamyl alcohol (24:1). After centrifugation at 12,000 rpm for 5 minutes, the supernatant was transferred to a new tube and mixed with 500 µL of isopropanol, then stored at –10°C for 30 minutes to precipitate the DNA.

The DNA pellet was obtained by centrifugation at 12,000 rpm for 2 minutes, washed with 500 µL of 70% ethanol, and air-dried. The DNA was eluted in 40 µL of TE buffer and stored at –10°C.

DNA Quantification

DNA concentration and purity were assessed using a UV spectrophotometer. A dilution containing 48 µL of TAE buffer and 2 µL of the DNA sample was prepared and measured at 260 and 280 nm wavelengths.

Gel Electrophoresis

DNA quality was verified using agarose gel electrophoresis. Five microliters of DNA sample and 2 µL of loading dye were loaded onto a 0.8% agarose gel prepared in TAE buffer. The gel was cast with 2 µL of SafeView dye, and electrophoresis was run at 120 volts for 10 minutes. DNA bands were visualized under a UV illuminator and documented.

RESULTS

Analysis of Variance

The analysis of variance (Table 1) revealed significant differences among the okra genotypes for most agronomic traits, including days to 50% flowering, plant height at maturity, days to maturity, fruit width, fruit length, number of fruits per plant, and total fruit yield per plant. However, differences in plant height at flowering and number of leaves per plant were not statistically significant, indicating less variation for these traits across genotypes.

Mean Performance of Genotypes

The mean performance of the eight genotypes is summarized in Table 2. Days to 50% flowering ranged from 63.73 days (G3) to 90.03 days (G8). Genotype G8 also recorded the tallest plants at flowering (78.01 cm) and maturity (181.03 cm), whereas the shortest plants were found in G7 at both stages (53.00 cm and 151.33 cm, respectively).

Genotype G1 exhibited the highest number of fruits per

Table 1. Analysis of Variance for the characters studied in the Okra genotypes, *Abelmoschus esculentus*

Source	Df	DT50%F	PHTF	PHTM	DTM	FW	FL (cm)	NFP	NLPF	TFY
Rep	2	25	34.98	100.81	10.51	0.76	0.69	81.43**	1.14	303.75
Genotypes	7	95.25**	92.20	177.05**	91.47**	7.99*	18.28*	15.62**	1.91	789.15*
Error	14	21.56	12.1	128.46	12.1	2.97	3.17	7.52	1.66	454.39

*, ** indicate significance at 5% and 1% level of probability, DF= degree of freedom, DT50%F = days to 50% flowering, PHTF = plant height at flowering, PHTM = plant height at maturity, DTM = days to maturity, FW = fruit width, FL = fruit length, NFP = number of fruit per plant, NLPF = number of leave per plant, TFY = total fruit yield per plant.

Table 2. Mean performance of agronomic characters studied in the okra genotypes, *Abelmoschus esculentus*

GENOTYPES	DT50%F (days)	PHTF (cm)	DTM (days)	PHTM (cm)	NLPF	FW (cm)	FL cm)	NFP	TFY (g)
G1	64.13	57.07	99.13	152.07	14.13	11.47	16.67	20.00	176.00
G2	73.13	62.07	107.13	159.73	12.67	10.20	10.87	15.67	120.38
G3	63.73	60.87	98.73	160.87	13.53	8.53	12.13	16.20	158.33
G4	81.20	71.20	116.20	167.87	13.47	9.13	14.93	17.27	145.33
G5	87.33	76.07	121.00	174.07	11.80	6.20	9.67	12.40	81.67
G6	75.93	56.00	112.60	156.00	12.33	8.40	13.93	15.27	125.67
G7	64.00	53.00	99.00	151.33	12.80	8.87	11.47	15.80	123.67
G8	90.03	78.01	125.03	181.03	11.12	4.61	7.23	9.41	70.71

DT50%F = days to 50% flowering, PHTF = plant height at flowering, PHTM = plant height at maturity, DTM = days to maturity, FW = fruit width, FL = fruit length, NFP = number of fruit per plant, NLPF = number of leave per plant, TFY = total fruit yield per plant.
G1= NGB00303, G2 = NGB00322, G3 = NGB00323, G4 = NGB00324, G5 = NGB00369, G6 = NGB00396, G7 = NGB00466, G8 = NGB00429

Table 3. Estimation of genetic parameters for characters studied among the Okra genotypes, *Abelmoschus esculentus*

CHARACTERS	MEAN	VG	VP	GCV%	PCV%	HB%	GA%	GAM%
DT50%F	74.935	24.563	46.123	6.614	9.063	53.256	744.910	9.941
PHTF	64.286	26.700	38.800	8.038	9.689	68.814	883.151	13.738
PHTM	162.871	16.197	144.657	2.471	7.385	11.197	277.473	1.704
DTM	109.853	26.457	38.557	4.682	5.652	68.618	877.798	7.991
FW	8.426	1.673	4.643	15.351	25.573	36.037	159.609	18.942
FL	12.113	5.037	8.207	18.528	23.651	61.373	362.849	29.957
NFP	15.253	2.700	10.220	10.773	20.959	26.419	174.153	11.418
NLPF	12.731	0.083	1.743	2.263	10.370	4.780	12.998	1.021
TFY	125.220	111.586	565.977	8.436	18.999	19.716	966.219	7.716

V_G = Genotypic variance; V_P= Phenotypic variance, PCV %= phenotypic coefficient of variation; GCV %= genotypic coefficient of variation; HB%= percentage heritability; GA%= Genetic advance; GAM%= Genetic advance as percentage of mean

plant (20.00) and the longest fruit length (16.67 cm), followed by G3 and G4. G8, on the other hand, produced the fewest fruits (9.41) and the shortest fruit length (7.23 cm). In terms of total fruit yield per plant, G1 led with 176.00 g, followed by G3 (158.33 g) and G4 (145.33 g). The lowest yield was recorded in G8 (70.71 g).

Genetic Parameters

The estimated genetic parameters for all measured traits are presented in Table 3. Genotypic variance ranged from 0.083 (number of leaves per plant) to 26.457 (days to maturity), while phenotypic variance ranged from 1.743 to 144.657.

Genotypic coefficient of variation (GCV) ranged between 2.26% (number of leaves) and 18.53% (fruit length), while phenotypic coefficient of variation (PCV) was highest for fruit width (25.57%), followed by fruit length (23.65%) and number of fruits per plant (20.96%). PCV values exceeded GCV for all traits, indicating environmental influence on

Table 4. Names and primer sequence of the SSR markers used for the analysis of 8 Okra genotypes, *Abelmoschus esculentus*

Name	Forward	Tm	Name	Reverse	Tm
OKRA103 F	5´GAATTCGATTCCAATACAGG 3´	47.68	OKRA103 R	5´ TCGTCGTCTTCATTTCTCTT 3´	47.68
OKRA104 F	5´ CGGTAAATCTTGTCTCTTGC 3´	49.73	OKRA104 R	5´ TATAGGAAAACCCCCAAGAT 3´	47.68
OKRA105 F	5´ CCTCAACGAGGAGTAGAAGA 3´	51.78	OKRA105 R	5´ CCTTCATCATAATCCATCTAGG 3´	51.11
OKRA108 F	5´ AAGAAGGAGAAGAGGGAATG 3´	49.73	OKRA108 R	5´ TAAACCGTCTAGGAACTCCA 3´	49.73
OKRA109 F	5´ TTTCCCTAATGAGTGGACC 3´	48.93	OKRA109 R	5´ GGGTCTGTTTTGTTGTTGTT 3´	47.68
OKRA110 F	5´ GGCAACAACAGTTCTCCTT 3´	48.93	OKRA110 R	5´ AATTGGGGTTAGTGACGATA 3´	47.68
OKRA111 F	5´ CATTTTAAGGAGCGAGTGTC 3´	49.73	OKRA111 R	5´ CTCTTCCTCAACAAACCAG 3´	49.73
OKRA112 F	5´ CTCAATTGGATTGGATGAGT 3´	49.73	OKRA112 R	5´ CCTCTCGAACTGAGAAAGAAA 3´	49.73

Table 5. Allele number, polymorphism information content (PIC), Major allele frequency and gene diversity for the primers

MARKER	ALLELE NO	PIC	MAJOR ALLELE FERQUENCY	GENE DIVERSITY
OKRA103	6.00	0.75	0.37	0.78
OKRA104	8.00	0.86	0.12	0.87
OKRA105	8.00	0.86	0.12	0.87
OKRA108	8.00	0.86	0.12	0.87
OKRA109	7.00	0.82	0.25	0.84
OKRA110	5.00	0.71	0.37	0.75
OKRA111	8.00	0.86	0.12	0.87
OKRA112	3.00	0.37	0.75	0.40
MEAN	6.63	0.76	0.29	0.78

phenotypic expression.

Heritability estimates ranged from 4.78% (number of leaves per plant) to 68.81% (plant height at flowering). High heritability coupled with high genetic advance was recorded for plant height at flowering, days to maturity, and fruit length, suggesting that these traits are controlled by additive gene action and could respond well to selection.

SSR Marker Polymorphism

The sequences of the SSR primers used are shown in Table 4, and the polymorphism data are summarized in Table 5. The number of alleles detected per marker ranged from 3 (OKRA112) to 8 (OKRA104, OKRA105, OKRA108, OKRA111), with an average of 6.63 alleles.

Polymorphic information content (PIC) values were high (>0.50) for all markers except OKRA112 (0.37), indicating that most markers were highly informative. OKRA104, OKRA105, OKRA108, and OKRA111 recorded the highest PIC values (0.86). Gene diversity ranged from 0.40 (OKRA112) to 0.87 (OKRA104, OKRA105, OKRA108, OKRA111), while major allele frequency ranged from 0.12 to 0.75.

Gel Electrophoresis Profiles

Plates 1 through 8 show the electrophoretic profiles of DNA fragments amplified by the SSR markers across the eight genotypes. The primers OKRA104, OKRA105, OKRA108, and OKRA111 exhibited clear polymorphic banding patterns, confirming their suitability for diversity analysis. In contrast, OKRA112 displayed weak and monomorphic patterns, indicating low discriminatory power.

DISCUSSION

The significant genotypic differences observed across most agronomic traits indicate substantial genetic variability among the eight okra genotypes. These findings align with previous studies (Amao et al., 2022; Makhdoomi et al., 2018), which similarly reported wide variability in okra germplasm. The significant differences found in traits such as total fruit yield, days to flowering, and plant height at maturity highlight the potential for genetic improvement through selection.

The broad range of mean values observed for traits like

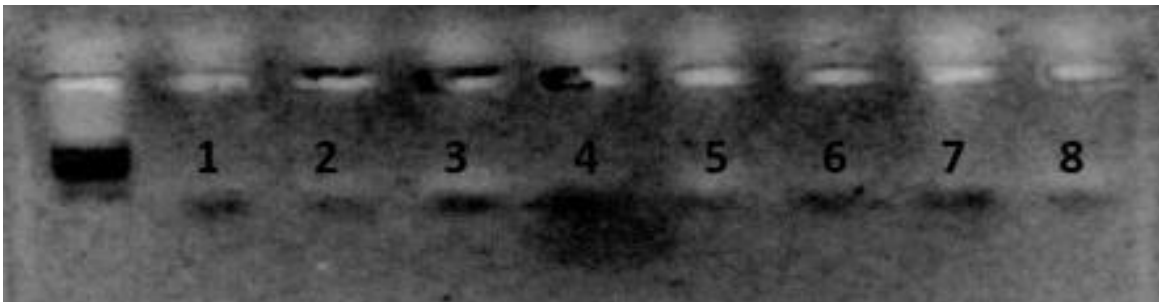

Plate 1. DNA bands amplified by OKRA103 marker across 8 Okra genotypes

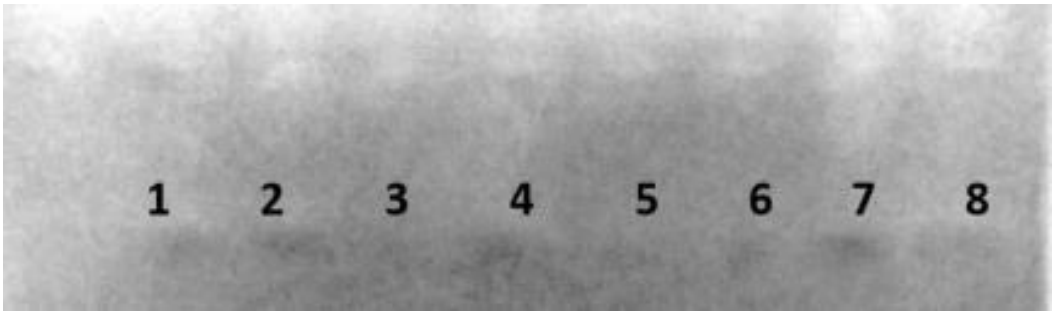

Plate 2. DNA bands amplified by OKRA104 marker across 8 Okra genotypes

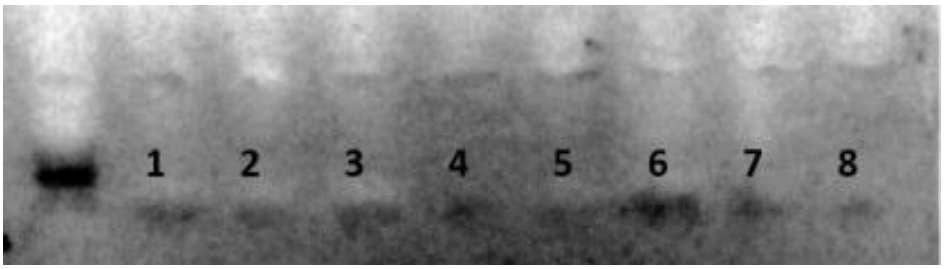

Plate 3. DNA bands amplified by OKRA105 marker across 8 Okra genotypes

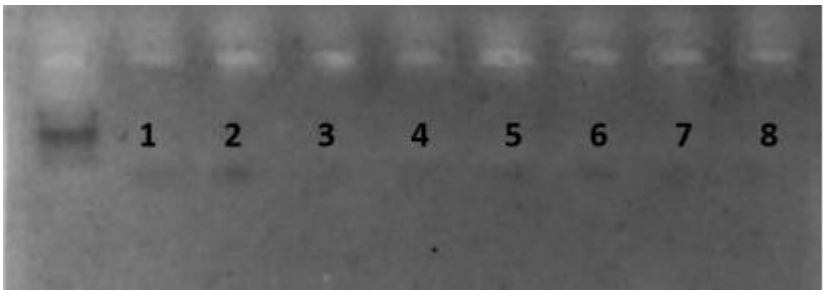

Plate 4. DNA bands amplified by OKRA108 marker across 8 Okra genotypes

fruit length, number of fruits, and total fruit yield confirms the presence of both early- and late-maturing genotypes, as well as high- and low-yielding accessions. For example, genotype G1 (NGB00303) outperformed others in fruit length and yield, suggesting it possesses superior yield potential and could serve as a valuable donor parent in

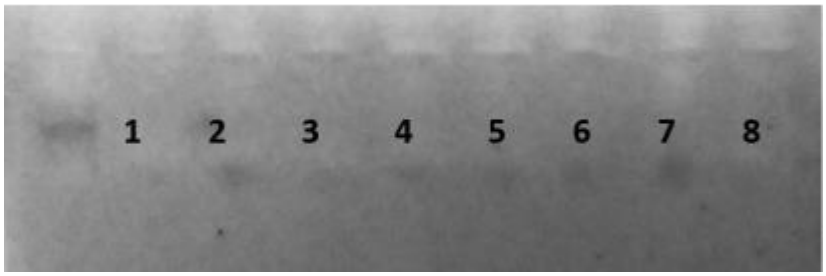

Plate 5. DNA bands amplified by OKRA109 marker across 8 Okra genotypes

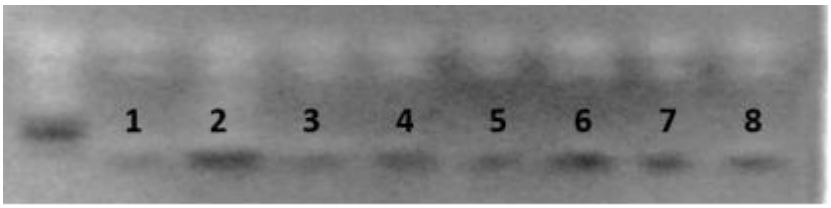

Plate 6. DNA bands amplified by OKRA110 marker across 8 Okra genotypes

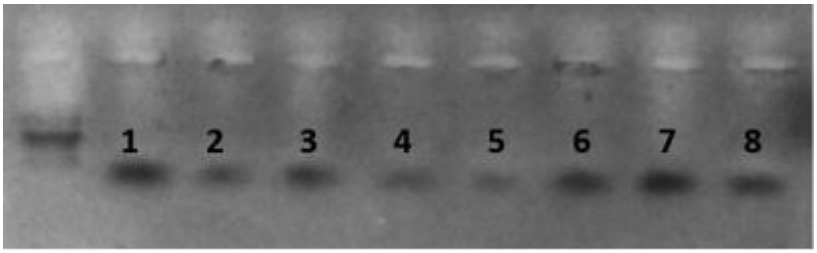

Plate 7. DNA bands amplified by OKRA111 marker across 8 Okra genotypes

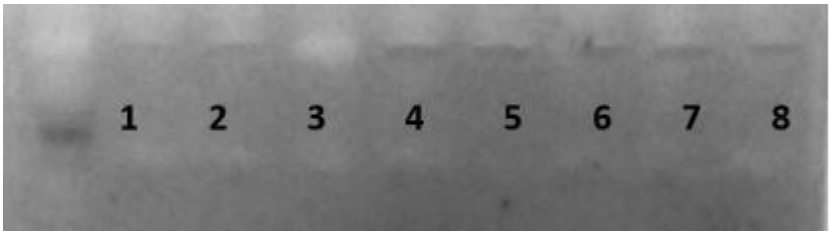

Plate 8. DNA bands amplified by OKRA112 marker across 8 Okra genotypes

breeding programs.

The higher phenotypic coefficient of variation (PCV) compared to genotypic coefficient of variation (GCV) for all traits suggests that environmental factors played a considerable role in trait expression. This trend is commonly observed in field-based plant breeding trials (Ashraf et al., 2020), where environmental variability can mask genetic effects.

Traits with both high heritability and high genetic advance—such as plant height at flowering, fruit length, and days to maturity—are likely governed by additive gene action. This suggests that these traits can be effectively improved through direct selection (Gohil et al., 2024; Singh et al., 2023). On the other hand, traits like number of leaves per plant and total fruit yield had lower heritability estimates, implying more complex inheritance likely involving non-additive gene effects and environmental interactions.

The SSR marker analysis revealed that markers OKRA104, OKRA105, OKRA108, and OKRA111 were highly polymorphic and informative, with high PIC values (>0.80), high gene diversity, and low major allele frequency. These markers are thus well-suited for assessing genetic diversity, constructing linkage maps,

and applying marker-assisted selection (Gayathri et al., 2020; Ibrahim et al., 2024). Conversely, OKRA112 exhibited the lowest allele number, gene diversity, and PIC value, indicating limited utility for diversity studies. These findings reinforce the importance of marker validation prior to inclusion in molecular breeding pipelines.

The variability in SSR profiles across genotypes supports the conclusion that the okra genotypes evaluated in this study originate from diverse genetic backgrounds. This diversity is critical for broadening the genetic base of breeding materials and developing improved varieties with better yield and adaptability.

CONCLUSION

This study demonstrates significant genetic variability among eight okra (*Abelmoschus esculentus* L. Moench) genotypes based on both morphological traits and SSR markers. The variability observed in key agronomic traits, such as fruit length, number of fruits per plant, and total fruit yield, highlights the potential for selection and genetic improvement.

Genotypes NGB00303, NGB00323, and NGB00324 exhibited superior performance in yield-related traits and can be recommended as donor parents for hybridization and development of high-yielding okra varieties. Additionally, genotypes NGB00303, NGB00323, and NGB00466 demonstrated relatively early flowering and maturity, making them suitable for developing early-maturing cultivars.

Molecular analysis confirmed that SSR markers OKRA104, OKRA105, OKRA108, and OKRA111 are highly polymorphic and informative, supporting their application in diversity assessment, population structure analysis, and marker-assisted selection. Conversely, OKRA112 was found to be weakly polymorphic and is not recommended for genetic diversity studies in okra.

The integration of morphological and molecular analyses provides a comprehensive understanding of genetic diversity and offers valuable tools for the improvement of okra breeding programs in Nigeria and similar agro-ecological zones.

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