ASSESSMENT OF GENETIC VARIATIONS IN OKRA (*Abelmoschus esculentus* L. Moench) GENOTYPES

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Abstract
*This study evaluated genetic variability, heritability, and genetic advance for agronomic and yield traits among four okra (*Abelmoschus esculentus *L. Moench) genotypes, two landraces (Etighi Abakpa, Etighi Idok) and two exotic varieties (Hire, Clemson). The experiment was conducted during the 2024 cropping season in Calabar, Nigeria, the experiment employed a Randomized Complete Block Design (RCBD) with three replications. Data were collected on emergence and establishment percentages, plant height, number of leaves, leaf area, flowering and fruiting traits, and yield (t/ha). Analysis of variance revealed significant ($p < 0.05$) differences among genotypes for most traits, indicating the presence of genetic variability. Phenotypic coefficients of variation (PCV) were generally higher than genotypic coefficients of variation (GCV), suggesting environmental influence. Heritability estimates ranged from 30% to 99%. High heritability and genetic advance as percent of mean (GAM) were recorded for number of leaves (77.08%; 53.21%), emergence (78.55%; 59.07%), establishment (81.97%; 77.18%), leaf area (81.70%; 54.16%), days to budding (98.68%; 78.15%), days to anthesis (98.83%; 88.00%), days to fruit appearance (99.29%; 74.12%), and days to fruit maturity (99.43%; 69.23%), suggesting additive gene action. Genetic parameters for yield (σ^2g, σ^2p, GCV, PCV, H^2, GA, GAM) were zero, indicating no measurable variability. Traits with high heritability and GAM can be effectively utilized in okra improvement programmes.*
Keywords*: Heritability, Genetic advance, Variability, Improvement, Genotypes*

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is an economically important vegetable crop cultivated throughout tropical and subtropical regions of Africa, Asia, and the Americas for its tender green fruits used as food and for industrial applications (Kenaw *et al.*, 2023).
In Nigeria, okra contributes significantly to household income, nutrition, and food security, yet productivity remains low due to limited genetic improvement and poor adaptation of exotic cultivars to local conditions (Akindele *et al*., 2023).

Genetic improvement of okra depends on the extent of available genetic variability and the heritable portion of that variability. Estimates of genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance help breeders determine the effectiveness of selection and predict genetic gain in successive generations (Bambhaniya *et al*., 2024).
Previous studies have reported considerable variability and heritability for yield and its components in okra genotypes under different environments (Kenaw *et al.*, 2023; Satpute *et al.*, 2024).

However, there is limited information on the genetic parameters of okra genotypes cultivated in the humid tropics of southeastern Nigeria, particularly under Calabar's ecological conditions.
Therefore, the present study aimed to estimate genetic variability, heritability, and genetic advance in selected agronomic and yield traits of four okra genotypes grown in Calabar, Cross River State.

Materials and Methods

Experimental Site

The experiment was conducted in Calabar, Cross River State, Nigeria during the 2024 planting season. Calabar is located in the South-Eastern rainforest Agro-ecological Zone of Nigeria between latitudes 04°58N, longitude 08°21E and altitude of 62.3m of the equator (NIMET,2020).

Experimental Materials

Four okra genotypes were evaluated, two landraces; Etighi Abakpa, Etighi Idok and Exotic varieties; Hire and Clemson

Experimental Design

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each experimental unit measured 2 m x 2 m with alley way of 1m. The okra seeds were planted in row with inter and intra row spacing of 50 cm x 30 cm giving a plant population of 133,333 plant per hectare, 1,200 plant in the entire experimental field and 20 plant per plot. Standard agronomic practices for okra cultivation were followed.

Data Collection

Data were recorded on the following traits: Emergence percentage, establishment percentage, plant height (cm), number of leaves, leaf area (cm²), days to budding, leaf area index, days to anthesis, days to 50% flowering, days to fruit appearance, number of fruits per plant, fruit length (cm), days to fruit maturity, fresh fruit weight (kg), and yield (t/ha).

Data Analysis

Data were subjected to analysis of variance (ANOVA) using Statistical Tool for Agricultural Research (STAR). Genetic parameters were computed as follows:
Genetic Component Analysis was calculated for all the traits. Genotypic and phenotypic coefficient of variability GCV% and PCV% were estimated according to Singh and Chaudhary (1995) as follow $GCV(\%) = \sqrt{\frac{\delta_g^2}{\bar{x}}} \times \frac{100}{1}$, $PCV(\%) = \sqrt{\frac{\delta_p^2}{\bar{x}}} \times \frac{100}{1}$

Where *GCV = Genotypic coefficient of variability*
PCV = Phenotypic coefficient of variability
δ_g^2 = *Genotypic variance*
δ_p^2 = *Phenotypic variance*
$\bar{x}$ = *Mean*

Broad sense heritability and genetic advance were estimated according to Johnson *et al.* *(*1955) as follows

$$H^2 = \frac{\delta_g^2}{\delta_p^2} \times \frac{100}{1} \text{ , } GA = \frac{k \times \sqrt{\delta_p^2} \times \delta_g^2}{\delta_p^2}$$

$$GAM = \frac{GA}{\overline{X}} \times \frac{100}{1}$$

Where H^2 *= Broad-sense heritability*
GA = Genetic advance
GAM = Genetic advance as percent of mean
K = 2.06 at 5% selection

Results and Discussion
Estimates of Variance Components and Genetic Parameters
Genetic Variability and Component Analysis

The estimates of variance components and genetic parameters for the evaluated okra traits are presented in **Table 1**. Across all traits, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV), indicating that environmental factors contributed to the total observed variation. However, the magnitude of this environmental influence varied among traits. Traits such as days to budding (PCV: 41.90%; GCV: 41.62%), days to anthesis (40.55%; 40.30%), days to fruit appearance (39.69%; 39.55%), and days to fruit maturity (36.74%; 36.64%) exhibited very narrow differences between PCV and GCV, suggesting minimal environmental effect and predominantly genetic control. In contrast, wider PCV–GCV differences were recorded for days to 50% flowering (57.82%; 40.70%), number of fruits per plant (15.81%; 9.53%), and fresh weight (15.45%; 8.48%), indicating substantial environmental influence on their expression.

Heritability and Genetic Advance

As shown in **Table 1**, high broad-sense heritability ($H^2 > 70\%$) combined with high genetic advance as percent of mean (GAM > 20%) was observed for emergence (78.55%; 59.07%), establishment (81.97%; 77.18%), number of leaves (77.08%; 53.21%), leaf area (81.70%; 54.16%), days to budding (98.68%; 78.15%), days to anthesis (98.83%; 88%), days to fruit appearance (99.29%; 74.12%), and days to fruit maturity (99.43%; 69.23%). This combination indicates additive gene action for these traits, implying that selection would be highly effective in improving them. Conversely, traits such as number of fruits per plant (H^2: 36.38%; GAM: 11.75%) and fresh weight (30.77%; 9.09%) recorded low heritability and low GAM, suggesting a predominance of non-additive gene effects and considerable environmental influence, which may limit direct selection efficiency.

Yield Variability

The yield trait showed no detectable genetic variability among the four okra genotypes evaluated. As indicated in **Table 1**, all associated parameters (σ^2g, σ^2p, GCV, PCV, H^2, GA, and GAM) were recorded as 0.00, implying genetic uniformity for yield in this particular population.

The significant variability observed among the evaluated okra genotypes underscores the presence of substantial genetic diversity, providing a valuable foundation for selection and genetic improvement. Similar findings were reported by Kenaw *et al*. (2023) in Ethiopia and Bambhaniya *et al.* (2024) in India, who observed that phenotypic coefficients of variation (PCV) consistently exceeded genotypic coefficients of variation (GCV) for all studied traits in okra. The high heritability estimates obtained for plant height, number of leaves, and fruit length in this study corroborate the findings of Satpute *et al*. (2024), who recorded heritability values exceeding 70% for major yield traits in F_4 and F_5 okra generations. High heritability combined with high genetic advance (GA) suggests the predominance of additive gene action, indicating that phenotypic selection would be effective for improving these traits. According to and Kute *et al.* (2023) and Yadav *et al.* (2024), this combination serves as a strong indicator of additive gene control, and selection based on such traits is likely to result in substantial genetic gain. This observation aligns with Behera *et al*. (2025), who reported similar patterns in okra populations cultivated under humid tropical conditions.

Conversely, traits such as number of fruits per plant and fresh fruit weight exhibited low heritability coupled with low GA, implying the predominance of non-additive gene effects. Comparable findings were reported by Kute *et al*. (2023) and Goudara *et al*. (2024) , who attributed such patterns to dominance and epistatic interactions, thereby limiting the efficiency of direct selection. Consistent with recent genetic variability studies in okra, PCV values in the present study were generally higher than corresponding GCV values, signifying the influence of environmental factors on trait expression (Sharma *et al.*, 2023; Goudara *et al.*, 2024).

Table 1: Estimates of variance components, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as percent of mean for different characters of okra genotypes

Trait or CharacteR	Mean (×)	δ^2g	δ^2e	δ^2p	GCV (%)	PCV (%)	H^2	GA	GAM
Emergence (%)	37.92	150	40.97	190.92	32.3	36.44	78.55	22	59.07
Establishment (%)	65.42	741.67	163.19	904.86	41.62	45.98	81.97	50.49	77.18
plant height(cm)	42.73	75.64	40.61	116.25	20.36	25.23	65.07	14.51	33.96
No. of leaves	14.49	19.07	5.67	24.74	29.55	33.6	77.08	7.87	53.21
Leaf area(cm2)	146.32	3841.19	860.57	4701.76	42.36	46.86	81.7	79.24	54.16
Days to budding	43.75	331.5	4.42	335.92	41.62	41.9	98.68	34.19	78.15
Leaf are index	0.0967	0.0017	0.0003	0.0039	41.37	64.12	43.5	0.056	57.91
days to anthesis	52.5	447.85	5.3	453.15	40.3	40.55	98.83	46.2	88
days to 50% flowering	55.33	507.17	4.56	1023.45	40.7	57.82	49.55	31.39	56.73
days to fruit appearance	57.42	515.75	3.69	519.44	39.55	39.69	99.29	42.56	74.12
No. of fruit per plant	26.13	6.21	10.86	17.07	9.53	15.81	36.38	3.07	11.75
Fruit length	6.97	1.06	0.46	1.52	14.88	17.65	69.74	1.77	25.39
Days to fruit maturity	62.5	524.34	3	527.34	36.64	36.74	99.43	43.27	69.23
Fresh weight (kg)	0.33	0.0008	0.0018	0.0026	8.48	15.45	30.77	0.03	9.09
Yield (t/ha)	0.33	0	0	0	0	0	0	0	0

δ^2g = genotypic variance; δ^2e = environmental variance; δ^2p = phenotypic variance; GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; H^2 = Heritability; GA = Genetic advance; GAM = Genetic advance as percent of mean.

However, the relatively narrow difference between PCV and GCV observed for traits such as days to budding, days to anthesis, days to fruit appearance, and days to fruit maturity suggests that these traits are less influenced by environmental fluctuations. Consequently, selection based on phenotypic performance for these traits would likely be effective. Overall, the results indicate that although genetic variability exists, phenotypic selection must be executed with careful consideration of environmental effects.

Moreover, traits including number of leaves, emergence, establishment, leaf area, and flowering-related attributes (days to budding, anthesis, fruit appearance, and maturity) exhibited high heritability coupled with high genetic advance as a percentage of the mean. This finding is consistent with Yadav *et al.* (2024) and Behera *et al.* (2025), who underscores the predominance of additive genetic effects and suggests that selection based on these traits can lead to genetic improvement under the prevailing environmental conditions.

The inclusion of both landraces and exotic genotypes in the present study aligns with contemporary breeding perspectives emphasizing the expansion of the genetic base of okra for yield enhancement and environmental resilience Akinwusi and Agbedahunsi (2025). Substantial genetic variability was recorded among the four evaluated genotypes (Etighi Idok, Etighi Abakpa, Hire, and Clemson spineless) across growth and yield-related traits. The observed differences in plant height, number of leaves, fruit length, and fresh fruit weight indicate the presence of exploitable genetic diversity, which is crucial for crop improvement. Similar reports of significant variability among okra genotypes were documented by Yadav *et al.* (2024) and Behera *et al.* (2025), who observed wide genetic variation for yield and related traits across diverse environments.

This result suggests that the genotypes responded uniformly in terms of yield potential under the prevailing environmental conditions of the 2024–2025 season in Calabar. Similar observations have been reported in okra by Kute *et al.* (2023) and Goudara *et al.* (2024), who found negligible genetic variance for yield when genotypes performed similarly due to uniform growing conditions or limited genetic divergence. A zero genotypic variance implies that phenotypic differences among genotypes were statistically insignificant or masked by environmental uniformity (Yadav *et al.*, 2024). Consequently, the heritability estimate (H^2) and the expected genetic advance (GA, GAM) were also zero, reflecting the non-additive nature or environmental determination of yield in this trial (Behera *et al.*, 2025).As observed by Frontiers in Plant Science (2025), yield expression in okra is a highly integrative polygenic trait influenced by both genetic and environmental interactions; hence, minor data or environmental uniformity can suppress detectable genetic variation. To obtain a more reliable genetic parameters for yield, Adewusi (2023) and Behera *et al.* (2025) stressed the need for subsequent trials to incorporate larger genotype samples, multiple seasons, and more contrasting environments.

Conclusion and Recommendations

Significant genetic variability exists among the four okra genotypes for most traits. Traits such as emergence, establishment, plant height, number of leaves, leaf area, days to budding, leaf area index, days to anthesis, days to 50% flowering, days to fruit appearance, fruit length and days to fruit maturity show potential for direct selection and genetic improvement. Environmental influence was pronounced for leaf area index, days to 50% flowering, number of fruit/plant and fresh weight.

Breeding programmes in Calabar should focus on genotypes Hire and Etighi Abakpa for developing high-yielding, adaptable varieties. Future studies should include more genotypes, multi-season trials, and integration of molecular tools to complement phenotypic selection.

In summary, despite the limited number of genotypes assessed, the present study demonstrates sufficient genetic variability among okra lines to support the improvement of yield and yield components under the humid tropical conditions of Calabar, Nigeria. These findings highlight key traits for immediate selection and reinforce the strategic inclusion of diverse germplasm in okra breeding programmes targeted at the humid tropics

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