RESEARCH ARTICLE

Genetic variability for selected tomato (*Lycopersicon esculentum* Mill.) varieties in the forest–Savanna transition zone of Ekpoma, Edo State, Nigeria

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ABSTRACT

A study was conducted at the Teaching and Research Farm of Ambrose Alli University, Ekpoma, to evaluate the genetic variability of four tomato (Lycopersicum esculentum) varieties. The experiment employed a Randomized Complete Block Design (RCBD) with four replicates and focused on both vegetative and yield-related traits. Among the tested varieties, Superstar consistently outperformed others in plant height, number of leaves, leaf area, stem girth, and branching across 2, 4, 6, and 8 weeks after planting (WAP). High heritability estimates coupled with substantial genetic gain for traits such as plant height, leaf number, and stem girth suggest strong additive gene effects, indicating that these traits are highly amenable to selection in breeding programs. For instance, plant height recorded heritability values of 90.22% and 95.95% at 2 and 4 WAP, with corresponding genetic gains of 11.90 and 6.48. In contrast, traits like leaf area exhibited low genetic gain at later stages (0.41–2.21), reflecting non-additive gene action. Superstar also demonstrated superior yield potential and early flowering, making it particularly suitable for cultivation under Ekpoma conditions. Based on these findings, the study recommends Superstar as a promising candidate for local tomato improvement programs aimed at enhancing productivity and adaptability in the region.

Keywords: Genetic variability, Heritability, Genetic gain, Tomato, Quantitative traits, Yield components

INTRODUCTION

Tomato (*Solanum lycopersicum* L.), a member of the Solanaceae family, is one of the most widely cultivated and economically significant vegetable crops globally. It is a versatile crop, consumed fresh, cooked, and processed into various products such as sauces, soups, pastes, and juices, making it essential to human nutrition and food security (Pinela et al., 2022). The tomato fruit is rich in essential nutrients, including vitamins A, C, E, potassium,

folate, lycopene, and β-carotene, contributing to its role in preventing chronic diseases through its antioxidant properties (Du et al., 2025).

In Nigeria, tomato is a major crop for smallholder farmers, particularly in regions where climatic conditions, such as those in the savannah zones, favor its growth (Olorunfemi et al., 2023). Despite its nutritional and economic importance, the productivity of tomato in Nigeria remains sub-optimal, primarily due to several constraints, including limited irrigation infrastructure, pest and disease pressures, post-harvest losses, and reliance on unimproved varieties (Akhter et al., 2023). Furthermore, the dependence on rain-fed agriculture severely limits production to the wet season, causing reduced market availability and, consequently, lower income for farmers (Olorunfemi et al., 2023).

Genetic improvement of tomato through breeding is a promising strategy to overcome these challenges. By developing high-yielding, pest-resistant, and climate-resilient varieties, significant improvements can be made in tomato production systems (Akhter et al., 2023). Evaluating the genetic variability within tomato varieties can provide essential insights into the heritable traits that contribute to yield and adaptability, thereby aiding in the selection of superior cultivars suited to local conditions (Bizouerne et al., 2023). Therefore, assessing the genetic variability, heritability, and genetic gain among tomato varieties under specific ecological conditions, such as the forest–savanna transition zone of Ekpoma, Edo State, Nigeria, is crucial for identifying high-yielding and adaptable varieties suitable for local production systems. Such knowledge will support targeted selection and improvement programs aimed at achieving sustainable tomato productivity and food security in the region (Akhter et al., 2023).

The overall objective of this study was to evaluate the genetic variability of four tomato (*Lycopersicon esculentum*) varieties: *Superstar*, *PADMA 108 F1*, *Roma*, and *Esan Tomatoes* and to determine how their component characters are associated. Specifically, the experiment aimed to determine variation in their genetic makeup, identify the genes or genetic factors responsible for high yield, detect the high-yielding varieties, and identify characters that can be improved through selection and breeding.

MATERIALS AND METHODS

Experiment Location

The experiment was conducted at the Teaching and Research Farm of the Faculty of Agriculture, Ambrose Alli University, Emaudo Annex, Ekpoma, Edo State, Nigeria. The site is located within the forest–savanna transition zone at Latitude 6°45′ N and Longitude 6°08′ E, providing a suitable agro-ecological environment for tomato cultivation.

Materials used

Four tomato (*Solanum lycopersicum* L.) varieties were used in the study, namely Super Star, PADMA 108 F1, Roma, and Esan. Seeds of these varieties were procured from Reputable Agro-Allied, Ibadan, Nigeria, ensuring genetic purity and quality for the experiment.

Experimental design

The field experiment was arranged in a Randomized Complete Block Design (RCBD) with four replicates. Land preparation was carried out manually using cutlasses, and plots were demarcated according to treatments. The experimental field measured 7.8 × 7.8 m and was divided into 16 plots of 1.2 × 1.2 m each, with a 1 m alley separating plots and replicates. Seedlings were raised on four nursery beds and transplanted into the field two weeks after germination. Each plot contained nine plants, spaced at 60 × 30 cm on flat ground in four rows, giving a total of 144 plants across the entire experiment.

Data Collection

Vegetative, Yield and Yield Components

Data collection focused on vegetative growth and yield parameters. Vegetative traits included number of leaves per plant, leaf length, leaf breadth, vine length, stem girth, and number of branches per plant. The number of leaves and branches was determined by visually counting four randomly selected plants per plot and recording the mean values. Leaf length and breadth were measured in centimeters using a calibrated measuring tape, while vine length was measured from the soil surface to the plant apex. Stem girth was measured at the base of

the stem using a flexible tape. Yield and yield components included number of fruits per plant, fruit weight per plant, days to 50% flowering, days to 50% maturity, and yield per plant. The number of fruits was obtained by counting all fruits from four randomly selected plants per plot, while fruit weight was measured using a sensitive electronic weighing scale. Days to 50% flowering were recorded from sowing to the day when half of the plants had flowered, and days to 50% maturity were determined from transplanting to the stage when 50% of plants reached physiological maturity. Yield per plant was calculated from the total fruit weight per plot and converted to yield per hectare using standard procedures.

Genetic analysis

Genetic analysis was carried out to estimate heritability, genotypic advance, and genetic gain based on agronomic and yield-related genotypic and phenotypic expressions, following the method described by Allard (1999). Phenotypic variance was obtained from mean squares at treatment levels, while genotypic variance was calculated by subtracting the error mean square from the corresponding phenotypic variance. Heritability in the broad sense was estimated as the ratio of genotypic variance to phenotypic variance expressed as a percentage. Genotypic advance was calculated as the product of the genotypic variance to phenotypic variance ratio and the selection intensity constant (K = 2.06, representing 10% selection intensity). Genetic gain was expressed as genotypic advance relative to the population mean, presented as a percentage.

Data analysis

Plant growth and yield data were analyzed using Genstat 12th Edition (VSN International, 2009). Analysis of Variance (ANOVA) was performed at the 5% significance level, and treatment means were separated using the Least Significant Difference (LSD) test when the F-ratio was significant.

RESULTS AND DISCUSSION

Significant variations were observed among the tomato varieties for most traits, indicating the presence of substantial genetic variability. Such variability provides an opportunity for effective selection and genetic improvement in tomato (*Lycopersicon esculentum* Mill.) breeding programs. Similar findings have been reported by Suresh et al. (2024), who emphasized the importance of genetic diversity in tomato populations for yield improvement and adaptability under varying agro-ecological conditions.

For plant height (Table 1) at 2 weeks after planting (WAP), the Superstar variety differed significantly compared with the other varieties, whereas Esan Tomatoes, PADMA 108 F1, and Roma were statistically similar. A similar trend was observed at 4 WAP, with Superstar and Roma exhibiting significant differences from the other two varieties. These results suggest that Superstar possesses superior early growth vigour, likely attributable to its genetic makeup and adaptive ability. Differences in plant height among tomato varieties have been attributed primarily to genetic composition and environmental interaction (Chandanshive, Gaikwad, Sonavane, & Bankar, 2024).

Regarding the number of leaves and branches (Tables 2 & 3), the Superstar variety also differed significantly in leaf number at 2 WAP, with significant differences persisting across subsequent weeks. The observed variation among varieties indicates that genetic factors strongly influence leaf proliferation, which directly affects photosynthetic potential. Leaf number and branch development are critical determinants of canopy structure and assimilate partitioning, both of which contribute to fruit set and yield. At 4 and 6 WAP, Superstar and Esan Tomatoes exhibited superior leaf and branch counts compared to PADMA 108 F1 and Roma. These observations are consistent with reports by Plant Archives (2024), which highlighted the role of leaf traits in determining yield potential in tomato.

For leaf area and stem girth (Tables 4 & 5), significant variation was observed among varieties at all stages of growth, with Superstar consistently maintaining the highest leaf area values. Larger leaf area enhances light interception and photosynthetic efficiency, thereby contributing to higher dry matter accumulation. Similarly, Superstar recorded the highest stem girth across all sampling periods, indicating superior structural development. These findings align with the results of Suresh et al. (2024), who reported strong associations between leaf area, stem girth, and overall plant vigour in tomato genotypes.

Table 1. Plant height (cm) of tomatoes at 2, 4, and 6 WAP

Variety	Weeks after planting		
	2	4	6
Esan tomatoes	14.77[b]	27.22[b]	64.54[b]
Super star	22.01[a]	41.21[a]	110.06[a]
PADMA 108 F1	14.44[b]	32.37[b]	78[b]
Roma	11.31[b]	21.38[c]	73.52[b]
LSD	4.53	5.41	22

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 2. Number of leaves/plant (cm) of tomatoes at 2, 4, and 6 WAP

Variety	Weeks after planting		
	2	4	6
Esan tomatoes	20.19[b]	27.56[bc]	39[c]
Super star	27.19[a]	41.21[a]	57.19[a]
PADMA 108 F1	15.31[c]	32.37[b]	45.19[b]
Roma	16b[c]	21.38[c]	37[c]
LSD	4.44	7.41	4.4

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 3. Number of branches (cm) of tomatoes at 2, 4, and 6 WAP

Variety	Weeks after planting		
	2	4	6
Esan tomatoes	0.00	1.58[c]	5.53[b]
Super star	0.00	4.88[a]	15.15
PADMA 108 F1	0.00	1.88[c]	13.96[a]
Roma	0.00	3.00[b]	13.65[a]
LSD	0.00	0.97	3.78

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 4. Leaf area (cm) of tomatoes at 2, 4, and 6 WAP

Variety	Weeks after planting		
	2	4	6
Esan tomatoes	84[b]	216.1[b]	353.2[b]
Super star	146.22[a]	392.8[a]	530.2[a]
PADMA 108 F1	55.24[b]	194.2[b]	384.5[ab]
Roma	48.06[b]	149.8[b]	275.8[b]
LSD	46.46	127.7	161.8

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 5. Stem girth (cm) of tomatoes at 2, 4, and 6 WAP

Variety	Weeks after planting		
	2	4	6
Esan tomatoes	0.14[b]	0.49[b]	0.997[b]
Super star	0.2275[a]	0.7525[a]	1.26[a]
PADMA 108 F1	0.13[b]	0.515[b]	0.98[b]
Roma	0.1225[b]	0.4125[b]	0.952[b]
LSD	0.07	0.14	0.21

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 6. Days to 50% flowering and maturity (cm) of tomatoes

Variety	Days to 50%	Days to 50%	Number of	Fruit yield

	flowering	maturity	fruits/plant	(t/ha)
Esan tomatoes	47.25[a]	66.00[a]	16.5[b]	7.82[ab]
Super star	32.25[b]	46.50[c]	30.69[a]	9.82[a]
PADMA 108 F1	37.00[b]	53.00[b]	14.94[b]	5.45[bc]
Roma	44.25[a]	66.50[aa]	14.06[b]	3.78[c]
LSD	7.00	4.25	11.27	3.76

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 7. Number of fruits and fruit yields of tomatoes

Variety	Number of fruits/plant	Fruit yield (t/ha)
Esan tomatoes	16.5[b]	7.82[ab]
Super star	30.69[a]	9.82[a]
PADMA 108 F1	14.94[b]	5.45[bc]
Roma	14.06[b]	3.78[c]
LSD	11.27	3.76

Values with the same alphabet on the same column are not significantly different (p<0.05)

Table 8. Heritability, genetic advance and genetic gain for plant traits

Plant traits	Genetic parameters	2WAP	4WAP	6WAP
Plant height	HO	90.22	95.95	87.97
	GA	1.86	1.98	1.81
	GG	11.90	6.48	2.22
Number of leaves per plant	HO	93.34	95.06	97.71
	GA	1.93	1.96	2.01
	GG	9.81	6.11	5.00
Leaf area	HO	89.44	86.01	77.45
	GA	1.84	1.77	1.60
	GG	2.21	0.74	0.41
Number of branches	HO	99.48	95.89	92.80
	GA	2.06	1.98	1.91
	GG	17.66	69.96	15.82
Stem girth	HO	99.48	91.27	79.69
	GA	2.06	1.88	1.64
	GG	17.66	346.86	156.64

HO (%) = Heritability, GA = Genetic Advance, GG = Genetic Gain

Table 9. Heritability, genetic advance and genetic gain for 50% flowering, 50% maturity, and the number of fruit of tomatoes

	Days to 50% flowering	Days to 50% maturity	Number of fruits/plant
HO	89.70	98.20	79.74
GA	1.85	2.02	1.64
GG	14.60	13.48	18.63

HO (%) = Heritability, GA = Genetic Advance, GG = Genetic Gain

Significant variation was observed among the tomato varieties for days to 50% flowering and maturity. The Superstar variety flowered earlier than the other varieties, suggesting an advantage in earliness and adaptability. Early flowering genotypes are often desirable in short-season environments where the growing period is limited (Jana et al., 2025). Conversely, Roma required the longest time to reach 50% maturity, implying a possible negative correlation between flowering and maturity duration. This finding contrasts with the report of Kanneh et al. (2020), who found no significant difference in flowering time among six tomato varieties, likely due to genotypic variation. Early flowering and maturity, as exhibited by Superstar, suggest efficient assimilate translocation, which enhances yield potential (Suresh et al., 2024).

Yield and Yield Components in (Table 7), yield and its components are the most important considerations for breeders and producers. *Superstar* recorded the highest number of fruits per plant and overall yield (Chandanshive et al., 2024). Genetic variability studies for qualitative and quantitative traits in tomato (*Solanum lycopersicum* L.). This may be attributed to its genetic potential for better flower retention and fruit set; a trait previously linked to higher sink strength and efficient carbohydrate partitioning. Genotypes with higher fruit counts tend to exhibit superior photosynthetic rates and source–sink efficiency, leading to increased productivity.

High heritability values were recorded for most traits, particularly number of leaves, stem girth, and days to 50% flowering, indicating that these traits are largely governed by additive gene action. High heritability coupled with moderate to high genetic gain suggests that selection based on phenotypic performance would be effective in improving these traits (Allard, 1999). The Superstar variety exhibited high heritability and genetic advance for vegetative and yield traits, suggesting strong genetic control and minimal environmental influence. The moderate genetic gain observed for flowering and maturity duration implies partial dominance, indicating that both additive and non-additive gene actions contribute to these traits. Overall, the significant genotypic variations observed in this study highlight the potential for improvement through selection and hybridization. Superstar demonstrated superior performance across most traits, confirming its suitability for breeding programs aimed at improving tomato yield and adaptability under the forest–savanna transition zone of Ekpoma.

CONCLUSION

The study evaluated the genetic variability, heritability, and genetic gain of four tomato varieties in Ekpoma, Edo State, revealing significant differences in most vegetative and yield-related traits, indicating substantial genetic variability. Among the varieties, *Superstar* consistently outperformed others in growth and yield characteristics, including plant height, number of leaves, leaf area, stem girth, and fruit yield. High heritability estimates for key traits, such as days to 50% flowering, maturity, and fruit yield, suggest that these traits are predominantly governed by additive gene effects, making them suitable for selection in breeding programs. Conversely, traits with low heritability and genetic gain, influenced by non-additive gene effects, may not respond well to selection. Given its superior performance, *Superstar* is recommended for cultivation in the forest–savanna transition zone of Ekpoma and similar regions. It should also be considered as a potential parental line in breeding programs focused on improving yield, early maturity, and adaptability in local tomato varieties. Further studies, including molecular characterization and multi-location trials, are suggested to confirm the stability of *Superstar*'s superior traits across different environments.

AUTHORS CONTRIBUTION

All the authors contributed equally to this work. All authors read and approved the final manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ETHICAL APPROVAL

Not applicable.

AVAILABILITY OF DATA AND MATERIALS

All datasets analyzed and described during the present study are available from the corresponding author upon reasonable request.

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