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Genetic Evaluation of Agronomic Traits in Early-maturing White Maize under Savannah Agroecologies

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ABSTRACT

Understanding genetic variability in maize is critical for identifying traits that enhance breeding efficiency, particularly in drought-prone environments. This study evaluated genetic variance, heritability, and genetic advance for grain yield and associated agronomic traits in early-maturing white maize cultivars. Eighteen cultivars obtained from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, were assessed during the 2023 and 2024 cropping seasons at the Lower Niger River Basin Development Authority, Oke-Oyi, Nigeria, using a randomized complete block design with three replications. Data on grain yield, plant height, days to silking, and other key traits were subjected to analysis of variance, and estimated of phenotypic and genotypic variance, phenotypic and genotypic coefficients of variation, broad-sense heritability, and genetic advance were computed to guide selection strategies. Across all traits, phenotypic coefficients of variation exceeded genotypic coefficients of variation (GCVs), indicating a significant environmental influence. Traits including number of grains per ear, grain yield, plant height, and days to silking exhibited high GCV, high heritability, and high genetic advance, indicating substantial potential for improvement through selection. Six cultivars, 2013 DTE STR-W SYN F_1 , 2012 TZE-W POP DT C_4 STR C_5 , EV DT-W 2000 STR, 2011 TZE-W DT STR SYN, 2009 DTE-W STR, and 2008 DTMA-W STR, demonstrated superior grain yield performance. These findings underscored the value of genetic variance, heritability, and genetic advance as tools for guiding maize improvement programs. The identified high-yielding cultivars were recommended for multi-location and on-farm trials to validate their performance and adaptability under drought-prone savannah agroecologies.

Keywords: Genetic variance, heritability, genetic advance, coefficient of variation, drought-adaptation

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important staple crops worldwide and particularly in sub-Saharan Africa, where it serves as a primary source of food, livestock feed, and industrial raw materials (FAOSTAT, 2025). Its broad ecological adaptation, high productivity potential, and economic value make it indispensable for subsistence and commercial agriculture. Globally, maize utilisation is primarily driven by livestock feed, accounting for approximately 67% of total production, followed by human consumption and industrial uses at 25%, with the remaining fraction allocated for seed production (Bello & Olawuyi, 2015; Dheeraj et al 2020). The crop's rich carbohydrate, starch, and oil content underpins its role in ensuring food and nutritional security. Moreover, the high solar radiation in the savannah regions of Nigeria provides favourable conditions for maize photosynthesis and biomass accumulation, supporting its potential for high grain yield.

Despite its adaptability, maize production in the savannah agroecologies is constrained by erratic rainfall, prolonged dry spells, and recurrent drought stress, which negatively affect growth, development, and yield. Water deficit during critical stages, particularly before or during flowering and grain-filling, could result in reductions in plant height, biomass, kernel number, grain weight, and overall yield. Empirical evidence suggested that drought stress during these stages could reduce grain yield by 21–50%, posing a significant threat to food security in the region (Bello et al 2014). Beyond drought, environmental stresses exacerbated vulnerability to pests and diseases, further limiting maize productivity. These challenges underscore the critical need for developing maize cultivars specifically adapted to the water-limited conditions of savannah agroecologies. Early-maturing maize varieties, with a life cycle of approximately 90–95 days, are a strategic adaptation to such environments (Bello et al 2025). By completing their growth cycle before the onset of terminal drought stress, these cultivars could escape late-season moisture deficits while maintaining high yield potential. Early-maturing genotypes also conferred additional agronomic benefits, including reduced exposure to pest and disease pressures, suitability for multiple cropping systems, and flexibility in planting schedules according to rainfall availability. Studies had shown that early-maturing maize cultivars could yield 20–50% more than late-maturing varieties under similar savannah conditions (Bello et al 2014), making them a vital component of climate-resilient maize production systems.

Breeding high-yielding, early-maturing, and stress-tolerant maize cultivars necessitated a thorough understanding of the genetic architecture of grain yield and associated traits. Maize grain yield was a quantitative trait governed by polygenic inheritance, including additive, dominance, and epistatic gene actions, which complicated improvement through conventional selection methods (Ishfaq et al 2025). Selection based solely on grain yield was often inefficient due to the trait's complex inheritance and strong environmental influence. Integrative breeding strategies that considered correlated agronomic traits, such as plant height, ear length, kernel number, and flowering time, were more effective in improving yield (Limbongan et al 2024). Comprehending trait correlations and genotype × environment interactions was therefore pivotal for designing effective selection strategies and accurately predicting potential genetic gains.

A key component of crop improvement was the assessment of genetic variability, which provided the basis for selection and breeding decisions. Genetic variance, partitioned into additive, dominance, and epistatic components, determines the proportion of phenotypic variation attributable to heritable factors and informed the choice of appropriate selection strategies (Nguyen et al 2022). Additive genetic variance, in particular, was crucial for predicting response to selection because it represented the proportion of variation that could be reliably passed to subsequent generations. Phenotypic variance, encompassing genetic and environmental effects, represented the total observable variation within a population. Heritability and genetic advance were complementary metrics that together provided insight into the potential response to selection and the efficiency of trait improvement. Broad-sense heritability considered all genetic effects, whereas narrow-sense heritability accounted only for additive effects, providing a more precise guide to selection potential (Amegbor et al 2022). High heritability suggested that phenotypic differences reflected underlying genetic variation, indicating that selection based on observed performance would likely be effective. However, heritability must be interpreted with genetic advance, which quantified the expected improvement under a defined selection intensity. Traits exhibiting high heritability and high genetic advance represented ideal targets for selection, as they were likely to respond predictably and substantially to breeding interventions (Bello, 2017). These parameters were particularly relevant for yield and yield-related traits, which were complex, environmentally sensitive, and critical for food security.

Research had documented substantial variability among early-maturing maize cultivars for agronomic traits, indicating significant potential for improvement through targeted breeding (Ige et al 2020; 2023). Traits, including plant height, ear length, kernel number, and grain weight, often displayed moderate to high heritability, allowing breeders to identify and select superior genotypes for improvement. Moreover, understanding correlations among these traits facilitated indirect selection strategies, whereby improvement in one trait contributes positively to gains in correlated traits, enhancing selection efficiency (Olajide et al 2025ab). The assessment of combining ability, heterosis, and gene action was also critical for informing hybrid development and parental line selection. Additive and non-additive gene effects influenced the expression of yield and associated traits, underscoring the need to identify superior parents for hybridization programs (Bello et al 2015). Diallel and line × tester analyses had been widely employed to characterize inheritance patterns, enabling the identification of high-performing genotypes and optimal cross combinations for breeding high-yielding hybrids (Bello et al 2017).

Despite these advances, several research gaps remained. First, most studies focussed on general maize germplasm, with limited attention to early-maturing white maize cultivars specifically adapted to savannah conditions. Second, while drought-tolerant cultivars had been developed, comprehensive evaluations integrating genetic variability, heritability, genetic advance, and trait correlations under local savannah environments were sparse. Third, knowledge of specific traits contributing to high grain yield and their potential for selection in early-maturing cultivars remained incomplete. These gaps hindered the efficient design of breeding programs targeted at drought-prone agroecologies and limited the deployment of high-performing cultivars to farmers. Addressing these gaps was critical given the projected challenges of climate variability, increasing population pressure, and the need for sustainable intensification of maize production in the savannah. By evaluating genetic parameters and trait associations in early-maturing white maize, breeders could identify superior genotypes, understand their genetic potential, and implement selection strategies that maximized genetic gain. Such research provides the foundation for breeding programs aimed at enhancing yield stability, drought adaptation, and productivity under suboptimal environmental conditions.

The present study is justified by the need to generate empirical data on the genetic potential of early-maturing white maize cultivars under savannah conditions. Its novelty lied in the integrated assessment of genetic variability, heritability, genetic advance, and trait correlations, which collectively inform selection strategies and breeding decisions. The study provided new insights into the performance and genetic control of yield-related traits specifically for early-maturing white maize, which had been underrepresented in previous research. The objectives of this study were

i. Evaluated genetic variability among eighteen early-maturing white maize cultivars for grain yield and associated agronomic traits under savannah agroecologies,
ii. Estimated broad- and narrow-sense heritability and genetic advance for key yield-related traits,
iii. Assessed correlations among agronomic traits to identify potential targets for indirect selection, and
iv. Identified cultivars with superior performance and high selection potential for breeding programs aimed at improving early-maturing maize productivity in drought-prone environments.

This study provided critical guidance for maize breeders seeking to develop high-yielding, early-maturing cultivars that were resilient to drought stress and adaptable to the savannah environment. The findings were expected to bridge existing research gaps, support strategic breeding decisions, and contributed to sustainable maize production and food security in sub-Saharan Africa.

MATERIALS AND METHODS

Experimental site and plant materials

The study was conducted at the Oke-Oyi substation of the Lower Niger River Basin Development Authority, Nigeria (8°30′ N, 8°36′ E), located within the southern Guinea savannah agroecological zone. Field trials were conducted under rainfed conditions during the 2023 and 2024 cropping seasons. A total of eighteen early-maturing white maize cultivars, with growth durations of 90–95 days and varying responses to abiotic and biotic stresses, were sourced from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. The site was an elevation of approximately 378 metres above sea level and experienced a tropical savannah climate (Köppen Aw) with distinct wet (April–October) and dry (November–March) seasons. Mean annual rainfall was about 852 mm, peaking around 211 mm in September, while average minimum and maximum temperatures were 21.8°C and 32.6°C, respectively. The experimental site consisted of Alfisol soils characterized by a sandy loam texture, slightly acidic pH (5.8–6.3), moderate organic matter content (1.4–1.8%), and adequate fertility and drainage, creating suitable conditions for maize cultivation. Baseline soil fertility was assessed using composite samples collected from the 0–20 cm soil layer to determine nitrogen, phosphorus, potassium, and organic matter levels. Key characteristics of the cultivars were presented in **Table** 1.

Table 1 Description of eighteen early white cultivars evaluated for grain yield and associated characters at the Lower Niger River Basin Development Authority, Oke-Oyi, Nigeria

S/N	Pedigree	Endosperm type	Reaction to Striga	Reaction to drought
1	Acr 90 Pool 16 Dt Str	Normal	Resistant	Resistant
2	Tze-W Dt Str C$_4$	Normal	Resistant	Resistant
3	Tze Comp 3 Dt C$_3$	Normal	Resistant	Susceptible
4	Tze-W Dt Str QPM C$_0$	Normal	Resistant	Resistant
5	Tze-W Pop Dt Str QPM	QPM	Resistant	Resistant
6	Acr 97 Tze Comp 3 x 4	Normal	Susceptible	Resistant
7	Dmr-Esr W C$_1$F$_2$	Normal	Susceptible	Resistant
8	Acr 95 Tze Comp 4 C$_3$	Normal	Susceptible	Resistant
9	Dte-W Str Syn	Normal	Resistant	Resistant
10	Dte Str-W Syn Pop C$_3$ F$_1$	Normal	Resistant	Resistant
11	Syn Dte Str-W	Normal	Resistant	Resistant
12	Ev Dt-W 2000 Str QPM	QPM	Resistant	Resistant
13	Ev Dt-W 2008 Str	Normal	Resistant	Resistant
14	2009 Dte-W Str	Normal	Resistant	Resistant
15	2008 Dtma-W Str	Normal	Resistant	Resistant
16	2011 Tze-W Dt Str Syn	Normal	Resistant	Resistant
17	2012 Tze-W Pop Dt C$_4$ Str C$_5$	Normal	Resistant	Resistant
18	2013 Dte Str-W Syn F$_1$	Normal	Resistant	Resistant

Cultural practices, experimental design, and layout

Standard agronomic practices for maize cultivation in the southern Guinea savannah of Nigeria were followed. The field was ploughed, harrowed, and ridged prior to planting. Weed management included pre- and post-emergence herbicide applications: post-emergence paraquat (3 kg a.i. ha^{-1}) was applied two weeks before planting, while a pre-emergence mixture of The field trials were laid out in a randomized complete block design (RCBD) with three replications. Within each replication, the maize cultivars were randomized across blocks to minimize experimental bias and enhance precision in evaluating genotype performance. Each plot consisted of a single row measuring 4 m in length, with 0.75 m spacing between rows and 0.25 m spacing between plants, resulting in an approximate population density of 53,000 plants ha^{-1}. This uniform layout was maintained across both seasons to facilitate reliable assessment of genotype × year interactions. Maize seeds were manually sown on 20 July 2023 and 18 July 2024 for the first and second cropping seasons, respectively. Three seeds were sown per hole at a depth of 3–4 cm and thinned to two plants per stand at two weeks after planting (WAP), resulting in a plant density of 53,333 plants ha^{-1}. Fertilization was applied at 4 WAP using side placement: 80 kg N ha^{-1} (Urea), 40 kg P_2O_5 ha^{-1} (Single Superphosphate), and 40 kg K_2O ha^{-1} (Muriate of Potash). Supplemental hand weeding and top-dressing with 30 kg N ha^{-1} of urea were performed at 6 WAP.

Data Collection

Data were recorded from the two middle rows of each plot, with measurements taken on an average of ten plants per row. Traits measured included days to 50% tasselling and silking, anthesis-silking interval (ASI), plant and ear height, number of grains per ear, plant and ear aspect, and grain yield. Plant height was measured from ground level to the first node of the flag leaf, and ear height from soil level to the highest ear-bearing node. Days to 50% anthesis, tasselling, and silking were recorded as the number of days from sowing to when half of the plants reached each respective stage. ASI was calculated as the interval between tasselling and silking. Plant and ear aspects were visually scored on a 1–5 scale, where 1 = excellent (uniform, healthy plants or well-filled ears) and 5 = poor (variable, weak plants or poorly filled ears). Grain yield was determined following the procedure described by Bello et al. (2012b). At crop maturity, ears were harvested and weighed separately for each plot. Grain yield per hectare (kg ha^{-1}) at 15% grain moisture content was calculated as:

$$\text{Grain yield (kg ha}^{-1}\text{)} = [\text{Fresh wt.} \times (100 - \text{MC}) \times 0.8 \times 10{,}000] / [(100 - 15) \times 7.5] \quad (1)$$

Where:
- Fresh wt. = weight of ears per plot at harvest (kg)
- MC = moisture content of the grain at harvest (%)
- 0.8 = shelling percentage (assumed 80%)
- 10,000 m^2 = area per hectare
- 15% = standard grain moisture for storage
- 7.5 m^2 = harvested plot area (5 m × 0.75 m × 2 rows)

Statistical Analyses

The PROC MIXED procedure in SAS (SAS version 9.1.3, SAS Institute, 2024) was used to compute variance components for all measured traits. Data from each year were first subjected to analysis of variance (ANOVA) to test for significant differences among genotypes. Homogeneity of variance was assessed using Levene's test, after which a combined ANOVA was performed to evaluate the effects of year, cultivar, and cultivar × year interaction on agronomic performance. In the model, cultivars and their interaction with year were considered random effects, while cropping years and replications within years were fixed effects. The combined analysis of genotypes across the two years of evaluation for the studied traits (Fehr, 1987) was represented by the following model:

$$Y_{(\square\square\square\square)} = \mu + \text{genotype}_{\square} + y_{\square} + (\text{genotype} \times y)_{\square\square} + \text{rep}(y)_{\square\square} + \text{block}(\text{rep} \times y)_{\square\square\square} + \varepsilon_{\square\square\square\square}$$
(2)

- μ = overall mean
- $\text{genotype}_{\square}$ = effect of the i-th genotype (**cultivar**)
- $y_{\square}$ = effect of the j-th year
- $(\text{genotype} \times y)_{\square\square}$ = interaction effect between the i-th genotype and the j-th year
- $\text{rep}(y)_{\square\square}$ = effect of the k-th replication within the j-th year
- $\text{block}(\text{rep} \times y)_{\square\square\square}$ = effect of the l-th incomplete block within the k-th replication in the j-th year
- $\varepsilon_{\square\square\square\square}$ = residual variance

The coefficient of variation (CV %) was used to describe the relative degree of variation for each trait. Standard errors (SE) for all effects were computed from error mean squares for the untransformed data. Differences in trait means were determined using the least significant difference (LSD) test at $p < 0.05$.

Phenotypic variance ($\delta^2_{\square}$)

$$\delta^2_{\square} = \delta^2 g + (\delta^2 gy / y) + (\delta^2 e / ry) \quad (3)$$

Broad-sense heritability (H)

$$H(\%) = (\delta^2 g / \delta^2 p) \times 100 \quad (4)$$

Genetic advance (GA)

$$GA = K \times \delta A \times H \qquad (5)$$

Where:
- $K = 2.063$ (selection differential at 5%)
- δA = phenotypic standard deviation of the mean yield of the original lines
- H = broad-sense heritability

Genetic gain (GG)

$$GG(\%) = (GA / X\square) \times 100 \qquad (6)$$

Genotypic coefficient of variation (GCV)

$$GCV(\%) = (\sqrt{\delta^2 g} / \bar{U}) \times 100 \qquad (7)$$

Phenotypic coefficient of variation (PCV)

$$PCV(\%) = (\sqrt{\delta^2 p} / \bar{U}) \times 100 \qquad (8)$$

Environmental coefficient of variation (ECV)

$$ECV(\%) = (\sqrt{\delta^2 e} / \bar{U}) \times 100 \qquad (9)$$

Where $\bar{U}$ is the mean value of the trait.

RESULTS

Combined analysis of variance for grain yield and associated characters

Analysis of variance revealed significant differences among cultivars for grain yield and associated agronomic traits, demonstrating the presence of substantial genetic variability (**Table** 2). The cultivar × year interaction was also highly significant for grain yield, highlighting differential responses of cultivars to varying environmental conditions across the two cropping seasons. This highlighted the necessity of multi-year evaluations to account for genotype × environment interactions, which were essential for identifying cultivars with stable and broad adaptation. Phenotypic variation among cultivars was sufficient to enable effective selection, consistent with previous reports in early-maturing maize under savannah conditions (Ige et al 2020). Traits such as plant height, days to silking, and number of grains per ear exhibited moderate to high heritability and genetic advance, suggesting that selection for these characters can substantially improve grain yield (Amegbor et al 2022). High phenotypic coefficients of variation relative to genotypic coefficients indicated environmental influence on trait expression, reinforcing the need for multi-location testing (Nguyen et al 2022).

Table 2 Mean squares from combined analysis of variance for grain yield and associated characters at the Lower Niger River Basin Development Authority, Oke-Oyi, Nigeria

Sources of variation	Days to 50% tasselling	Days to 50% silking	Anthesis -silking interval (days)	Plant height (cm)	Ear height (cm)	Number of grains ear-1	Plant aspect	Ear aspect	Grain yield (t ha-1)
Year	4.55	2.54	3.58	3.45	6.58	8.25	10.22	10.18	2.48
Rep/Year	4.11	6.23	8.45	2.79	2.49	3.12	7.56	6.44	3.66
Cultivars	7.52	8.36	2.11	7.83	7.94	9.22	11.34	11.26	88.25*
Cultivars × Year	11.23	9.23	2.48	9.18	7.34	9.37	12.22	13.36	92.98*
Pool Error	7.76	9.62	11.22	137.74	7.11	12.62	13.75	10.11	11.48

Note: *, **, significant at $P < 0.05$ and 0.01, respectively

Performance of early-maturing white maize cultivars

Table 3 presented the average performance of the eighteen early-maturing white maize cultivars across two cropping seasons. Grain yield varied significantly among cultivars, ranging from 4.11 to 5.49 t ha^{-1}, with a mean of 4.66 ± 0.42 t ha^{-1} and a highly significant F-value (122.68; $P < 0.01$), reflecting substantial genetic contributions to yield differences. The top-performing cultivars were 2013 DTE STR-W SYN F$_1$, 2012 TZE-W POP DT C$_4$ STR C$_5$, EV DT-W 2000 STR, 2011 TZE-W DT STR SYN, 2009 DTE-W STR, and 2008 DTMA-W STR in descending order. These genotypes warrant further multi-location evaluation in drought-prone environments to confirm stability and adaptability (Konate et al 2023; Ige et al 2024). Flowering traits were relatively uniform, with days to 50% tasselling (55 ± 0.48) and silking (57 ± 0.66) ranging narrowly from 52 to 56 and 54 to 59 days, respectively. In contrast, the anthesis–silking interval (ASI) exhibited greater variability (3 ± 1.42 days; F = 64.75), highlighting differences in flowering synchronization among genotypes, a trait critical for pollination efficiency and yield stability under stress conditions (Ishfaq et al 2025).

Table 3 Combined mean performance of 18 early white maize cultivars for grain yield and associated characters at the Lower Niger River Basin Development Authority, Oke-Oyi, Nigeria

Cultivars	**Days to 50% tasselling**	**Days to 50% silking**	**Anthesis-silking interval (days)**	**Plant height (cm)**	**Ear height (cm)**	**Number of grains ear-1**	**Plant Aspect (No)**	**Ear Aspect (No)**	**Grain yield (t ha-1)**
Acr 90 Pool 16 Dt Str	53	55	2	124	38	59	3	2	4.36
Tze-W Dt Str C_4	56	58	2	127	37	59	2	2	4.37
Tze Comp 3 Dt C_3	55	57	2	128	38	60	3	3	4.41
Tze-W Dt Str QPM C_0	54	56	2	126	37	58	2	3	4.43
Tze-W Pop Dt Str QPM	56	57	3	119	36	59	3	2	4.11
Acr 97 Tze Comp 3 x 4	56	57	3	121	35	58	2	2	4.39
Dmr-Esr W C_1F_2	55	57	2	123	35	58	3	3	4.43
Acr 95 Tze Comp 4 C_3	53	55	2	123	37	59	3	3	4.39
Dte-W Str Syn	57	59	2	119	36	58	3	3	4.45
Dte Str-W Syn Pop C_3 F_1	55	57	2	121	38	58	3	2	4.12
Syn Dte Str-W	52	54	2	118	35	58	2	2	4.59
Ev Dt-W 2000 Str QPM	54	57	3	126	37	59	2	2	4.57
Ev Dt-W 2008 Str	54	57	3	127	38	57	3	2	5.18
2009 Dte-W Str	53	56	3	125	34	56	2	3	5.16
2008 Dtma-W Str	56	58	2	123	39	58	2	3	5.12
2011 Tze-W Dt Str Syn	55	57	2	121	37	58	2	2	5.17
2012 Tze-W Pop Dt C_4 Str C_5	54	57	3	119	34	58	3	3	5.21
2013 Dte Str-W Syn F_1	55	57	2	124	36	60	2	2	5.49
Means	55	57	3	123	37	58	3	2	4.66
Standard deviation	1.33	1.18	0.49	3.12	1.47	0.97	0.51	0.51	0.43
CV %	20.15	18.22	11.55	6.98	15.22	9.32	12.55	17.74	8.62
LSD (0.05)	0.03	0.01	0.05	0.01	0.07	0.04	0.02	0.01	0.75

Table 4. Ranges, F-values, and means from evaluation for grain yield and related characters among 18 early white maize cultivars evaluated in 2023 and 2024 at the Lower Niger River Basin Development Authority, Oke-Oyi, Nigeria

Characters	Range of variation	Means	Standard deviation	Error variance	F observed
Days to 50% tasselling	52-56	55	1.33	0.65	34.83
Days to 50% silking	54-59	57	1.18	0.23	25.11
Anthesis-silking interval	2-3	3	0.49	5.61	64.75
Plant height (cm)	118-197	123	3.12	0.22	22.12
Ear height (cm)	34-38	37	1.47	0.98	10.86
Number of grain ear^{-1}	56-60	58	0.97	0.45	14.67
Plant aspect	2-3	3	0.51	1.33	70.34
Ear aspect	2-3	2	0.51	0.74	44.42
Grain yield (t ha^{-1})	4.11-5.49	4.66	0.43	2.14	122.68**

Note: **, significant at $P < 0.01$

Phenotypic and Genotypic Coefficients of Variation

Maize grain yield and related agronomic traits were complex, polygenic, and influenced by interactions between genetic and environmental factors (Table 5). The GCV and PCV) were essential for assessing the relative contributions of genetic and environmental factors and estimating potential genetic gains (Amegbor et al 2022). Traits exhibiting high GCV values were more reliable for selection, highlighting the potential for improving drought-tolerant maize cultivars in water-limited environments. The present study showed that GCVs were generally close to, but slightly lower than, PCVs for most traits, indicating a modest environmental influence on expression (Dheeraj et al 2020). The small differences between phenotypic variance (σ^2p) and genotypic variance (σ^2g) suggested that phenotypic variation was largely genetically determined, with limited environmental contribution. The cultivar × year interaction variance (σ^2gy) was low for most traits, implying stable expression across the two cropping seasons and supporting previous observations that heterozygosity could buffer against environmental fluctuations, whereas inbreeding reduces this buffering capacity (Konate et al 2023).

Table 5. Phenotypic variance, genetic variance cultivar × year interaction variance, environmental, phenotypic and genotypic coefficient of variations for grain yield and associated characters

Characters	δ2p	PCV	δ2g	GCV	δ2gy	ECV
Days to 50% tasselling	8.42	7.63	6.38	7.54	11.53	18.56
Days to 50% silking	6.98	10.73	9.73	11.86	16.13	13.51
Anthesis-silking interval	12.35	13.82	14.36	22.11	26.65	17.06
Plant height (cm)	532.62	62.15	72.11	76.27	27.11	26.82
Ear height (cm)	127.83	82.36	92.83	87.73	23.82	17.17
Number of grain ear^{-1}	2341.32	111.83	136.36	163.62	17.73	16.63
Plant aspect	234.92	89.39	77.91	69.26	27.61	23.42
Ear aspect	123.51	116.56	127.45	151.77	23.75	19.62
Grain yield (t ha^{-1})	261.37	146.89	152.61	161.23	22.82	20.55
Standard error	1.34	2.83	1.43	1.94	0.67	0.72

Heritability and Genetic Advance

Genetic variance and heritability were key determinants of selection efficiency in maize breeding, as they reflected the potential for genetic improvement and guide breeding strategy. High genetic variance offered opportunities for combining desirable alleles, while heritability indicates the proportion of phenotypic variation attributable to genetic factors (Bello et al 2012ab; Amegbor et al 2022). In this study, broad-sense heritability was generally high for most traits (Table 6), indicating the scope for effective selection under savannah agroecologies.

Table 6. Estimate of heritability and genetic advance for grain yield and other related characters among 18 early white maize cultivars evaluated in 2023 and 2024 at Oke-Oyi, Nigeria

Cultivars	**Days to 50% tasselling**	**Days to 50% silking**	**Anthesis-silking interval**	**Plant height**	**Ear height**	**Number of grains ear-1**	**Plant aspect**	**Ear aspect**	**Grain yield**
Heritability (%)	78.47	77.47	63.52	97.38	95.79	98.54	54.65	53.54	98.63
Genetic Advance	8.43	9.82	8.41	9.22	10.62	7.62	5.11	5.73	22.22
Genetic advance (% of mean)	7.89	8.37	5.72	7.17	8.64	8.22	6.54	6.82	19.89
Standard error	0.98	1.73	0.93	0.46	0.61	2.72	1.46	0.95	0.58

DISCUSSION

The observed variability provided a strong basis for selecting superior early-maturing white maize cultivars with enhanced yield potential in drought-prone savannah agroecologies. These results aligned with prior studies emphasizing the value of integrating genetic variance, heritability, and genotype × environment interaction analyses in maize breeding programs (Olajide et al 2025a).

The observed variation in the number of grains per ear (58□±□0.99; F□=□14.67) reflected significant genetic differences in ear productivity, providing a reliable basis for selection aimed at enhancing grain yield. Plant aspect (3 ± 0.53) and ear aspect (2 ± 0.93) were highly significant (F = 70.34 and 44.42, respectively), revealing substantial variation in traits influencing plant performance and grain quality (Bello et al 2019). Overall, these results confirmed that early-maturing white maize cultivars possessed significant genetic variability for key agronomic traits, providing opportunities for selection and breeding of high-yielding, stress-resilient genotypes suitable for savannah agroecologies.

Plant height (123 ± 0.78 cm) and ear height (37 ± 0.63 cm) showed moderate variation (F = 22.12 and 10.86, respectively), consistent with their roles in lodging resistance and harvestability, aligning with observations on maize plant architecture optimization (Bello et al 2013ab).

High PCV and GCV values were observed for grain yield, number of grains per ear, and plant and ear height, indicating significant variability and the potential for effective selection (Ige et al 2020;). In contrast, anthesis–silking interval, days to silking, and days to tasselling exhibited low PCV and GCV, reflecting limited genetic variability. These findings aligned with previous studies on early-maturing maize and highlighted the traits most amenable to selection for improving productivity under savannah conditions (Limbongan et al 2024).

Traits such as grain yield, number of grains per ear, plant height, and ear height exhibited high heritability and high genetic advance, suggesting strong additive gene action and significant potential for improvement through direct selection (Bello et al 2013ab; 2025). Conversely, low genetic advance in combination with high heritability for days to silking and tasselling indicated the predominance of non-additive genetic effects, which are better exploited through hybridization and heterosis (Ige et al 2020). Although anthesis–silking interval showed moderate heritability, its high genetic advance indicated environmental sensitivity, limiting gains from direct selection (Nguyen et al 2022). Similarly, plant and ear aspects exhibited low heritability and genetic advance, suggesting strong environmental influence and non-additive control, thereby reducing the efficiency of selection for these traits (Bello et al 2015, 2024). These results provided critical guidance for selecting early-maturing white maize cultivars, emphasizing traits with additive genetic control for yield improvement in drought-prone savannah agroecologies.

The genetic advance, expressed as a percentage of the mean, varied from 59.87 for the number of grains per ear to 5.23 for days to silking, highlighting the differential potential for improvement among traits and aligning with previous findings (Amegbor et al 2022).

The present study provided a comprehensive evaluation of genetic variability, heritability, and genetic advance for grain yield and associated agronomic traits in early-maturing white maize cultivars grown under savannah agroecologies. Significant differences among cultivars for grain yield and related traits, along with notable cultivar × year interactions, indicated substantial genetic variation and highlight differential genotypic responses to environmental fluctuations across cropping seasons. This underscored the importance of multi-environment evaluation in identifying stable, high-performing cultivars suitable for drought-prone regions, where erratic rainfall and terminal water stress often limitted maize productivity. Among the eighteen cultivars evaluated, 2013 DTE STR-W SYN F_1 , 2012 TZE-W POP DT C_4 STR C_5 , EV DT-W 2000 STR, 2011 TZE-W DT STR SYN, 2009 DTE-W STR, and 2008 DTMA-W STR consistently exhibited superior grain yield, ranging from 5.12 to 5.49 t ha^{-1}, demonstrating their potential for further multi-location testing and deployment in drought-prone environments. The minimal differences between phenotypic and genotypic variances for most traits, along with high phenotypic and genotypic coefficients of variation, suggested that key yield-related traits, including grain yield, number of grains per ear, and plant and ear height,were predominantly under genetic control and were highly amenable to selection.

Traits such as days to tasselling, days to silking, and anthesis-silking interval exhibited relatively low genetic variability, indicating limited potential for direct selection. Conversely, traits displaying high heritability and high genetic advance, such as grain yield, plant height, ear height, and number of grains per ear, reflect strong additive genetic control, making them highly suitable for improvement through conventional selection. Traits with high heritability but low genetic advance, such as flowering time, are likely influenced by non-additive genetic effects and might be more effectively improved through hybrid breeding strategies. The significant cultivar × year interactions observed for key traits further highlight the need for multi-season and multi-location evaluation to identify genotypes with stable performance across variable environmental conditions. Traits related to plant and ear aspects exhibited low heritability and genetic advance, suggesting strong environmental influence, and therefore required careful consideration when designing breeding strategies for improved plant architecture and harvestability.

CONCLUSION

The study demonstrated that early-maturing white maize cultivars possess substantial genetic variation for grain yield and associated traits, providing a strong foundation for targeted selection and breeding. The identification of superior cultivars and traits with high additive genetic control offered clear avenues for enhancing maize productivity under favourable and water-limited conditions. These results offerred valuable insights for breeding programs aimed at developing high-yielding, drought-resilient maize cultivars, thereby supporting enhanced food security and promoting sustainable agricultural production in savannah regions characterized by environmental variability and recurrent water stress.

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