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Genetic Variability and Yield Determinants of Upland Rice Genotypes in Akungba Akoko Agro-Ecology

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Abstract

Background Rice is one of the world's most important cereal crops and a major source of food and income for millions of people, especially Nigeria, which has almost reach her self-sufficient production capacity. However, genetic variability significantly influences yield component traits in rice for stability and adaptability. Therefore, this study assessed the genetic variability and trait associations influencing grain yield in upland rice genotypes evaluated under the Akungba Akoko agro-ecology.

Methods Fourteen genotypes were tested under field conditions in a randomized complete block design at the experimental field of the department of Plant Science and Biotechnology, and data were collected on yield and related agronomic traits, analyzed using GLM models of SPSS version 27.

Result The analysis of variance revealed highly significant differences among genotypes, confirming the presence of considerable genetic diversity. Plant height, number of tillers, effective tillers, flag leaf length, panicle length, panicle weight, number of grains per panicle, number of spikelets, thousand grain weight, grain length and width, days to panicle initiation, days to maturity, and grain yield per hill all vary significantly among the genotypes. These significant differences suggest considerable genetic variability within the tested genotypes, which is favorable for selection and breeding. Coefficient of variation (CV) provides a measure of experimental precision and variability relative to the mean. Most traits have CV values below 20%, with some lower than 10%, which suggests good experimental consistency. For example: Plant height CV 5.8% (high precision). Number of tillers CV 16.4%. Grain yield CV 25.8%, which is typical for yield traits due to their inherent variability. Estimates of genotypic and phenotypic coefficients of variation indicated that while some traits were strongly under genetic control, others were more sensitive to environmental influence. Grain yield showed positive and significant correlations with key yield components, particularly productive tillers, panicle weight, number of grains per panicle, and thousand-grain weight, highlighting their value as indirect selection criteria. Genetic parameter estimates further demonstrated high heritability (> 90%) for traits such as plant height, number of tillers, panicle weight, and maturity, coupled with high genetic advance values, suggesting strong additive gene action and effective selection potential. Conversely, traits like panicle length exhibited lower heritability, reflecting greater environmental influence.

Conclusion

The study shows good genetic variability and heritability for most important yield and agronomic traits in upland rice genotypes from this agro-ecology, indicating strong potential for selection and breeding improvements. Traits like panicle weight, grain yield, and tiller number are particularly promising targets for breeders.

1.0 Background

Rice (*Oryza sativa* L.) is one of the world's most important cereal crops and a major source of food and income for millions of people. Its production is especially important in developing countries, particularly Nigeria, where population growth and changing climatic conditions continue to increase food demand [1]. However, rice productivity is constrained by several biotic and abiotic factors, including drought, poor soil fertility, weeds, pests, and diseases [2]. These constraints are often more pronounced in upland rice production systems, where crops depend largely on rainfall and are frequently exposed to intermittent water stress. Consequently, increasing the productivity and stability of upland rice through genetic improvement remains an important objective of rice breeding programs.

Genetic variability is fundamental to the success of any crop improvement program because selection can only be effective when sufficient genetic differences exist among the breeding materials. Therefore, substantial variation among rice genotypes for agronomic and yield-related traits provides opportunities to identify superior genotypes and exploit desirable genetic combinations in enhancing rice productivity. Studies using diverse rice materials have reported significant differences among genotypes for grain yield and other agronomic characteristics, demonstrating exploitable genetic variation in rice populations [3,4]. For example, considerable variation in grain yield has been observed among rice cultivars representing different production ecologies, with significant genotype effects and genotype × environment interactions influencing yield performance [5].

The assessment of genetic variability is commonly complemented by estimates of genotypic and phenotypic coefficients of variation, heritability, and genetic advance. These parameters help breeders to determine the extent with which observed differences among genotypes are genetically controlled and therefore useful for selection. High heritability, particularly when accompanied by substantial genetic advance, generally indicates that a considerable proportion of the observed variation may be attributable to genetic effects and that selection based on phenotypic performance could be effective. In rice, studies have reported considerable heritability for several yield and yield-related traits, although the magnitude varies across traits and environments. For example, a study of 319 rice genotypes reported broad-sense heritability estimates ranging from 0.35 to 0.99 for 19 agronomic traits [6]. Hence, selection could be initiated on these agronomic traits as a result of the reported estimates.

Grain yield is a complex quantitative trait controlled by several genes and strongly influenced by environmental conditions [7]. Direct selection for grain yield can therefore be difficult, particularly when environmental variation masks genetic differences among genotypes [1]. For this reason, understanding the association between grain yield and its component traits is essential for developing effective selection strategies [8]. Correlation analysis provides a measure of the degree and direction of association between traits and can help identify characters that may be useful as indirect selection criteria for improving grain yield. In rice breeding studies, grain yield is significantly associated with traits such as number of panicles per plant, thousand-grain weight, grain width, filled grains, and yield per plant, although the strength and direction of these relationships may vary with season and environment [9].

The distinction between genotypic and phenotypic correlations is also important because phenotypic associations is always influenced by environmental effects which is an important variable in phenotypic correlations. Genotypic correlation provides a better indication of the inherent genetic relationship between traits and may therefore be more useful in predicting the response to selection. Where a yield component exhibits a strong positive genetic

association with grain yield, improvement of that component traits may contribute to simultaneous improvement in yield. Conversely, a negative association between important traits may indicate the existence of trade-offs that breeders need to consider during selection.

Upland rice improvement presents additional challenges because yield performance is often affected by water availability and other environmental stresses, this may be corrected by providing steady supply of water when there is shortage of rainfall. Genotype × environment interactions can cause genotypes to perform differently across locations or growing conditions, making the identification of broadly adapted and high-yielding genotypes an important breeding objective [10]. Research in rainfed and upland environments has demonstrated significant genotype × environment effects for grain yield, while direct selection under the target production conditions can be important for achieving genetic gain.

Against this background, the present study is undertaken to assess the genetic variability and yield-determining traits of upland rice genotypes. The study will provide information on the extent of genetic variation present in the materials and identify yield-related traits that could serve as useful selection criteria for developing high-yielding and well-adapted upland rice varieties.

2.0 Materials and Methods

2.1 Location and field layout

The experiment was conducted in the experimental plot of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba Akoko, to evaluate genetic variability in yield determinants among upland rice genotypes. During the experiment, moisture supply relied on rainfall, and all other agronomic practices were adequately followed. A Randomized Complete Block Design (RCBD) with three replications and 14 rice genotypes (Table 1) was adopted. The selected lines used in this experiment were screened in different experiments based on high yield potential and short duration. Pre-germinated seeds were planted in a wet seedbed, and 21-day-old seedlings were transplanted with one seedling per hill, spaced evenly at 25 × 25 cm between and within rows. Nitrogen fertilizer was applied in four splits with a total of 120 kg N ha^{-1}: 30% as a basal application, 20% at the mid-tillering stage, 30% at panicle initiation, and 20% at heading. Additionally, 30 kg P_2O_5 and 30 kg K_2O were applied as basal. Other crop care measures, including insect, disease, and weed management, were carefully managed as required.

2.2. Trait measurements

Phenotypic data on 14 traits (Table 2), including plant height (PLTHT), number of tillers (NOT), effective tillers (ETP), flag leaf length (FLL), panicle length (PANL), panicle weight (PANWT), number of filled grains per panicle (NGP), number of spikelets per panicle (NSPKP), 1000-grain weight (TGW), grain length (GL), grain width (GW), number of days to panicle initiation (NDPI), number of days to maturity (NDM), and grain yield (GYD), were collected from 5 randomly selected representative plants in each plot.

2.3. Statistical analysis

The data obtained from the trait measurements were subjected to statistical analysis of treatment means and compared using the Duncan Multiple Range Test (DMRT) at a 5% significance level with SPSS version 20. Genetic parameters were estimated following the procedure of Osekita and Ajayi (2013). Genotypic Variance (VG) and Phenotypic Variance (VP) were estimated according to Wricke and Weber [1986]:

$$\mathrm{VG} = \left(\frac{MSg - MSe}{r}\right)$$

VP = VG + MSe

where MSg = mean square for genotype, MSe = mean square for error, and r = number of replicates.

The Phenotypic Coefficient of Variation (PCV) and the Genotypic Coefficient of Variation (GCV) were computed following Osekita and Ajayi [2013]:

$$\mathrm{PCV}\ (\%) = \left(\frac{\sqrt{VP}}{\bar{x}}\right) \times 100$$

$$\mathrm{GCV}\ (\%) = \left(\frac{\sqrt{VG}}{\bar{x}}\right) \times 100$$

where $\bar{x}$ is the grand mean. Values were classified according to Sivasubramanian and Madhavamenon [1973] as low (0–10%), moderate (10–20%), and high (> 20%). The Coefficient of Variation (CV) was calculated as follows:

$$\mathrm{CV}\ (\%) = \left(\frac{\sqrt{MSe}}{Gm}\right) \times 100$$

where *Gm* = grand mean.

Broad-sense heritability (H^2B) was estimated as the ratio of VG to VP and classified according to Robinson et al. [1949] as low (0–30%), moderate (30–60%), and high (> 60%). Genetic Advance (GA) and genetic advance as a percentage of the mean (GAM) were estimated following Johnson et al. [1955]:

$$\mathrm{GA} = \left(\frac{H^2 B}{100}\right) \times K \times \sqrt{VP}$$

$$\mathrm{GAM}\ (\%) = \left(\frac{GA}{GM}\right) \times 100$$

where K = 2.06 (selection intensity at 5%) and GM = grand mean. GAM was categorized as low (0–10%), moderate (10–20%), and high (> 20%). Pearson's correlation coefficients among yield traits were computed in SPSS version 20, with significance assessed at $p \leq 0.05$ and $p \leq 0.01$, and degrees of freedom set to n − 2.

Table 1
Genotypes and its source

S/N	Genotypes	Source
1	NER 2	IITA
2	NER 6	IITA
3	NER 8	IITA
4	OS 6	IITA
5	LAC 23	IITA
6	IWA 10	ABAKALIKI
7	LADY's	IITA
8	IR06N	IRRI
9	IR06A	IRRI
10	FAD 42	IITA
11	IR07A	IRRI
12	INPARI	ABAKALIKI
13	IWA 8	ABAKALIKI
14	UPIA	ABAKALIKI

Table 2. List of studied traits of rice genotypes evaluated in Akungba Akoko Agro ecology with acronym and unit of measurement.

Trait acronym	Trait description	Unit
PLTHT	Plant height at harvest	cm
NOT	number of Tillers hill^{-1} at harvest	count
ETP	Effective tillers hill^{-1} at harvest	count
FLL	Flag leaf length	cm
PANL	Panicle length	cm
PANWT	Panicle weight	g
NGP	Number of filled grain panicle^{-1}	count
NSPK	Number of spikelets per panicle	count
TGW	1000-grain weight	g
GL	Grain Length	cm
GW	Grain width	cm
NDPI	Number of days to panicle initiation	count
NDM	Days to maturity at harvest	count
GYDH	Grain yield hill^{-1}	g

3.0 Results

3.1 Mean performance

Table 3 presents the mean performance of fourteen upland rice genotypes evaluated in the Akungba Akoko agro-ecology, focusing on several agronomic traits.

Table 3
Mean performance of fourteen upland rice genotypes evaluated in Akungba Akoko agro ecology.

Genotypes	PLHT	NOT	ETP	FLL	PANL	PAWT	NGP	NSPK	TGW	GL	GW	NDPI	NDM	GYDH
NER 2	99.9^{ab}	13.0^{bcd}	12.0^{cd}	37.1^{def}	28.6^{ab}	6.4^{c}	277.3^{cde}	14.3^{de}	23.8^{bc}	0.9^{c}	0.4^{c}	101.0^{g}	131.0^{i}	60.4^{d}
NER 6	97.9^{ab}	6.3^{a}	5.3^{a}	30.2^{ab}	30.6^{bc}	8.8^{d}	340.6^{g}	20.3^{g}	31.1^{g}	0.9^{c}	0.4^{c}	109.3^{h}	139.3^{j}	42.1^{bc}
NER 8	97.2^{ab}	11.0^{bc}	9.3^{bc}	32.5^{bcd}	26.7^{a}	5.8^{c}	217.3^{abcd}	14.7^{de}	30.1^{e}	0.9^{c}	0.4^{c}	94.7^{f}	124.7^{g}	42.9^{bc}
OS 6	113.0^{cd}	11.3^{bc}	10.0^{bcd}	42.5^{g}	31.3^{c}	7.6^{d}	267.3^{cde}	16.3^{ef}	28.4^{de}	0.9^{c}	0.4^{c}	99.7^{g}	129.7^{h}	43.9^{bc}
LAC 23	117.9^{d}	9.0^{ab}	8.3^{b}	37.2^{ef}	29.6^{bc}	8.4^{d}	340.0^{e}	18.3^{fg}	30.1^{e}	0.9^{c}	0.4^{c}	110.0^{h}	140.0^{j}	29.3^{ab}
IWA 10	101.0^{ab}	15.7^{def}	13.3^{de}	32.8^{bcde}	37.7^{f}	4.4^{b}	238.7^{bcd}	12.7^{cd}	24.3^{bcd}	0.8^{b}	0.3^{b}	80.0^{b}	109.7^{bc}	49.0^{cc}
LADY's	103.3^{bc}	14.7^{cde}	12.3^{cde}	32.2^{bc}	35.0^{ef}	3.3^{ab}	255.3^{cd}	10.7^{abc}	25.4^{cd}	0.7^{a}	0.2^{a}	89.3^{e}	119.7^{f}	42.4^{bc}
IR06N	102.0^{ab}	13.7^{cd}	11.7cd	34.0^{bcdef}	36.4^{ef}	3.7^{ab}	224.0^{abcd}	12.7^{cd}	20.6^{ab}	0.8^{b}	0.3^{b}	79.3^{b}	109.0^{b}	30.3^{ab}
IR06A	98.4^{ab}	19.3^{f}	13.3^{de}	33.7^{bcde}	35.7^{ef}	3.4^{ab}	198.3^{abc}	12.0^{bcd}	21.7^{bc}	0.9^{c}	0.3^{b}	80.7^{bc}	110.7^{cd}	32.9^{ab}
FAD 42	154.9^{c}	14.3^{cde}	12.3^{cde}	38.3^{f}	34.1^{de}	4.3^{b}	301.0^{de}	11.7^{abcd}	22.3^{bc}	0.9^{c}	0.3^{b}	81.7^{cd}	111.7^{d}	24.0^{a}
IR07A	96.2^{ab}	18.0^{ef}	15.3^{e}	26.4^{a}	34.2^{de}	3.8^{ab}	287.3^{de}	14.7^{de}	17.3^{a}	0.9^{c}	0.3^{b}	90.3^{e}	120.3^{f}	17.6^{a}
INPARI	90.3^{a}	14.3^{cde}	13.0^{de}	27.1^{a}	35.2^{ef}	2.9^{a}	162.7^{ab}	9.3^{ab}	23.1^{bc}	0.9^{c}	0.3^{b}	83.0^{d}	113.0^{e}	19.1^{a}
IWA 8	93.7^{ab}	11.3^{bc}	10.3^{bcd}	35.9^{cdef}	32.1^{cd}	2.7^{a}	142.3^{a}	9.0^{a}	22.6^{bc}	0.8^{bc}	0.3^{b}	72.7^{a}	102.7^{a}	31.0^{ab}
UPIA	102.6^{bc}	18.0^{ef}	13.0^{de}	34.9^{cdef}	32.3^{cd}	3.6^{ab}	235.3^{bcd}	12.3^{cd}	22.2^{bc}	0.9^{c}	0.3^{b}	100.0^{g}	130.0^{h}	43.4^{bc}

PLTHT = plant height, NOT = number of tillers per hill, ETP = effective tillers, FLL = flag leaf length, PANL = panicle length, PANWT = panicle weight, NGP = number of grains per panicle, NSPKP = number of spikelet per panicle, TGW = thousand grain weight, GL = grain length, GWDT = grain width, NDTPI = number of days to panicle initiation, NDTM = number of days to maturity, GYDH = grain yield per hill

Plant Growth and Morphological Traits

Plant Height: FAD 42 shows the tallest plants (154.9 cm), which may indicate robust growth potential. INPARI has the shortest height (90.3 cm). Number of Tillers per Hill and Effective Tillers: IR06A and IR07A have a relatively high number of tillers (18.0 and 18.0, respectively) and effective tillers, suggesting good productive tillering capacity. NER 6, however, shows the lowest tillering. Flag Leaf Length: OS 6 has the longest flag leaf (42.5 cm), which can be linked to photosynthetic capacity impacting yield. Panicle length: IWA 10 shows the longest panicles (37.7 cm), which might contribute to higher grain-bearing potential.

Yield Components

Panicle Weight: The genotypes NER 6 (8.8 g) and LAC 23 (8.4 g) have the heaviest panicles, indicating more biomass allocation to grain. Number of Grains per Panicle: NER 6 and LAC 23 show the highest number of grains per panicle (340.6 and 340.0), which is a positive yield component. Number of Spikelets per Panicle: NER 6 also leads in spikelets (20.3), supporting its superior grain number. Thousand Grain Weight: The highest TGW is 31.1 g (NER 6), indicating grains are heavier, which can improve yield quality.

Grain Characteristics

Grain Length and Grain Width: All genotypes have similar grain length (~ 0.7–0.9 cm) and width (~ 0.2–0.4 cm), with minor variations.

Phenological Traits

Days to Panicle Initiation and Days to Maturity: LAC 23 and NER 6 take longer to initiate panicle and mature (~ 110 to 140 days), which may influence cycle length and adaptability.

Grain Yield

Grain Yield per Hill: The highest grain yield is by NER 2 (60.4 g), followed by IWA 10 (49.0 g) and NER 8 (42.9 g). Despite NER 6's high panicle weight and grain number, its grain yield per hill is moderate (42.1 g). Lower yield genotypes include IR07A (17.6 g), INPARI (19.1 g), and FAD 42 (24.0 g).

3.2 Genotypic differences

Table 4 presents the Analysis of Variance (ANOVA) and Coefficient of Variation (CV) for fourteen quantitative traits of upland rice genotypes evaluated in the Akungba Akoko agro-ecology.

Table 4
Analysis of variance and coefficient of variation for fourteen quantitative traits of upland rice genotypes evaluated in Akungba Agro ecology

SV	DF	PLHT	NOT	ETP	FLL	PANL	PAWT	NGP	NSPK	TGW	GL	GW	NDPI	NDM	GY
Gen	13	775.84**	39.10**	19.3**	55.9**	30.9**	13.0**	10466.7**	31.3**	49.4**	0.01**	0.01**	420.1**	423.4**	43
Error	28	36.9	4.9	3.0	5.7	2.2	0.5	1974.4	2.5	5.7	0.00	0.00	0.6	0.5	87.
CV(%)		5.8	16.4	15.1	7.1	4.5	14.7	17.8	11.7	9.7	0.0	0.00	0.9	0.6	25.
$\bar{G}x$		104.9	13.6	11.4	33.9	32.8	4.9	249.1	13.5	24.5	0.9	0.3	90.8	120.8	36.

SV = source of variation, DF = degree of freedom, PLTHT = plant height, NOT = number of tillers per hill, ETP = effective tillers, FLL = flag leaf length, PANL = panicle length, PANWT = panicle weight, NGP = number of grains per panicle, NSPKP = number of spikelet per panicle, TGW = thousand grain weight, GL = gra length, GWDT = grain width, NDTPI = number of days to panicle initiation, NDTM = number of days to maturity, GYDH = grain yield per hill

All traits show highly significant differences among genotypes, often indicating significance at $p < 0.01$. This means: Plant height, number of tillers, effective tillers, flag leaf length, panicle length, panicle weight, number of grains per panicle, number of spikelets, thousand grain weight, grain length and width, days to panicle initiation, days to maturity, and grain yield per hill all vary significantly among the genotypes. These significant differences suggest considerable genetic variability within the tested genotypes, which is favorable for selection and breeding.

Coefficient of Variation (CV%)

CV% provides a measure of experimental precision and variability relative to the mean. Most traits have CV values below 20%, with some lower than 10%, which suggests good experimental consistency. For example: Plant height CV = 5.8% (high precision), number of tillers CV = 16.4%, and Grain yield CV = 25.8%, which is typical for yield traits due to their inherent variability.

3.2.1 Genotypic Means ($G\bar{x}$)

The Genotypic Mean values show average trait values across the genotypes: Plant height (104.9 cm), number of tillers (13.6), and grain yield (36.3 g) per hill. These means can be compared with individual genotypes in Table 3 to assess which perform above or below average.

3.3 Broad-sense heritability

Table 5 presents key genetic parameters estimated for quantitative traits of upland rice genotypes. These parameters help assess the potential for genetic improvement through selection.

Table 5
Estimates of genetic parameters on quantitative traits of upland rice genotypes.

Characters	Broad sense heritability (%)	Genetic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Genetic advance	Genetic advance as percent of mean
Plant height (cm)	97.0	668.1	688.8	23.31	23.67	52.44	47.29
Number of tillers	97.0	16.7	20.1	30.50	33.46	7.67	57.21
Effective tillers/hill	80.9	9.3	11.5	20.56	29.54	6.19	53.85
Flag leaf length (cm)	85.7	27.2	31.8	15.08	16.29	9.95	28.76
Panicle length (cm)	57.7	6.9	12.0	7.69	10.12	4.12	12.04
Panicle weight (g)	91.4	6.1	6.6	53.52	55.98	4.85	105.4
Number of grains/panicle	79.3	4194	5289	27.78	31.20	118.80	50.97
Number of spikelet/panicle	89.9	12.3	13.7	26.82	28.29	6.86	52.37
Thousand grain weight (g)	77.8	26.2	33.7	19.70	22.34	9.31	35.81
Grain length (cm)	85.7	0.006	0.007	8.61	9.30	0.15	16.41
Grain width (cm)	91.4	0.008	0.009	30.73	32.15	0.18	60.00
Number of days to panicle initiation	99.8	273.8	274.6	18.21	18.23	34.04	37.45
Number of days to maturity	99.7	275.0	275.7	13.72	13.74	34.12	28.22
Grain yield per hill (g)	79.8	256.6	321.5	41.83	46.81	29.48	76.98

Broad-sense heritability values range from moderate to very high, indicating the proportion of total phenotypic variance due to genetic variance.

High heritability (> 80%) observed for traits like plant height (97.0%), number of tillers (97.0%), panicle weight (91.4%), number of spikelets (89.9%), and maturity traits (> 99%) implies that these traits are largely controlled by genetics rather than environment, making them reliable targets for selection. Moderate heritability is seen in panicle length (57.7%), suggesting greater environmental influence on this trait.

Genetic Variance (σ^2g) and Phenotypic Variance (σ^2p)

Genetic variance measures the variability due to genetic factors, while phenotypic variance includes both genetic and environmental factors. Traits such as the number of grains per panicle show large genetic variance (4194) compared to others, signifying ample variability among genotypes. Phenotypic variance is generally slightly higher than genetic variance, reflecting environmental effects.

Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV)

These coefficients show the relative variability of traits. Most traits have moderately high GCV and PCV values, for example, panicle weight (GCV 53.52%, PCV 55.98%) and grain yield (GCV 41.83%, PCV 46.81%), indicating high variability for these traits and good scope for improvement through selection.

The close values of GCV and PCV for many traits (e.g., plant height, days to maturity) suggest low environmental influence, which supports reliable phenotypic selection.

Genetic Advance (GA) and Genetic Advance as Percent of Mean (GAM)

Genetic advance estimates the expected improvement from selection, while GAM contextualizes it relative to the trait mean.

High genetic advance as a percentage of mean (> 50%) is seen in number of tillers (57.21%), effective tillers (53.85%), panicle weight (105.4%), number of grains (50.97%), grain width (60.00%), and grain yield (76.98%), indicating strong potential for improvement through selection.

Traits like panicle length show lower genetic advance (12.04%), highlighting reduced prospects for improvement via selection.

3.4 Trait correlation

Table 6 displays genotypic correlations among various quantitative traits of upland rice genotypes in the Akungba Akoko environment. These correlations help understand how traits are genetically related, which is crucial for selection strategies in breeding.

Table 6
Genotypic correlations among quantitative traits evaluated in Akungba Akoko environment

Traits	NOT	ETP	FLL	PANL	PANWT	NGP	NSPKP	TGW	GL	GWDT	NDTPI	NDTM	GYDH
PLTHT	-0.414	-0.243	0.499*	0.583*	0.680**	0.189	0.034	0.839**	0.058	-0.753**	0.666**	0.666**	0.534*
NOT		0.969**	-0.356	-0.377	-0.485	-0.456	-0.287	-0.487	-0.108	0.485	-0.368	-0.368	-0.086
ETP			-0.442	-0.361	-0.390	-0.467	-0.405	-0.401	-0.229	0.307	-0.152	-0.152	0.143
FLL				0.673**	-0.387	0.491*	0.597*	0.239	0.455	-0.337	0.312	0.312	-0.315
PANL					0.633**	0.603*	0.622*	0.416	0.368	-0.241	0.605*	0.605*	0.017
PANWT						0.660**	0.424	0.616*	0.249	-0.369	0.681**	0.681**	0.537*
NGP							0.887**	-0.019	0.262	0.068	0.451	0.451	0.012
NSPKP								-0.107	0.547*	0.332	0.153	0.153	-0.176
TGW									0.149	-0.660**	0.436	0.436	0.632**
GL										0.448	-0.122	-0.122	-0.180
GWDT											-0.514*	-0.514*	-0.302
NDTPI												0.999**	0.445
NDTM													0.445

Key: *, ** indicate significant and highly significant ($p \leq 0.05, 0.01$), respectively. PLTHT = plant height, NOT = number of tillers per hill, ETP = effective tillers, FLL = flag leaf length, PANL = panicle length, PANWT = panicle weight, NGP = number of grains per panicle, NSPKP = number of spikelet per panicle, TGW = thousand grain weight, GL = grain length, GWDT = grain width, NDTPI = number of days to panicle initiation, NDTM = number of days to maturity, GYDH = grain yield per hill

Positive Significant Correlations

Plant Height positively correlated with flag leaf length (0.499), panicle length (0.583), panicle weight (0.680), thousand-grain weight (0.839), days to panicle initiation (0.666), days to maturity (0.666), and grain yield per hill (0.534). This suggests taller plants tend to have longer leaves, larger/heavier panicles, heavier grains, longer growth periods, and higher yield.

Flag Leaf Length is positively correlated with panicle length (0.673), number of grains per panicle (0.491), number of spikelets per panicle (0.597), and grain yield (0.312, not significant). This indicates that longer leaves are associated with larger panicles and better grain production.

Panicle Length, Panicle Weight, Number of Grains: Strong positive correlations exist among these traits (e.g., PANL with PANWT 0.633, PANL with NGP 0.603, and PANWT with NGP 0.660). This cluster shows that bigger panicles tend to be heavier and have more grains.

Days to Panicle Initiation and Days to Maturity:

Extremely strongly correlated (0.999), reflecting that they measure related mature stages. Both positively associated with plant height and grain yield, suggesting longer crop duration supports taller plants and better yield.

Grain Yield per hill was positively correlated with plant height, panicle weight, days to panicle initiation, and maturity, emphasizing these traits' contributions to yield.

Negative Significant Correlations

Plant Height negatively correlated with number of tillers (-0.414), effective tillers (-0.243), and significantly correlated with grain width (-0.753), suggesting that taller plants tend to have fewer tillers and narrower grain width.

Number of Tillers and Effective Tillers: Both negatively correlated with panicle traits (PANL, PANWT) and grain yield, implying that higher tillering does not necessarily translate into larger panicles or higher yield.

Thousand Grain Weight is negatively correlated with days to panicle initiation (-0.660) and days to maturity, suggesting heavier grains might be associated with shorter crop durations.

Grain width is negatively correlated with days to panicle initiation and maturity (-0.514), suggesting that early maturing genotypes have wider grains.

4.0 Discussion

Genetic variability is central to improving upland rice because effective selection depends on heritable variation in grain yield and its component traits. Studies across diverse upland rice environments have consistently reported significant differences among genotypes in yield and associated agronomic traits, demonstrating substantial exploitable genetic diversity [16]. A study of 43 upland rice genotypes found considerable variation and high heritability for several quantitative traits, supporting the potential for selection and genetic improvement [17]. Similar findings have been reported in Ethiopia, India, Brazil, and Nigeria, although the magnitude of variability varies with genotype composition and environment. Genotypes such as NER 2 combine moderate plant height with good tiller number, panicle traits, and the highest grain yield, making it a strong candidate for upland rice cultivation in this zone. NER 6 stands out for high biomass traits (tillers, grains per panicle, panicle weight) but does not translate into the highest grain yield, possibly due to grain filling or other physiological factors [18]. Genotypes with shorter maturity durations tend to have lower yields. Knowing the local environment and constraints (e.g., growing season length, soil type) helps determine the most suitable genotype. Early maturing types with reasonable yield might be preferred where the season is shorter.

The highly significant genotypic differences confirm that there is substantial variability in the upland rice genotypes tested for all traits. This variability is crucial for breeding programs aiming to improve specific traits such as yield, plant height, tiller number, and maturity period. The relatively low CV% suggests the trial was well managed and the data are reliable. Grain yield, despite being variable, shows good genotypic variation, indicating potential for selecting high-yielding genotypes suited to this agro-ecology. Genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance are commonly used to assess the nature of this variability. Yield per plant often shows relatively high GCV and PCV, indicating substantial variation and appreciable environmental influence [19]. High heritability coupled with high genetic advance for traits such as grain yield, panicle weight, number of grains per panicle, test weight, and tiller number suggests that additive genetic effects contribute importantly to their expression and that direct selection can be effective [18]. Traits with high heritability and high genetic advance (e.g., panicle weight, grain yield, number of grains per panicle, number of tillers) are excellent candidates for direct selection as they are likely controlled by additive genes. Maturity-related traits have very high heritability but moderate genetic advance, suggesting that while they are genetically controlled, the scope for rapid improvement might be more limited. Moderate heritability and lower genetic advance for traits like panicle length suggest environmental factors play a greater role, and selection may be less effective. Traits like plant height, panicle weight, and grain yield are positively correlated, so selecting for one may improve the others. Correlation studies generally show that grain yield is positively associated with key yield components, particularly the number of panicles or productive tillers, panicle weight, grains per panicle, and filled grains, and, in some populations, plant height and harvest index. For example, [17] found significant positive associations between grain yield and plant height, ear-bearing tillers, panicle length, and panicle weight in upland rice. Likewise, studies in Nagaland identified panicle weight as a useful selection criterion because of its positive association with yield. However, correlations are population- and environment-dependent; therefore, a trait showing a strong association in one environment may not necessarily show the same relationship elsewhere [20].

Negative correlations between tiller number and yield components suggest a trade-off: focusing solely on increasing tiller number might reduce panicle size and yield. Grain yield is positively associated with plant height, panicle traits, and longer maturity, suggesting these should be considered in selection for yield [21]. The strong correlations among developmental timing traits (NDTPI and NDTM) confirm their tight genetic link and importance in phenology [18]. Breeders targeting increased yield in upland rice should focus on phenotypes with taller plants, heavier panicles, and longer maturity [22]. Selecting for more tillers alone may not enhance yield because of its negative association with panicle size and grain weight. Understanding these correlations helps design better breeding strategies for simultaneous improvement of multiple traits.

Conclusion

The evaluation of fourteen upland rice genotypes in the Akungba Akoko agro-ecology revealed significant genetic variability across a wide range of important agronomic and yield-related traits. High heritability and genetic advance for key traits such as plant height, number of tillers, panicle weight, number of grains per panicle, and grain yield indicate strong potential for effective selection and genetic improvement. Genotypic correlations suggest that traits such as plant height, panicle weight, and maturity duration are positively associated with grain yield, whereas high tiller numbers may not directly contribute to yield improvement due to negative correlations with panicle size and grain weight. This comprehensive analysis supports the identification of superior genotypes such as NER 2, which combine favorable traits and yield potential suitable for the local environment.

Abbreviations

ANOVA Analysis of variance

CV Coefficient of variation

GA Genetic advance

GAM Genetic advance as percent of mean

GCV Genotypic coefficient of variance

NER Nerica

PCV Phenotypic coefficient of variance

σ^2g Genetic Variance

σ^2p Phenotypic Variance

$G\bar{x}$ Genotypic Means

Declarations

Ethics approval and consent to participate

The plant materials used in this study consisted of rice (*Oryza sativa* L.) genotypes obtained from the International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria.

Consent to publication

Not applicable

Competing interests

The authors declare no competing interests

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Author Contribution

OSO = Conceptualization, Methodology, Data collection and analysis, Writing, review and editing. OSA = Investigation, Data collection, Drafting and editing of the manuscript. DOO = Data analysis and report writing. OAO = Review and editing of the manuscript, FMM = Investigation and visualization, KGO = Data analysis and formatting.

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Data Availability

The data can be obtained from the corresponding author upon reasonable request.

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