# ASSESSMENT OF GENETIC VARIABILITY OF SELECTED UPLAND RICE GENOTYPES GROWN IN A HUMID TROPICAL ENVIRONMENT

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**Abstract**
A field experiment was conducted in the growing season (May to August) of 2020 and 2021 in Calabar, Cross River State to assess the genetic variability of selected upland rice and evaluate the attributes that contribute to high yields. The experiment was laid out in a randomized complete block design replicated two times. The results showed that genotypes varied significantly for most of the traits studied. For tillering capacity, WAB 56-104, IR90, IRAT109, WAB 638-1 and Moroberekan performed better than others. High to medium phenotypic and genotypic coefficients of variation (11 to 48 %), heritability (71 to 91 %) and genetic advance was observed for number of leaves, number of panicles, leaf area, panicle length and total number of grains. These genotypes could be used for further breeding studies. The following traits; number of leaves, number of panicles, number of spikelets per panicle, number of filled grains per panicle and total number of grains could be exploited for further studies because of their high heritability and genetic advance which provides a basis for selection.

**Keywords:** Heritability, Traits, Variance components, and Yield.

## Introduction

The importance of rice (*Oryza sativa* L.) as a staple cereal crop across several continents cannot be overemphasized. Rice is a popular global food crop and a primary source of calories for more than half of the world's population (Mohidem *et al.*, 2022). The world's population is predicted to reach 12.3 billion by the year 2100 (Gerland *et al.* 2014). As a result of the ever-increasing population, making sure that people have access to enough nourishing food to prevent hunger and food insecurity is one of the biggest challenges of the twenty-first century (Cunha *et al*. 2022). To meet the demand for food, production is predicted to rise from 60 to 110 % by 2050 (Tilman *et al.*, 2011). The Food and Agriculture Organization (FAO) estimate for world rice production is forecast to reach 541.51 million tonnes (milled basis) in 2024/25, implying a 3 percent expansion from the 2023/24 (USDA, 2025). In an effort to attain self-sufficiency in rice, for example, the Federal Government of Nigeria channeled credit assistance to the rice sector through the Anchor Borrowers' Programme, with steps also taken to expand rice processing and storage capacity (Muhammad *et al.*, 2024). These interventions were set out by the Agricultural Sector Policy Roadmap (Green Alternative) (Muhammad *et al.*, 2024). This happened because of the hike in rice quotations as a result of a reduction in rice imports. Producers in the country started responding to the incentives provided by the states and the strength of local quotations by expanding plantings.

Upland rice is cultivated on well-drained soil. The yield is usually low compared to paddy rice (Tang *et al.*, 2023). Yield is a polygenic trait controlled by a combination of other traits or factors. To meet with the challenge of producing more rice from the existing land resources for the ever-increasing population, upland rice varieties with high yield potential are required. To achieve this, there is need to know the tillering capacity and identify other traits particularly with high heritability which is a key success to high potential yields. Number of tillers is a crucial phenological phase in rice as it greatly influences yield (Martínez-Eixarch *et al.*, 2015). The growth and development of tillers is a component of factors such as environment, temperature, nutrition and varietal characteristics (Martínez-Eixarch *et al.*, 2015). Other factors which can cause increasing tiller number include heritability and growing conditions. Generally, high-tillering varieties have a higher number of panicles and their contribution to the yield is higher than that of the low-tillering varieties (Martínez-Eixarch *et al.*, 2015). An effective breeding program entails generating genetic variability, identifying promising lines, selecting and using selected genotypes, and its ability to enhance grain yield and other characteristics depends on the type and extent of genetic variability as well as the corresponding heritability (Yadav *et al.*, 2010).

The persistent increase in global population poses a significant risk to global food security. There is limited research on the variability studies of the selected genotypes used for this study and to meet the needs of the ever-growing population, it is important for us to continually explore traits that directly or indirectly contribute to yield. Therefore, high-yielding rice varieties with greater yield stability and adaptability to different ecological zones should be produced to boost the economy and ameliorate food security problems. Therefore, the objective of this study was to estimate variance components, and investigate trait relationships in upland rice grown under humid tropical region. This research will help to improve understanding of genetic variability for increasing upland rice yield in tropical regions by identifying essential agronomic traits and their interrelationships.

## Materials and methods

The field experiment was carried out in the growing season (May to August) of 2020 and 2021 at the University of Calabar teaching and research farm Calabar, Nigeria. Calabar is a humid tropical environment located at latitude 4° 58' N and Longitude 8° 20' E of about 32 m above sea level (a.s.l). A total of fifteen genotypes used for this research were obtained from the AfricaRice center, International Institute of Tropical Agriculture (IITA, Ibadan, Nigeria) (Table 1). The experiment was laid out in a randomized complete block design (RCBD) replicated two times across two years. The experimental site was cleared manually and tilled to a depth of about 30 cm before field layout. The plot size was 1m x 1 m. The plots were separated from each other by a distance of 0.5 m and the distance between replication was 1 m. Four seeds were sown per hill at a spacing of 20 cm x 20 cm and later thinned to two seedlings per hill 14 days after emergence, giving a total plant population of 500,000 plants per hectare. All plots received 200 kg / ha of NPK 15: 15: 15 as basal application. Urea was applied as nitrogen source in two equal splits 50 kg / ha of urea (46% N) at 21 days after sowing (DAS) and another 50 kg / ha of urea at 42 DAS.

Table 1: List of genotypes used for this study with their descriptions

| **Plant Materials-----** | **Characteristics** |
|---|---|
| WAB56-104 -------- | *O. sativa* parent of upland NERICAs |
| IRAT109 ------------ | Early maturing and highly drought tolerant tropical japonica rice |
| PRIMAVERA ------ | High yielding with long grain |
| MOROBEREKAN | Moderately drought tolerant |
| IR90020-22-283-B | Early maturing variety with qDTY12.1 |
| NERICA4 ----------- | Interspecific rice (*O. sativa* x *O. glaberrima*) |
| WAB638-1----------- | *O. sativa* parent of upland NERICAs with aromatic fragrance |
| IR64------------------ | Interspecific rice |
| RCS 2C --------------- | High yielding recurrent selection lines |
| RCS 3A----------------- | High yielding recurrent selection lines |
| RCS 3D----------------- | High yielding recurrent selection lines |
| RCS 273A------------- | High yielding recurrent selection lines |
| RCS 273B------------- | High yielding recurrent selection lines |
| RCS 302B------------- | High yielding recurrent selection lines |
| RCS 302C------------- | High yielding recurrent selection lines |

The plots were kept weed free manually throughout the duration of the experiment. Data were collected from ten (10) plants in each plot on the following attributes: seedling vigour at 15 and 30 DAS; which was assessed by scoring using the scale reported in SES, 2002. Where: 1 (extra vigorous, very fast growing with plants at 5 to 6 leaf stage), 3 (vigorous, fast growing with plants at 4 to 5 leaf stage), 5 (normal with plants at 4 leaf stage), 7 (weak somewhat stunted with plants at 3 to 4 leaf stage) and 9 (very weak, stunted growth and yellowing of leaves). Number of tillers at 42 DAS and at maturity, plant height at 21, 42 DAS and at maturity, leaf area ($cm^2$), leaf area index, number of days to 50 % flowering, number of days to 85 % maturity, panicle number, panicle length, the number of spikelets per panicle, number of filled grains per panicle, total number of grains and grain yield in tons per hectare.

Analysis of variance was done using Genstat (16th ed.; VSN International, 2013). The data on each trait was subjected to analysis of variance, which was used to partition the gross (phenotypic) variability into the components due to genetic (hereditary) and non-genetic (environmental) factors. Variance components (genotypic, phenotypic and error variance) were estimated using the formula of Prasad *et al* (1981), Wricke and Weber (1986) as follows:

VG = [MSG – MSE / r]
VP= [MSG / r]
VE = [MSE / r]

Where MSG, MSE and r are the mean squares of genotypes, mean squares of error and number of replications, respectively. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were evaluated according to the methods of Burton (1953), Kumar *et al* (1985) as follows:

$$GCV = \frac{(\sigma_g^{2})^{0.5}}{\bar{x}} \times 100$$

$$PCV = \frac{(\sigma_p^{2})^{0.5}}{\bar{x}} \times 100$$

Where $\sigma_p^{2}$, $\sigma_g^{2}$ and $\bar{x}$ are the phenotypic variance, genotypic variance and grand mean per season, respectively for the characters under consideration.

Broad sense heritability ($h^2bs$) = $\sigma_g^{2} / \sigma_p^{2}$ was estimated on genotypic mean basis as described by Allard (1999). Genetic advance (GA) expected and GA as percent of the mean assuming selection of the superior 5% of the genotypes were estimated in accordance with the methods illustrated by Fehr (1987) as:

$GA = k (Sp) h^2 B$

GA (as % of the mean) = $(GA / \bar{x}) \times 100$

Where k is a constant (which varies depending upon the selection intensity and, if the latter is 5%, it stands at 2.06), Sp is the phenotypic standard deviation ($\sqrt{\sigma_p^{2}}$), $h^2 B$ is the broad sense heritability and $\bar{x}$ refers to the season mean of the character.

We assessed the distribution of the vigour data using the Shapiro–Wilk tes) and by inspecting residual plots. The results indicated deviation from normality. The vigour data was then transformed by $\log_{10}(x + 1)$ to obtain a normal distribution (Gomez and Gomez, 1984).

## Results and discussion

### Agronomic performance of the upland rice genotypes

The result of the combined analysis showed that genotypes varied significantly for the reproductive traits under consideration. The interaction between genotype and year was not significant for all the traits studied except number of tillers at maturity, number of panicles and panicle length (Table 2). There was no significant difference among genotypes for number of tillers at 42 DAS but Genotypes highly varied at maturity. Genotypes with the highest number of tillers were Moroberekan, IR90, IRAT109 and Nerica 4 (8 to 26). It was also observed that although some of the genotypes had vigorous growth, they matured later than others. The earliest maturing genotypes were IR90, IRAT109, Nerica 4 and WAB56 (102 to 108 days) while Moroberekan matured very late (121 days) followed by IR 64. Genotypes highly varied significantly for the yield attributes. For number of panicles, length of panicles, number of filled grains and number of spikelets per panicle, WAB 56, Moroberekan, IR90, WAB 638-1 and IRAT109 performed better than others. Grain yield ranged from 0.67 to 3.16 tons per hectare. The high yielding genotypes from this study were, WAB56, Moroberekan, IR90, IRAT109 and Nerica 4 (Table 2). Across the years, IRAT109 and IR900020-22-B-4 flowered and matured earlier than others. They flowered between 63 to 73 DAS and matured at 102 DAS.

Table 2: Yield and related attributes of the rice genotypes in 2020 and 2021

| Genotype | T42 | TM | FLW | MT | PN | PL | SPL | FG | TG | YLD |
|---|---|---|---|---|---|---|---|---|---|---|
| Moroberekan | 7.75 | 18.30 | 80.50 | 121.00 | 9.32 | 30.26 | 12.52 | 195.33 | 203.00 | 3.16 |
| IR 90020-22-283-B-4 | 7.26 | 16.40 | 66.50 | 102.00 | 8.70 | 25.20 | 9.40 | 55.25 | 73.90 | 2.23 |
| IRAT 109 | 6.36 | 14.25 | 73.50 | 102.50 | 9.60 | 19.72 | 10.27 | 97.08 | 103.83 | 2.34 |
| Nerica 4 | 6.05 | 14.13 | 73.00 | 102.50 | 6.70 | 25.27 | 11.44 | 125.73 | 140.77 | 2.01 |
| WAB 638-1 | 5.28 | 13.33 | 81.75 | 103.00 | 7.75 | 27.79 | 14.20 | 137.25 | 225.87 | 1.95 |
| IR 64 | 4.80 | 13.13 | 78.50 | 116.00 | 6.80 | 25.67 | 9.88 | 88.75 | 107.00 | 2.00 |
| Primavera | 4.10 | 12.20 | 79.00 | 113.00 | 5.82 | 25.20 | 8.96 | 104.07 | 128.53 | 1.14 |
| WAB 56-104 | 7.50 | 26.20 | 80.00 | 111.50 | 17.41 | 27.74 | 13.05 | 147.33 | 159.40 | 3.20 |
| RCS 2C | 3.88 | 8.20 | 80.00 | 113.00 | 5.35 | 23.86 | 9.10 | 108.08 | 128.30 | 1.38 |
| RCS 3A | 4.85 | 9.10 | 74.50 | 106.00 | 6.67 | 24.61 | 12.32 | 139.31 | 166.85 | 1.33 |
| RCS 3D | 4.25 | 9.23 | 76.50 | 113.00 | 6.77 | 24.79 | 9.65 | 123.10 | 151.91 | 0.92 |
| RCS 273A | 5.40 | 7.25 | 78.50 | 113.00 | 6.82 | 25.67 | 12.34 | 96.50 | 116.10 | 1.38 |
| RCS 273B | 3.15 | 9.58 | 80.50 | 108.50 | 5.75 | 25.90 | 11.85 | 114.12 | 127.71 | 1.32 |
| RCS 302B | 4.50 | 10.68 | 75.50 | 110.00 | 4.97 | 19.75 | 10.15 | 72.55 | 99.22 | 0.67 |
| RCS 302C | 4.55 | 11.65 | 76.50 | 111.00 | 5.56 | 21.29 | 8.80 | 81.75 | 116.75 | 0.89 |
| Grand Mean | 5.31 | 10.77 | 76.82 | 109.50 | 7.70 | 24.85 | 10.93 | 112.41 | 136.61 | 1.73 |
| Genotype (G) | P=0.620 | P=0.026 | P<0.001 | P=0.002 | P<0.001 | P<0.001 | P<0.001 | P<0.001 | P<0.001 | P<0.001 |
| Year (Y) | P=0.073 | P=0.002 | P=0.154 | P=0.527 | P=0.069 | P=0.208 | P=0.753 | P=0.519 | P=0.695 | P=0.519 |
| G x Y | P=0.732 | P=0.016 | P=0.891 | P=0.944 | P<0.001 | P=0.050 | P=1.000 | P=1.000 | P=1.000 | P=1.000 |
| SED | 1.68 | 3.05 | 2.68 | 4.13 | 1 | 1.79 | 1.21 | 22.99 | 25.04 | 0.52 |
| CV (%) | 44.7 | 33.2 | 4.9 | 5.3 | 18.4 | 10.2 | 15.6 | 28.9 | 25.9 | 42.7 |

T42 = Number of tillers at 42 DAS, TM = Number of tillers at maturity, FLW = Number of days to 50 % flowering, MT = Number of days to 85 % maturity, PN = Number of panicles, PL = Panicle length, SPL = Number of spikelets per panicle, FG = Number of filled grains per panicle, TG = Total number of grains, YLD = Grain yield t / ha. SED = standard error of difference, CV = Coefficient of variation.

**Estimation of variance components, heritability and genetic advance**

The result obtained from the pooled analysis showed that genotypes varied significantly across the traits (Table 3). Estimates of variance components showed that phenotypic variance VP
was generally higher than genotypic variance VG for all the traits under consideration in this study (Table 4). Phenotypic variance is a combination of both genotypic and environmental factors. Phenotypic variance ranged from 0.10 for leaf area to 319.6 for total number of grains while genotypic variance ranged from 0.07 to 256.90 (Table 4). Error variance also ranged from 0.03 to 62.7. From the result, it was also observed that phenotypic coefficient of variation, PCV was generally higher that GCV for all the traits studied. PCV ranged from 7.06 to 63.32 while genotypic coefficient of variation, GCV ranged from 5.98 to 55.59 with the days to 85% maturity having the lowest and grain yield having the highest value. Heritability in broad sense ranged from 57.25 to 90.16 % with the lowest value in number of tillers at maturity and the highest value for number of panicles. Genetic advance (GA) ranged from 46.9 to 2960 while GA as percentage of mean ranged from 1042.62 to 19704.60 with number of days to 85 % maturity having the lowest value. Among the traits, number of days to 85 % maturity had the lowest PCV and GCV (Table 4). Heritability value ranged from 57.25 to 90.16 with number of

Table 3: Mean squares, variance ratios and means obtained from pooled analysis of variance for yield and associated traits of the rice genotypes

| | **Mean squares** | | | |
|---|---|---|---|---|
| **Attributes** | **Genotype** | **Error** | **V. ratio** | **Mean** |
| Number of filled grains | 476.10 | 105.80 | 4.50*** | 112.41 |
| Leaf area | 0.19 | 0.056 | 3.27** | 74.47 |
| Leaf area index | 124.48 | 35.26 | 3.53*** | 0.75 |
| Number of days to 85% maturity | 120.34 | 34.11 | 3.53*** | 18.62 |
| Number of leaves at 21 DAS | 15.54 | 1.60 | 9.69*** | 6.25 |
| Number of leaves at maturity | 180.25 | 28.25 | 6.38*** | 19.67 |
| Panicle length | 29.45 | 6.41 | 4.59*** | 24.85 |
| Plant height at 21 DAS | 157.04 | 39.55 | 3.97*** | 38.83 |
| Number of panicles | 20.43 | 2.01 | 10.15*** | 7.70 |
| Spikelets / panicle | 11.60 | 2.90 | 4.00*** | 10.93 |
| Vigour at 30 DAS | 0.35 | 0.13 | 2.75** | 1.21 |
| Number of tillers at maturity | 43.42 | 18.56 | 2.34** | 12.96 |
| Total number of grains | 6392 | 1254 | 5.10*** | 136.61 |
| Grain yield (t/ha) | 2.40 | 0.55 | 4.00*** | 1.73 |

** Significant at P <0.01; *** Significant at P < 0. 001. V ratio =, DAS =

Table 4: Genetic variation from the pooled analysis of yield and associated traits of upland rice

| Attributes | VP | VG | VE | GCV | PCV | $h^2$bs (%) | GA | GA (%MEAN) |
|---|---|---|---|---|---|---|---|---|
| Number of filled grains | 238.05 | 185.15 | 52.90 | 12.10 | 13.73 | 77.78 | 2472.05 | 2199.14 |
| Leaf area | 32.17 | 24.98 | 7.20 | 35.89 | 42.34 | 71.86 | 907.08 | 1180.79 |
| Leaf area index | 62.24 | 44.61 | 17.63 | 35.87 | 42.37 | 71.67 | 46.69 | 6267.66 |
| Number of days to 85% maturity | 60.17 | 43.12 | 17.06 | 5.98 | 7.06 | 71.66 | 1145.00 | 1042.62 |
| Nunmber of leaves at 21 DAS | 7.77 | 6.97 | 0.80 | 42.24 | 44.60 | 89.70 | 515.10 | 8241.56 |
| Number of leaves at maturity | 90.13 | 76.00 | 14.13 | 44.32 | 48.26 | 84.33 | 1649.14 | 8384.05 |
| Panicle length | 14.73 | 11.52 | 3.21 | 13.66 | 15.44 | 78.23 | 618.43 | 2488.66 |
| Plant height at 21 DAS | 78.52 | 58.75 | 19.78 | 19.74 | 22.82 | 74.82 | 1365.68 | 3517.07 |
| Number of panicles | 10.22 | 9.21 | 1.01 | 39.41 | 41.51 | 90.16 | 593.62 | 7709.34 |
| Spikelets / panicle | 5.80 | 4.35 | 1.45 | 19.08 | 22.03 | 75.00 | 372.09 | 3404.26 |
| Vigour at 30 DAS | 0.18 | 0.11 | 0.07 | 27.41 | 34.57 | 62.86 | 54.17 | 4476.67 |
| Number of tillers at maturity | 21.71 | 12.43 | 9.28 | 27.20 | 35.95 | 57.25 | 549.55 | 4240.37 |
| Total number of grains | 319.60 | 256.90 | 62.70 | 11.73 | 13.09 | 80.38 | 2960.25 | 2166.93 |
| Grain yield t/ha | 1.20 | 0.93 | 0.28 | 55.59 | 63.32 | 77.08 | 173.95 | 10054.8 |

VP = Phenotypic variance, VG = Genotypic variance, VE = Error variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, $h^2$bs = Broad sense heritability, GA = Genetic advance.

tillers having the lowest value while number of panicles had the highest heritability value of 90.16 %. Other traits with high heritability include, number of leaves, panicle length, number of filled grains per panicle, number of days to 50 % flowering, leaf area and total number of grains with heritability values ranging from 71 to 89 %. High GCV and GA was recorded for number of panicles.

This study was necessitated due to the growing concern of improving yield through other traits for an important staple cereal crop as rice. In essence, because of the varying climatic conditions across various regions, it becomes imperative to test genotypes and select the best performing ones as well as attributes which contribute to their high yields. By identifying key agronomic traits and their interrelationships, this research provides valuable insights for breeders and agronomists working to enhance upland rice performance under tropical conditions. Fertility level of the soil could also affect plant growth if the required nutrient is not available. For example, WAB 56-104 had the highest number of tillers but was not as vigorous in the early growth stage and also was not as tall as Moroberekan There was an initial slow growth at seedling stage before the nutrients were fully absorbed though the fertilizer application. It was observed that WAB 56-104 and Moroberekan had the highest yield. This was followed by IR90, IRAT109, and Nerica 4. This could have resulted from the high number of tillers, number of panicles longer panicles and high number of spikelets per panicle. This result agrees with the findings of *Islam et al., (*2025) who in their experiment reported that number of tillers could contribute to yield. The phenotypic variance which was generally higher than the genotypic variance in this study indicates that the expression of these characters was subject to the influence of environmental factors. The proportion of the total variation attributable to error variance was lower than the genotypic variance for all the traits. This low error variance shows that the genotypic component was the major contributing factor to the total variance for the traits under consideration. Similar results have also been reported by David *et al.,* 2021. This also suggests the possibility of improving these traits through genotypic selection. GCV provides information on the genetic variability present in various quantitative characters but it cannot be used alone to determine the amount of the variation that was heritable without the heritability estimates. The high heritability estimates and GA obtained for number of leaves, number of tillers, panicle number and total number of grains in both years suggests that these characters are highly heritable and therefore the traits can be easily transferred from parent to offspring hence, selection for these traits is possible. From the results obtained in this study it was observed that environmental factors did not greatly affect phenotypic variation for the traits, rather genetic constitution of the genotypes was responsible for the variations. High values of genetic advance are indicative of additive gene action involved in the expression of various polygenic traits, and low values are of non-additive gene action. The fact that yield is a complex, polygenically inherited characteristic controlled by many genes makes direct selection based on it challenging in breeding programs (Ahktar *et al.,* 2011). As a result, increasing yield involves a number of factors, not just the environment and variety. The results obtained from this study agrees with the findings of Islam *et al.* (2025) in their study on rice reported notable variations in the agro-morphological characteristics that were examined. They recorded high genetic advance and heritability for flag leaf area, filled grain number per panicle, thousand-grain weight and grain yield. Martínez-Eixarch *et al.,* (2015) in their study on japonica rice reported that maximum tiller number was the main explanatory variable which immensely contributed to yield. Likewise, David *et al.*, (2021) in their study on upland rice genotypes also reported variability among upland rice genotypes. GCV provides information on the genetic variability present in various quantitative characters but it is not possible to determine the amount of the variation that was heritable from GCV. Low error variances indicate that the genotypic component is the major contributor to the total variance for characters and can be concluded that most of the variability observed in the phenotype for the different characters has more of a genetic than a non-genetic basis. This result is comparable to the findings of Saito *et al*. (2010), who found that vigour was either moderately or highly heritable in their study of rice grown in lowland and upland environments. This counters previous findings by Zhao *et al.* (2006), who demonstrated the significance of early vigorous growth (at 2-4 weeks after sowing) in their investigation on rice. Low heritability for some of the traits may also be as a result of high error variance.

## Conclusion

From this study, the early vigorous upland rice genotypes at seedling stage were not necessarily the best performing genotypes considering other traits. The best performing genotypes WAB 56-104, IR90, IRAT109, WAB 638-1 and Moroberekan could be used for further studies and tested across other regions. Furthermore, genotypes showed considerable variation for all the traits studied, which is an indication of the presence of sufficient variability that can be exploited through selection. Finally, from this study, the following traits could be used for further studies in an effort to improve the yield of rice; number of panicles, number of spikelets per panicle, number of tillers, number of filled grains per panicle and total number of grains. Therefore, selection based on these traits may contribute to the simultaneous enhancement of yield and related attributes.

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