Moroccan Journal of Agricultural Sciences
Vol 6 No 2 (2025): (June 2025), 73-77
Crop Production and Environment

Trait correlation and heritability analysis in diverse upland rice (Oryza sativa) genotypes

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This study evaluated agronomic traits' performance, correlation, and heritability in ten rice (*Oryza sativa L.*) genotypes grown at the Teaching and Research Farm of Federal University Dutse during the 2024 rainy season. The experiment followed a randomized complete block design with three replications. Analysis of variance revealed significant differences ($p < 0.01$) among genotypes for most traits, indicating substantial genetic variability. FARO 44 exhibited the highest grain yield per hill (145.3 g), followed by FARO 16 (138.6 g) and FARO 52 (140.7 g), while FARO 47 recorded the lowest yield (103.5 g). Days to heading (DTH) and days to flowering (DTF) showed high broad-sense heritability (99.9%), along with floret per panicle (99.6%) and grain yield per hill (98.5%), suggesting strong genetic influence. However, panicle length (59.4%) and fertility percentage (55.5%) had moderate heritability, implying environmental effects. Correlation analysis revealed a strong positive association between DTH and DTF (r = 0.970**) and between plant height and tillers per hill (r = 0.610**). However, plant height negatively correlated with DTH (r = -0.430*) and DTF (r = -0.405*), while grain yield exhibited weak associations with most traits. These findings highlight the potential for selecting high-yielding genotypes based on traits with strong heritability, particularly floret per panicle and grain yield per hill. The results provide useful insights for breeding programs aimed at improving rice productivity under similar agroecological conditions.

Keywords: Upland rice, trait heritability, yield, days to heading, days to flowering, Nigeria

INTRODUCTION

Rice (Oryza sativa L.) serves as a staple food for over half of the global population, making its productivity crucial for global food security (Khush and Brar, 2002). Enhancing rice yields necessitates a comprehensive understanding of the genetic factors influencing agronomic traits. Heritability estimates provide insight into the proportion of phenotypic variation attributable to genetic factors, guiding breeders in selecting traits with the highest potential for improvement (El-Malky et al., 2003). Studies have reported high heritability estimates for traits such as days to maturity and 1000-grain weight, indicating the potential for effective selection in breeding programs (Meitei et al., 2014).

Furthermore, examining trait associations through correlation and path coefficient analyses elucidates the relationships between yield and its components, informing selection strategies (Rahman et al., 2011). For instance, research has demonstrated significant correlations between grain yield and traits like plant height and panicle length, highlighting their importance in yield improvement efforts (Hossain et al., 2015). Additionally, studies have shown that traits such as the number of filled grains per panicle and panicle weight exhibit strong positive correlations with grain yield, emphasizing their significance in selection criteria (Jain et al., 2004). Path coefficient analysis further reveals that biological yield and harvest index have strong direct positive effects on grain yield, suggesting their potential as selection targets in breeding programs (Rathod and Mishra, 2017).

The integration of molecular tools, such as genome-wide association studies (GWAS), has enhanced our understanding of the genetic architecture of complex traits in rice (Waluyo and Kurniawan, 2022). GWAS enables the identification of genetic variants associated with important agronomic traits, facilitating marker-assisted selection and accelerating the development of high-yielding, resilient rice varieties (Babar et al., 2007).

This study aims to estimate the heritability of key agronomic traits and analyze their associations in various rice genotypes, providing valuable information for the development of high-yielding rice varieties. By integrating phenotypic evaluations with molecular insights, the research seeks to provide a comprehensive understanding of the genetic factors influencing rice yield and its components, thereby informing breeding strategies for improved rice varieties.

MATERIAL AND METHOD

A field experiment was conducted during the 2023 cropping season at the Teaching and Research Farm, Federal University Dutse, Jigawa, Nigeria, to assess the heritability and trait associations among ten upland rice (Oryza sativa L.) genotypes. The experiment was laid out in a randomized complete block design (RCBD) with three replications to ensure reliable statistical analysis.

The seeds were directly sown at a spacing of 20 cm between rows and hills in plots comprising 12 rows, covering an area of 6 m^2. Fertilization followed a split-application method, where 200 kg/ha of NPK (15:15:15) was applied as a basal dose before transplanting. Additionally, urea was top-dressed in two stages: 65 kg/ha at the tillering stage and 35 kg/ha at the booting stage to enhance plant growth and grain development.

Water management was maintained with an approximate standing water depth of 5 cm, which was drained before harvest. Weed control was achieved through a combination of pre-emergence herbicide application and manual hand weeding at critical growth stages to minimize competition and optimize yield potential.

Days to Heading (DTH) and Days to Flowering (DTF)

Days to heading (DTH) was recorded as the number of days from sowing until 50% of the plants in a plot exhibited panicle emergence. Similarly, days to flowering (DTF) was determined by counting the number of days from sowing until 50% of the panicles displayed at least one fully opened floret. Observations were made daily, and the dates were recorded accordingly (Vergara et al., 1976).

Plant Height (PH)

Plant height was measured at physiological maturity from the base of the plant to the tip of the tallest panicle (excluding awns). A meter scale was used to record the height of five randomly selected plants per plot, and the average value was taken as the final measurement (Gomez, 1972).

Tillers per Hill (TPH)

The total number of productive tillers per hill was counted manually. Five hills were randomly selected per plot, and the number of tillers per hill was recorded at the reproductive stage. The mean number of tillers per hill was calculated (Yoshida et al., 1976).

Panicle Length (PL)

Panicle length was measured from the base of the panicle to the tip, excluding awns. Five randomly selected panicles per genotype were measured using a meter scale, and the average was taken as the representative value (IRRI, 2002).

Number of Florets per Panicle (FPP)

The total number of spikelets per panicle was counted manually from five randomly selected panicles per genotype. The average number of florets per panicle was calculated and recorded (Yoshida, 1981).

Fertility Percentage (FPCT%)

Fertility percentage was determined by counting the number of filled and unfilled spikelets from five randomly selected panicles per genotype. The fertility percentage was calculated using the following formula (IRRI, 2013):

where FFF represents the number of filled grains, and UUU represents the number of unfilled grains.

Grain Yield per Hill (GYPH)

Grain yield per hill was measured by harvesting and weighing grains from randomly selected hills. The grains were dried to a standard moisture content of 14% before weighing. The final yield per hill was computed as follows (Peng et al., 1996):

Variance and Heritability Estimation

To assess the genetic parameters of the rice genotypes, genotypic variance, phenotypic variance, and broad-sense heritability were estimated following standard statistical procedures.

Genotypic and Phenotypic Variance

Genotypic variance (σg2\sigma_g^2σg2) and phenotypic variance (σp2\sigma_p^2σp2) were estimated using the method described by Falconer and Mackay (1996). The variance components were calculated using the mean square values obtained from the analysis of variance (ANOVA) as follows:

where:

MSG = mean square of genotypes

MSE = mean square of error

r = number of replications

σe2 = environmental variance (equal to the error mean square)

Broad-Sense Heritability (H2)

Broad-sense heritability (H2) was estimated to determine the proportion of total phenotypic variation attributed to genetic factors. It was computed as:

H2 = broad-sense heritability (%),

σg2 = genotypic variance,

σp2 = phenotypic variance.

Heritability estimates were classified according to Robinson et al. (1949).

Statistical Analysis

The statistical analyses were performed using Statistix 8.1 software, which was used to conduct analysis of variance (ANOVA) and least significant difference (LSD) tests to compare mean values. Correlation coefficients were calculated following the method outlined by Snedecor and Cochran (1980), while broad-sense heritability was estimated based on the approach suggested by Falconer (1989).

RESULTS AND DISCUSSION

Analysis of variance ANOVA

The ANOVA results indicated that all the genotypes exhibited significant differences at both the 5% ($p<0.05$) and 1% ($p<0.01$) probability levels. However, fertility percentage was not significantly affected. This suggests that while most traits varied significantly among the genotypes, fertility percentage remained consistent. Our findings (Table 1) align with those of Poudel et al. (2014), Gyawali et al. (2018), and Bhangar et al. (2024).

Performance from Various traits of rice genotype

The performance evaluation of various rice genotypes revealed significant differences across multiple traits. Days to heading (DTH) and days to flowering (DTF) varied significantly among genotypes, with genotype 3 exhibiting the longest durations (114.8 and 119.3 days, respectively) and genotype 8 the shortest (104.5 and 102.6 days, respectively). Plant height (PH) also differed, with genotype 7 being the tallest (110.2 cm) and genotype 6 the shortest (94.5 cm).

Total productive tillers per hill (TPH) and panicle length (PL) showed significant variation. Genotype 3 had the highest TPH (40.2), whereas genotype 6 had the lowest (25.0). Similarly, genotype 3 recorded the longest panicle length (30.5 cm), while genotype 7 had the shortest (26.5 cm). Filled panicles per plant (FPP) and the percentage of filled panicles to the total count (FPTC%) also varied, with genotype 8 having the highest FPP (230.0) and genotype 6 the lowest (170.2). Fertility percentage remained largely consistent across genotypes.

Grain yield per hill (GYPH) was significantly influenced by genotype, with genotype 1 achieving the highest yield (145.3 g), followed by genotype 2 (138.6 g), whereas genotype 6 recorded the lowest (103.5 g). These findings align with the work of Singh et al. (2013) and Akinwale et al. (2011), who reported significant genotype-dependent variations in yield-related traits among rice cultivars. Conversely, Rahman et al. (2017) observed minimal variation in some agronomic traits across specific genotypes, differing slightly from our findings (Table 2).

Correlation Coefficient

The correlation analysis among various rice genotypic traits revealed significant relationships between several key parameters. Days to flowering (DTF) exhibited a strong positive correlation with days to heading (DTH) ($r = 0.970$, $p<0.01$), indicating that genotypes with delayed heading also had extended flowering periods. However, plant height (PH) showed a significant negative correlation with both DTF ($r = -0.430$, $p<0.05$) and DTH ($r = -0.405$, $p<0.05$), suggesting that early flowering genotypes tend to be taller.

Total productive tillers per hill (TPH) showed a positive correlation with DTF ($r = 0.540$, $p<0.01$)

and PH (r = 0.610, $p<0.01$), implying that genotypes with more tillers tended to be taller and flowered later. Panicle length (PL), on the other hand, had a significant negative correlation with both DTF (r = -0.590, $p<0.01$) and PH (r = -0.580, $p<0.01$), while maintaining a positive association with TPH (r = 0.500, $p<0.01$).

Filled panicles per plant (FPP) showed a weak negative correlation with both DTF (r = -0.390, $p<0.05$) and PH (r= -0.470, $p<0.01$), while a weak positive correlation was found with TPH (r = 0.350, $p<0.05$). Fertility percentage (FPCNT) did not show significant correlations with most traits, indicating its relative independence from other agronomic parameters.

Grain yield per hill (GYPH) exhibited a weak positive correlation with DTF (r = 0.350, $p<0.05$) and PH (r = 0.440, $p<0.05$) but a negative correlation with FPP (r = -0.410, $p<0.05$), suggesting that while taller and late-flowering genotypes had higher yield potential, increased filled panicle numbers did not necessarily translate to higher grain yield.

These findings align with those of Prasad et al. (2017) and Kumar et al. (2019), who reported strong correlations between flowering time, plant height, and grain yield in rice genotypes (Table 3). However, contrary to our results, Patel et al. (2020) found a stronger positive correlation between panicle traits and yield components, indicating potential genotype-specific differences in trait interactions.

Genetic Variability

The genetic variability analysis for various rice traits revealed high heritability estimates across most characteristics, indicating a strong genetic influence on their expression. Days to heading (DTH) and days to flowering (DTF) exhibited exceptionally high heritability (99.9%), suggesting that these traits are predominantly governed by genetic factors with minimal environmental influence. Similarly, floret per panicle (99.6%) and grain yield per hill (98.5%) showed high heritability, emphasizing their potential for effective selection in breeding programs.

Plant height (PH) and tillers per hill (TPH) displayed relatively high heritability values of 92.8% and 94.1%, respectively, indicating that genetic factors largely control these traits but may still be slightly influenced by the environment. Panicle length (PL) and fertility percentage (FPCNT) had moderate heritability values of 59.4% and 55.5%, respectively, implying that environmental conditions play a more substantial role in their variation compared to other traits.

These findings align with the work of Johnson et al. (2019) and Singh et al. (2020), who also reported high heritability for flowering time, plant height, and yield-related traits in rice genotypes, making them suitable for genetic improvement. However, contrary to our results, Sharma et al. (2021) found lower heritability for grain yield, suggesting possible differences in environmental conditions or genetic backgrounds of the studied populations (Table 4).

CONCLUSION

This study assessed the genetic variability, correlation, and heritability of key agronomic traits in ten rice (Oryza sativa L.) genotypes under field conditions at Federal University Dutse during the 2024 rainy season. The findings revealed significant genetic differences among the genotypes, suggesting a strong potential for selection and improvement. The high heritability observed for grain yield per hill (98.5%), floret per panicle (99.6%), and days to heading (99.9%) indicates that these traits are largely controlled by genetic factors, making them ideal candidates for selection in breeding programs. However, moderate heritability in panicle length (59.4%) and fertility percentage (55.5%) suggests environmental influences, necessitating further studies on genotype-environment interactions. Correlation analysis showed that days to heading and days to flowering were highly associated (r = 0.970**), implying that early flowering genotypes can be selected to optimize maturity duration. The positive correlation between plant height and tillers per hill (r = 0.610**) suggests that selecting taller genotypes may enhance tillering capacity. However, the negative association of plant height with days to heading (r = -0.430*) and days to flowering (r = -0.405*) indicates that taller genotypes tend to mature earlier. Overall, the study provides valuable insights into the genetic potential of rice genotypes for yield improvement. Future breeding efforts should focus on selecting genotypes with high yield potential, early maturity, and favourable agronomic traits to enhance rice productivity in similar agroecological conditions.

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