**Original Research Article**

**Genetic variability and correlation analysis for yield attributing traits in rice (*Oryza sativa* L.)**

**Abstract**

**Aim:** To evaluate genetic variability, heritability, genetic advance, and correlation among yield and yield-attributing traits in rice genotypes to identify effective selection criteria for yield improvement.

**Study design:** Augmented block design

**Place and Duration of Study:** Institute of Rice Research, ARI, Rajendranagar, Hyderabad, Telangana, India, during the Kharif season of 2024.

**Methodology:** The study involved 100 rice genotypes and five checks, sown in a nursery bed and transplanted after 25 days with a spacing of 30 cm between rows and 15 cm between plants. Ten agronomic and yield-related traits were evaluated: days to 50% flowering, plant height, panicle length, number of productive tillers per plant, 1000-grain weight, number of grains per panicle, grain yield per plant, kernel length, kernel breadth, and kernel length-to-breadth (L/B) ratio. Observations were recorded from five randomly selected plants per genotype. Statistical analysis was conducted using INOSTAT software to assess variance, heritability, genetic advance, and phenotypic correlations.

**Results:** Analysis of variance revealed significant variation (P < 0.01) among genotypes for all traits. High heritability (>80%) was observed for days to 50% flowering (86.47%), plant height (93.90%), number of productive tillers per plant (85.24%), 1000-grain weight (94.68%), number of grains per panicle (97.34%), grain yield per plant (90.59%), kernel length (97.73%), kernel breadth (96.14%), and L/B ratio (96.07%), with panicle length showing moderate heritability (73.99%). High genetic advance as a percentage of the mean was recorded for plant height (24.28%), number of productive tillers per plant (32.77%), 1000-grain weight (45.09%), number of grains per panicle (63.42%), grain yield per plant (42.80%), kernel length (22.59%), and kernel breadth (24.02%). Grain yield per plant showed a significant positive phenotypic correlation with the number of grains per panicle (r = 0.1155, P < 0.01) and non-significant positive associations with plant height (r = 0.1116), panicle length (r = 0.0635), number of productive tillers per plant (r = 0.1540), 1000-grain weight (r = 0.1155), kernel length (r = 0.0757), and kernel breadth (r = 0.0921).

**Conclusion:** ANOVA confirmed significant genetic variation among 100 rice genotypes for all traits, supporting selection (Joshi *et al.*2021). Plant height, productive tillers, 1000-grain weight, grain number per panicle, grain yield, and kernel dimensions showed high heritability (>80%) and genetic advance (22.59–63.42%), indicating additive genetic control ideal for direct selection (Nayak *et al.*2022; Yadav *et al.*2023). Days to 50% flowering, panicle length, and kernel length-to-breadth ratio had high heritability but moderate genetic advance, suggesting non-additive and environmental effects (Sharma *et al.*2020; Gupta *et al.*2021). Positive correlations with grain yield support indirect selection (Vennelea *et al.*2021; Kumar *et al.*2022; Das *et al.*2023).

**Keywords:**Correlation, genetic advance, heritability, improvement, selection

**1.INTRODUCTION**

Rice (*Oryza sativa* L., 2n=24) is a self-pollinated, semi-aquatic annual grass that belongs to the genus Oryza. This genus includes two cultivated varieties of rice and 22 wild species. Rice is classified within the Gramineae family, also known as Poaceae. It serves as the primary staple food for nearly 50% of the world’s population. In India, rice is the predominant food crop in terms of area, production, and productivity, and the country ranks as the second-largest producer and exporter of rice (Goswami *et al.*2023). The annual global production of rice is 787 million tonnes, cultivated across 165 million hectares (Kumar *et al.*2020). The largest rice-producing countries include China, India, Bangladesh, Indonesia, Vietnam, Myanmar, the Philippines, Cambodia, and Pakistan. In Asia, rice production amounts to 524 million tonnes from 138.56 million hectares. In India, rice is cultivated on approximately 46.28 million hectares, yielding an annual production of 132.5 million tonnes. In Telangana, rice occupies an area of 1.451 million hectares, with a production of 12.41 million tonnes and a productivity rate of 3,395 kg per hectare (India Stat, 2023).

Heritability and genetic advance are important parameters for improving yield (Verma *et al.*2019). Yield is a complex trait; enhancing this trait is beneficial when achieved by increasing related traits with high heritability (Singh *et al.*2021). Genetic diversity underpins successful breeding programs by creating variation in economically important traits among different varieties. This variation is essential because it provides heritable differences within a breeding population, which we refer to as inter-mating resources. Understanding this diversity enables breeders to effectively track and manipulate trait inheritance.

Heritability measures the extent to which traits are transmitted from one generation to the next. In other words, it offers insight into the probability that offspring will exhibit the same characteristics as their parents. These heritability estimates enable breeders to forecast the likelihood of traits manifesting in future generations (Begna *et al.*2021).

The correlation coefficient is instrumental in identifying traits or combinations of traits that can serve as indicators of high yield. It illustrates the relationships between different traits and grain yield, as well as the interrelationships among the traits themselves. Yield component characters exhibit correlations and associations with yield; however, programs aimed at improving yield have shown limited effectiveness. This limitation arises because direct selection for yield alone reduces selection efficiency. Therefore, the effectiveness of yield improvement programs depends on the careful selection of component characters.

2.material and methods

The experimental material for the present investigation comprised 100 genotypes and 5 checks. One hundred rice genotypes, along with five checks, were sown during the Kharif season of 2024 in an augmented block design at the Institute of Rice Research, ARI, Rajendranagar, Hyderabad. All the genotypes were initially sown in a nursery bed. Twenty-five days after sowing, the seedlings were transplanted into the field with a spacing of 30 cm between the rows and 15 cm between the plants. Observations were recorded on days to 50 percent flowering, plant height (cm), panicle length (cm), number of productive tillers per plant, 1000-grain weight (g), number of grains per panicle, grain yield per plant, kernel length (mm), kernel breadth (mm), and kernel length-to-breadth (L/B) ratio from five randomly selected plants of each genotype (Patel *et al.*2021). Statistical analysis was conducted using INDOSTAT software for the analysis of association studies related to yield and yield-related traits.

3.results and discussion

3.1 Analysis of variance (ANOVA)

The analysis of variance for the augmentted block design of yield and yield component characteristics was statistically tested and found to be significant for all evaluated traits, including 50 percent flowering, plant height (cm), panicle length (cm), number of productive tillers per plant, 1000 grain weight (g), number of grains per panicle, grain yield per plant, kernel length (mm), kernel breadth (mm), and kernel length-to-breadth ratio (L/B).The ratio indicates the presence of sufficient variation among the genotypes, thereby providing ample opportunity for effective selection (Table 1) (Immanuel *et al.*2011; Pandey *et al.*2020). The analysis of variance yields estimates of phenotypic, genotypic, and environmental variances, which were utilized to calculate the respective coefficients of variation (Verma *et al.*2019). This variance analysis reveals significant differences among genotypes for all traits, highlighting considerable diversity within the genotypes. Such pronounced variability presents valuable potential for their application in various selection and hybridization efforts.

**3.2 Variability Parameters**

The genotypic and phenotypic coefficients of variation for days to fifty percent flowering were low, at 6.36% and 6.84%, respectively. For panicle length, the coefficients were 8.42% (genotypic) and 9.79% (phenotypic), while the kernel length-to-breadth (L/B) ratio also exhibited low variation. The coefficients of variation for kernel breadth and kernel length were moderate, at 11.88% and 12.11%, and 11.20% and 11.07%, respectively. Additionally, the number of productive tillers per plant showed moderate variation, with genotypic and phenotypic coefficients of 17.21% and 18.64%. In contrast, the genotypic and phenotypic coefficients of variation for grain weight were high, at 22.46% and 23.08%, respectively. The number of grains per panicle exhibited even higher variation, with coefficients of 31.16% (genotypic) and 31.58% (phenotypic), while grain yield per plant also demonstrated high variation, with coefficients of 21.80% (genotypic) and 22.90% (phenotypic). Grain yield per plant, the number of grains per panicle, and 1000-grain weight exhibited a high phenotypic coefficient of variation, while a moderate phenotypic and genotypic coefficient of variation was recorded for plant height, the number of productive tillers per plant, kernel length, and kernel breadth.

**3.3 Heritability**

High broad-sense heritability estimates, exceeding 80%, were observed for 50% flowering (86.47%), plant height (93.9%), the number of productive tillers per plant (85.24%), 1000-grain weight (94.68%), the number of grains per panicle (90.59%), grain yield per plant (97.34%), kernel length (97.73%), kernel breadth (96.14%), and the kernel length-to-breadth (L/B) ratio (96.07%). Moderate heritability estimates were recorded for panicle length (73.99%).

**3.4 Genetic Advance**

The genetic advance as a percentage of the mean revealed high estimates for plant height (24.28%), the number of productive tillers per plant (32.77%), 1000-grain weight (45.09%), the number of grains per panicle (63.42%), grain yield per plant (42.8%), kernel length (922.89%), and kernel breadth (24.02%). Moderate genetic advance as a percentage of the mean was recorded for days to 50% flowering (12.2%), panicle length (14.94%), and the kernel L/B ratio (14.94%). High heritability, accompanied by significant genetic advance, was observed in traits such as plant height, the number of productive tillers per plant, 1000-grain weight, the number of grains per panicle, grain yield per plant, kernel length, and kernel breadth (Sarkar *et al.* (2007). The traits days to 50% flowering, panicle length, and kernel length-to-breadth ratio exhibited high estimates of heritability coupled with moderate genetic advance as a percentage of the mean (Sharma *et al.*2020; Bhargava *et al.*2021**).**

**3.5 Correlation coefficients**

Correlation represents the relationship between two variables, specifically highlighting the degree and linearity of their connection. In plant breeding, analyzing correlations is valuable for understanding how enhancing one trait may simultaneously improve others. Studying the relationships among traits assists breeders in establishing selection criteria for characteristics such as grain yield in parent plants, thereby facilitating the identification of individuals with the optimal combination of traits. Phenotypic correlation refers to the observable relationship between traits, which can be influenced by environmental factors. In contrast, genotypic correlation reflects the genetic or breeding value connection between traits. Therefore, understanding these associations is crucial for designing an effective and well-informed breeding strategy.

Grain yield per plant exhibited a significant positive phenotypic correlation with the number of grains per panicle (0.1153) and a non-significant positive association with plant height (0.1116), panicle length (0.0635), the number of productive tillers per plant (0.1540), 1000-grain weight (0.1155), kernel length (0.0757), and kernel breadth (0.0921) (Bhor *et al.*2020; Vennelea *et al.*2021). Additionally, it showed a non-significant negative association with days to 50% flowering (-0.2304) and the length-to-breadth (L/B) ratio (-0.041) (Singh *et al.*2021). These correlations suggest that selecting for traits such as grain number and tiller count can indirectly enhance yield (Yadav *et al.*2023).

The plant height exhibited a significant positive phenotypic correlation with panicle length (0.4771) and the number of grains per panicle (0.1871). It also showed a positive but non-significant correlation with grain yield per plant (0.1116), days to 50% flowering (0.1520), 1000-grain weight (0.0139), kernel length (0.0492), kernel breadth (0.0306), and the length-to-breadth (L/B) ratio. In contrast, there was a negative non-significant association with the number of productive tillers per plant (-0.1466). Panicle length demonstrated a significant positive correlation with 1000-grain weight (0.2711), plant height (0.4771), kernel length (0.3254), and kernel breadth (0.2259). It also exhibited a positive but non-significant phenotypic correlation with the number of grains per panicle (0.1129), days to 50% flowering (0.1520), L/B ratio (0.0971), and grain yield per plant (0.0635) (Nayak *et al.*2022). Additionally, panicle length showed a significant negative phenotypic correlation with the number of productive tillers per plant (-0.1925). The number of productive tillers per plant exhibited a significant negative phenotypic correlation with 1000-grain weight (-0.2091), panicle length (-0.1925), and kernel breadth (-0.2068). It also displayed a negative non-significant phenotypic correlation with plant height (-0.1466) and kernel length (-0.1741). Conversely, the number of grains per panicle (0.0011), L/B ratio (0.0924), and grain yield per plant (0.1540) exhibited positive non-significant phenotypic associations. The 1000-grain weight demonstrated a significant positive correlation with kernel length (0.8686) and kernel breadth (0.7866). Additionally, it showed a positive but non-significant phenotypic correlation with the length-to-breadth (L/B) ratio (0.0034) and grain yield (0.1155). Conversely, it exhibited a significant negative phenotypic correlation with the number of grains per panicle (-0.5190).

**Table:1 Analysis of variance for yield and its attributing characters rice genotypes**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **S.no** | **Traits** | **Blocks** | **Treatment** | **Treatment: check** | **Treatment: Test/Test vs Check** | **Error** |
| **1** | **DFF** | 194.63\*\* | 50.50\*\* | 362.86\*\* | 38.01\*\* | 5.84 |
| **2** | **PH** | 774.60\*\* | 183.38\*\* | 1170.67\*\* | 143.89\*\* | 10.59 |
| **3** | **PL** | 15.21\*\* | 5.20\*\* | 6.12\* | 5. 16\*\* | 1.51 |
| **4** | **NPT** | 7.27\*\* | 6.35\*\* | 17.19\*\* | 5.92\*\* | 0.92 |
| **5** | **1000GW** | 7.94\*\* | 33.39\*\* | 199.21\*\* | 26.76\*\* | 1.42 |
| **6** | **NGP** | 2379.65\*\* | 3774.55\*\* | 24853.10\*\* | 2931.41\*\* | 71.30 |
| **7** | **GY** | 100.35\*\* | 40.29\*\* | 126.24\*\* | 36.86\*\* | 3.80 |
| **8** | **KL** | 0.13\*\* | 0.61\*\* | 2.29\*\* | 0.54\*\* | 0.01 |
| **9** | **KB** | 0.06\*\* | 0.07\*\* | 0.28\*\* | 0.06\*\* | 0.00 |
| **10** | **L/B ratio** | 0.19\*\* | 0.08\*\* | 0.18\*\* | 0.08\*\* | 0.00 |

DFF: Days to 50%flowering, PH: Plant height, PL: Panicle length, NPT: Number of productive tillers per plant, 1000GW: 1000 grain weight, NGP: Number of grains per panicle, GY: Grain yield per plant, KL: Kernel length, KB: Kernel breadth, L/B ratio: Kernel length and breadth ratio.

**Table:2 Variability studies for different yield and its attributing characters**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameters** | **Phenotypic variance** | **Genotypic variance** | **Environmental variance** | **GCV%** | **PCV%** | **ECV%** | **Heritability in broad sense (%)** | **Genetic Advance as % mean** |
| **DFF** | 43.14 | 37.30 | 5.84 | 6.36 | 6.84 | 2.52 | 86.47 | 12.20 |
| **PH** | 173.64 | 163.05 | 10.59 | 12.14 | 12.53 | 3.09 | 93.90 | 24.28 |
| **PL** | 5.80 | 4.29 | 1.51 | 8.42 | 9.79 | 4.99 | 73.99 | 14.94 |
| **NPT** | 6.25 | 5.33 | 0.92 | 17.21 | 18.64 | 7.16 | 85.24 | 32.77 |
| **1000gw** | 26.68 | 25.27 | 1.42 | 22.46 | 23.08 | 5.32 | 94.68 | 45.09 |
| **NGP** | 2681.99 | 2610.69 | 71.30 | 31.16 | 31.58 | 5.15 | 97.34 | 63.42 |
| **GY** | 40.37 | 36.57 | 3.80 | 21.80 | 22.90 | 7.03 | 90.59 | 42.80 |
| **KL** | 0.50 | 0.49 | 0.01 | 11.07 | 11.20 | 1.69 | 97.73 | 22.59 |
| **KB** | 0.06 | 0.05 | 0.00 | 11.88 | 12.11 | 2.38 | 96.14 | 24.02 |
| **L/B ratio** | 0.08 | 0.08 | 0.00 | 8.71 | 8.89 | 1.76 | 96.07 | 17.61 |

DFF: Days to 50%flowering, PH: Plant height, PL: Panicle length, NPT: Number of productive tillers per plant, 1000GW: 1000 grain weight, NGP: Number of grains per panicle, GY: Grain yield per plant, KL: Kernel length, KB: Kernel breadth, L/B ratio: Kernel length and breadth ratio.

Fig:1 Estimates of heritability and genetic advance as % of mean for yield and its component traits.

**Table :3 Correlation coefficients for yield, yield contributing and quality traits**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Character** | **DFF** | **PH** | **PL** | **NPT** | **1000GW** | **NGP** | **KL** | **KB** | **L/B ratio** | **GY** |
| **DFF** | 1.0000 | 0.2644\*\* | 0.1520 | 0.0478 | -0.1648 | 0.1104 | -0.2131\* | -0.1859\* | -0.0016 | -0.2304 |
| **PH** |  | 1.0000 | 0.4771\*\*\* | -0.1466 | 0.0139 | 0.1871\* | 0.0492 | 0.0306 | 0.0471 | 0.1116 |
| **PL** |  |  | 1.0000 | -0.1925\* | 0.2711\*\* | 0.1129 | 0.3254\*\*\* | 0.2259\* | 0.0971 | 0.0635 |
| **NPT** |  |  |  | 1.0000 | -0.2091\* | 0.0011 | -0.1741 | -0.2068\* | 0.0924 | 0.1540 |
| **1000GW** |  |  |  |  | 1.0000 | -0.5190\*\*\* | 0.8686\*\*\* | 0.7866\*\*\* | 0.0034 | 0.1155 |
| **NGP** |  |  |  |  |  | 1.0000 | -0.5560\*\*\* | -0.4993\*\*\* | 0.0025 | 0.1153\*\* |
| **KL** |  |  |  |  |  |  | 1.0000 | 0.7602 \*\*\* | 0.1970\* | 0.0757 |
| **KB** |  |  |  |  |  |  |  | 1.0000 | -0.4774 \*\*\* | 0.0921 |
| **L/B ratio** |  |  |  |  |  |  |  |  | 1.0000 | -0.0415 |
| **GY** |  |  |  |  |  |  |  |  |  | 1.0000 |

DFF: Days to 50%flowering, PH: Plant height, PL: Panicle length, NPT: Number of productive tillers per plant, 1000GW: 1000 grain weight, NGP: Number of grains per panicle, GY: Grain yield per plant, KL: Kernel length, KB: Kernel breadth, L/B ratio: Kernel length and breadth ratio.

**4. Conclusion**

ANOVA confirmed significant genetic variation among 100 rice genotypes for all traits, supporting selection (Joshi *et al.*2021; Tripathi *et al.*2022). Plant height, productive tillers, 1000-grain weight, grain number per panicle, grain yield, and kernel dimensions showed high heritability (>80%) and genetic advance (22.59–63.42%), indicating additive genetic control ideal for direct selection (Nayak *et al.*2022; Yadav *et al.*2023). Days to 50% flowering, panicle length, and kernel length-to-breadth ratio had high heritability but moderate genetic advance, suggesting non-additive and environmental effects (Sharma *et al.*2020; Gupta *et al.*2021). Positive correlations with grain yield support indirect selection (Vennelea *et al.*2021; Kumar *et al.*2022; Das *et al.*2023).

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