***Original Research Article***

**ASSESSMENT OF VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN RICE (*Oryza sativa* L.)**

**ABSTRACT**

Variation in genetic composition within a population is often referred to as genetic variability, which serves as the basis for developing breeding techniques aimed at further crop improvement. Estimates of genetic advance, heritability, and coefficients of variability were calculated for 14 yield-contributing traits during the kharif seasons of 2022 and 2023. These genetic parameters were evaluated across twenty-one paddy varieties. For all traits, the phenotypic coefficients of variation (PCV) were consistently higher than the corresponding genotypic coefficients of variation (GCV), indicating environmental influence on trait expression. Moderate to high genetic advance as a percentage of mean was recorded for all traits studied, which included: leaf blade length (cm), leaf blade width (cm), time of heading, stem length (cm), panicle length (cm), number of panicles per plant, days to maturity, 1000-grain weight (g), grain length (mm), grain width (mm), decorticated grain length (mm), decorticated grain width (mm), amylose content in the endosperm, and awn length. Overall, the study revealed low to moderate genetic variability coupled with moderate to high genetic advance as a percent of mean for all traits, suggesting the potential for genetic improvement through selection.

***Keywords:*** *Variability, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance*

**INTRODUCTION**

Rice (*Oryza sativa* L.) is the most widely consumed cereal and serves as a staple food for nearly two-thirds of the world's population. More than 50% of the global population relies on rice as a part of their daily diet, contributing approximately 20% of the world's caloric intake, according to the Food and Agriculture Organization of the United Nations (FAO). By 2050, the demand for cereals-for both human consumption and animal feed is projected to rise from the current level of approximately 2.1 billion tonnes to about 3 billion tonnes. To meet the food requirements of a global population estimated to reach 9.1 billion by 2050, it will be necessary to increase total food production by nearly 70% compared to the levels of 2005-07.

 Growing high-yielding rice varieties with superior quantitative traits adapted to various ecosystems is crucial to meeting the rising global demand for rice. However, due to its polygenic nature and the diversity and complexity of genetic traits, as noted by Singh *et al.* (2000), grain yield is primarily influenced by both genetic and environmental factors. Genetic diversity in agronomic traits is essential for effective breeding programs. The extent to which traits are transmitted from one generation to the next is partly determined by heritability; high heritability indicates a strong genetic influence. However, for meaningful genetic improvement, heritability must be considered alongside genetic advance. When both heritability and genetic advance are high, it suggests the presence of additive gene action, which enhances the effectiveness of selection and accelerates breeding progress.

**MATERIAL AND METHODS**

Twenty-one rice varieties JGL 24423, JGL 27356, RNR 15048, RNR 11718, RNR 15435, RNR 29325, RNR 15459, RNR 21278, RNR 28361, KNM 118, KNM 1638, KNM 733, KPS 2874, KPS 6251, WGL 44, WGL 14, WGL 20471, WGL 915, WGL 962, WGL 1119 and WGL 1246 were used in the study. The 21 rice varieties were sown in randomized block design (RBD) with 2 replications during *Kharif,* 2022 and 2023 in Seed Production Farm, Agricultural Research Institute, and Department of Seed Science and Technology of Seed Research and Technology Centre, PJTAU, Rajendranagar, Hyderabad, Telanana, India.

For planting, a spacing of 20 cm × 15 cm was maintained. The recommended package of practices was followed throughout the crop growth period. Observations were recorded for fourteen traits, namely: leaf blade length (cm), leaf blade width (cm), time of heading, stem length (cm), panicle length (cm), number of panicles per plant, days to maturity, 1000-grain weight (g), grain length (mm), grain width (mm), decorticated grain length (mm), decorticated grain width (mm), amylose content in the endosperm, and awn length. For each of these fourteen traits, estimates of genetic advance, heritability, and genotypic and phenotypic coefficients of variation were computed.

**STATISTICAL ANALYSIS**

Statistical analysis was performed using WINDOSTAT software (Version 9.1). The standard procedures were followed for the estimation of heritability, genetic advance, and phenotypic and genotypic coefficients of variation (PCV and GCV).

**Estimation of variances**

According to Johnson *et al.* (1955), phenotypic variances (σ²p) and genotypic variances (σ²g) were measured.

σ²g = (GMS–EMS)/r

Where, r is the number of replications,

 GMS is the genotypic mean square,

EMS is the error mean square.

σ²p = σ²g + EMS.

**Estimation of coefficient of variation (PCV and GCV)**

PCV and GCV were calculated based on formula given by Falconer (1981).

$$Genotypic Coefficient of Variation=\frac{Genotypic standard Deviation}{Mean}×100$$

$$Phenotypic Coefficient of Variation=\frac{Phenotypic standard Deviation}{Mean}×100$$

**Estimation of heritability**

Heritability (h2) in the broad sense was calculated as per formula given by Allard (1960).



Where,

h2 (b) = Heritability in the broad sense

𝜎2g = Genotypic variance

𝜎2p = Phenotypic variance

𝜎2e = Environmental variance

**Genetic advance as per cent of mean**

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent for mean (GAM) was obtained.

$$GAM= \frac{GA}{Grand Mean \overbar{(X)}} ×100$$

Where,

GA = Expected genetic advance

$\overbar{(X)}$= General mean of the character in the population

**RESULTS AND DISCUSSION**

The findings of genetic advancement, heritability, and coefficient of variation were displayed in Table-1. For every characteristic, the phenotypic coefficient of variation (PCV) was generally greater than the corresponding genotypic coefficient of variation (GCV). The high PCV and GCV (> 20%) were recorded for the traits, 1000 grain weight (g) (PCV 27.93%, GCV 27.90%) and awn length (PCV 239.52%, GCV 203.73%). The moderate estimates of PCV and GCV (10-20%) were recorded for leaf blade length (PCV 17.35%, GCV 17.00%), leaf blade width (PCV 17.34%, GCV 16.24%), Stem length (PCV 15.26%, GCV 14.93%), panicle length (PCV 10.57%, GCV 10.21%), panicle number per plant (PCV 20.07%, GCV 19.07%), days to maturity (PCV 10.11%, GCV 10.09%), grain length (PCV 18.30%, GCV 16.34%), grain width (PCV 18.12%, GCV 16.85%), decorticated grain length (PCV 15.54%, GCV 15.50%) and decorticated grain width (PCV 12.13%, GCV 11.09%). The low (<10%) PCV and GCV were recorded in time of heading (PCV 9.29%, GCV 9.28%) and content of amylose in the endosperm (PCV 7.21%, GCV 7.15%). Similar outcomes were noted for the fourteen characters mentioned above, which are largely consistent with past observations in rice. These finding were also provided by Aravind *et al.* 2019; Sahu 2021; Behera *et al.* 2020; Bastola *et al.* 2023; Demeke *et al.* 2023.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| S.No. | Character | Range | Mean | Genotypic variance | Phenotypic variance | Environmental variance | CV (%) | h2 (bs) | GAM |
| Max | Min  | PCV | GCV |
| 1 | Leaf Blade Length (cm) | 50.83 | 23.98 | 33.50 | 32.48 | 33.82 | 1.35 | 17.35 | 17.00 | 0.96 | 34.32 |
| 2 | Leaf Blade Width (cm) | 1.86 | 0.88 | 1.50 | 0.06 | 0.07 | 0.01 | 17.34 | 16.24 | 0.88 | 31.33 |
| 3 | Time of heading (50% of plants with panicles) | 109.50 | 85.50 | 97.00 | 80.27 | 80.53 | 0.26 | 9.29 | 9.28 | 1.00 | 19.08 |
| 4 | Stem: Length (cm) | 120.64 | 70.57 | 92.02 | 188.82 | 197.27 | 8.45 | 15.26 | 14.93 | 0.96 | 30.10 |
| 5 | Panicle: Length of main axis (cm) | 31.06 | 21.49 | 25.10 | 6.59 | 7.07 | 0.48 | 10.57 | 10.21 | 0.93 | 20.31 |
| 6 | Panicle: Number per plant | 17.75 | 8.45 | 14.80 | 7.88 | 8.72 | 0.84 | 20.07 | 19.07 | 0.90 | 37.34 |
| 7 | Time maturity (Days) | 141.25 | 101.75 | 123.90 | 156.40 | 157.00 | 0.61 | 10.11 | 10.09 | 1.00 | 20.74 |
| 8 | Grain: Weight of 1000 fully developed grains (g) | 30.53 | 12.11 | 19.03 | 28.33 | 28.40 | 0.07 | 27.93 | 27.90 | 1.00 | 57.40 |
| 9 | Grain: Length (mm) | 11.33 | 5.24 | 8.50 | 1.93 | 2.42 | 0.49 | 18.30 | 16.34 | 0.80 | 30.06 |
| 10 | Grain: width (mm) | 3.14 | 1.46 | 2.00 | 0.12 | 0.14 | 0.02 | 18.12 | 16.85 | 0.86 | 32.28 |
| 11 | Decorticated Grain: Length (mm) | 8.21 | 3.54 | 6.00 | 0.86 | 0.86 | 0.00 | 15.54 | 15.50 | 0.99 | 31.85 |
| 12 | Decorticated Grain: width (mm) | 2.22 | 1.46 | 1.80 | 0.04 | 0.05 | 0.01 | 12.13 | 11.09 | 0.84 | 20.90 |
| 13 | Endosperm: Content of amylose | 25.61 | 20.35 | 23.10 | 2.73 | 2.78 | 0.05 | 7.21 | 7.15 | 0.98 | 14.62 |
| 14 | Awn: Length (mm) | 1.37 | 0.00 | 0.15 | 0.10 | 0.13 | 0.04 | 239.52 | 1.00 | 0.72 | 356.96 |

**Table 1. Estimates of range, mean and variability for 14 quantitative parameters in twenty-one rice genotypes**

Note: CV: Coefficient of variation, PCV and GCV: Phenotypic and Genotypic Coefficient of variation, h2 (bs): Heritability (broad sense), GAM: Genetic Advance as per cent of mean.

Heritability in broad sense (h2bs) have been classified by Robinson (1966) into three categories viz., high (> 75%), medium (50-75%) and low (< 50%). All the fourteen traits exhibited lowest heritability. The moderate estimates of genetic advance as per cent of mean was found in time of heading (19.08%) and content of amylose in the endosperm (14.62). The high genetic advance as per cent of mean (>20%) using broad sense heritability was documented among all the twelve traits *i.e.,* leaf blade length (34.32), leaf blade width (31.33), stem length (30.10), panicle length (20.31), panicle number per plant (37.34), days to maturity (20.74), 1000 grain weight (57.40), grain length (30.06), grain width (32.28), decorticated grain length (31.85), decorticated grain width (20.90) and awn length (356.96). The results obtained for the above characters are broadly in agreement with earlier reports in rice which were documented by Behera *et al.* 2020; Ratnam *et al.* 2024; Shrestha *et al.* 2021; Bastola *et al.* (2023), Demeke *et al.* (2023), Ivin *et al.* 2022; Aravind *et al.* 2019; Sudeepthi *et al.* 2020 and Sahu, 2021.

**CONCLUSION**

The 21 rice genotypes under study were evaluated for 14 yield and yield-attributing traits in this experiment. The results on variability, heritability, and genetic advance revealed the presence of sufficient genetic variability among the traits, indicating a promising scope for improvement in grain yield through selection. These findings may prove valuable in identifying suitable genetic materials for breeding programs, which can be further investigated and utilized for crop improvement.

**DECLARATIONS**

**Ethical Approval and Consent to participate:** Not Applicable

**Consent for publication:** Not Applicable

**Availability of supporting data:** The data used and/or analysed during the current study will be made available from the corresponding author on reasonable request.

**COMPETING INTERESTS DISCLAIMER:**

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

**REFERENCES**

Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and Sons Inc. Publishing Co. Pvt. Ltd. New York, USA. pp. 485.

Aravind, K., Banumathy, S., Vanniarajan, C., Arunachalam, P., Ilamaran, M and Kalpana, K. 2019. DUS characterization and genetic variability studies of rice mutants. *Electronic journal of plant breeding*. 10(2): 451-461.

Bastola, B.R., Adhikari, U., Poudel, B.P., Yadav, R.K., Basnet, R., Poudel, A., Yadaw, R.B. and Bhattarai, D. 2023. Genetic variation and trait association of fine rice genotypes. *Archives of Agriculture and Environmental Science*. 8(4): 590-596.

Behera, P. P., Singh, S. K., Singh, D. K and Longkho, K. 2020. Genetic parameters study for yield and yield contributing characters in rice (*Oryza sativa* L.) genotypes with high grain zinc content. *International Journal of Current Microbiology and Applied Sciences.* 9(3): 357-364.

Demeke, B., Dejene, T and Abebe, D. 2023. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at Pawe, northwestern Ethiopia. *Cogent Food & Agriculture*. 9(1): 2157099.

Falconer, D.S. 1981. Introduction to quantitative genetics. Olive Boyd, London. 340.

<https://openknowledge.fao.org/server/api/core/bitstreams/2a91baaf-c2e2-4a86-a327-f75c244108fe/content>

Ivin, J. J. S., Kayathri, S., Raveendra, C., Anbarasu, M and Anbuselvam, Y. 2022. Evaluation of morphological and molecular characterization of rice (Oryza sativa L.) through SSR marker under saline stress condition. *Journal of Environmental Biology*. 43(6): 786-793.

Johnson, H. W., Robinson, H. F and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybeans.

Ratnam, T. V., Kumar, B. R., Rao, L. V., Srinivas, T and Kumar, A. A. 2024. Assessment of genetic variability, character association and path analysis for yield and quality traits in zinc and iron rich landraces of rice. *Agricultural Science Digest*. 44(2): 289-294.

Sahu, S. 2021. Agro-morphological characterization and diversity analysis for yield and quality traits of rice (*Oryza sativa* L.) accessions (Doctoral dissertation, Indira Gandhi Krishi Vishwavidyalaya, Raipur).

Shrestha, J., Subedi, S., Kushwaha, U. K. S. and Maharjan, B. 2021. Evaluation of growth and yield traits in rice genotypes using multivariate analysis. *Heliyon*. 7(9).

Singh, R. K., Gautam, P. L., Saxena, S. and Singh, S. 2000. Scented rice germplasm: conservation, evaluation and utilization. *Aromatic rices. Kalyani, New Delhi*, 107-133.

Sudeepthi, K., Srinivas, T. V. S. R., Kumar, B. R., Jyothula, D. P. B and Umar, S. N. 2020. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 11(01): 144-148.