***Original Research Article***

**MULTISEASONAL ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN RICE (*Oryza sativa* L.): IMPLICATIONS FOR TRAIT IMPROVEMENT THROUGH SELECTION**

**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. The study assessed genetic variability, heritability and genetic advance in 14 yield related traits across 21 paddy genotypes during the 2022 and 2023 *kharif* seasons. The traits include; leaf blade length (cm), leaf blade width (cm), time of heading, stem length (cm), panicle length (cm), number of panicles per hill, 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. Phenotypic variation was consistently higher than genotypic variation, indicating environmental influence. Despite low to moderate genetic variability, moderate to high genetic advance as percent of mean was observed for all traits, suggesting good potential for genetic improvement through selection.

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

**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 [1]. More than 50% of the global population relies on rice as a part of their daily diet [2], contributing approximately 20% of the world's caloric intake [3]. 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 [4]. To meet the food requirements of a global population estimated to reach 9.3 billion by 2050, it will be necessary to increase total food production by nearly 70-100% compared to the levels of 2005-07 [5].

The variability of traits within and among different rice genotypes is statistically measured using the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). GCV quantifies the extent of genetic variability present for a trait, while PCV reflects the total observable variation, including both genetic and environmental influences [6]. Heritability estimates the proportion of phenotypic variation in a trait that is due to genetic factors. High heritability indicates a strong genetic influence making selection more effective, whereas low heritability suggests greater environmental influence on trait expression [7]. Genetic advance estimates the expected improvement in a trait through selection in a breeding program. It reflects the difference between the mean performance of selected individuals and the overall population, indicating the trait’s potential for genetic gain and effectiveness of selection, especially when coupled with high heritability [8].

Genetic variability in agronomic traits is a crucial component of breeding programs aimed at broadening the gene pool of rice. The heritability (h²) of a trait plays a significant role in determining its potential response to selection, thereby guiding effective genetic improvement strategies [9]. 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, diversity and complexity of genetic traits, grain yield is primarily influenced by both genetic and environmental factors[10]. The extent to which traits are transmitted from one generation to the next is partly determined by heritability; However, for meaningful genetic improvement, heritability must be considered alongside genetic advance. When both heritability and genetic advance as percent of mean 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 genotypes 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 genotypes were sown in randomized block design (RBD) with 2 replications during *Kharif,* 2022 and 2023 under ambient conditions in Seed Production Farm, Agricultural Research Institute, and Department of Seed Science and Technology of Seed Research and Technology Centre, PJTAU, Rajendranagar, Hyderabad, Telangana, India.

Data was recorded at key crop growth stages following the DUS Test guidelines for rice (*Oryza sativa* L.) by PPV & FRA (2007) *viz.,* booting, anthesis to dough development, ripening, and caryopsis hard stages. For planting, a spacing of 20 cm × 15 cm was maintained with a plot size of 6 sq. m. The recommended package of practices was followed throughout the crop growth period and followed the standard agronomic practices. Observations were recorded on 10 plants 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 [11], phenotypic variances (σ²p) and genotypic variances (σ²g) were measured.

$$σ^{2}g=\frac{(GMS-EMS)}{r}$$

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 [12].

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

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

**Estimation of heritability**

Heritability (h2) in the broad sense was calculated as per formula given by Allard [13]. Heritability in broad sense (h2bs) have been classified by Robinson (1966) into three categories viz., high (> 75%), medium (50-75%) and low (< 50%).

$$h^{2}(b)=\frac{Genotypic variance (σ²g) }{Phenotypic variance (σ²p)}$$

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, Analysis of variance was presented in Table-2. 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%), indicating genetic control is strong while the environmental influence is low and the selection will be effective. Moderate to high GCV and PCV in test weight suggest that the traits were under the influence of genetic control and are least affected by environment [14].

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, [15], [16], [17], [18] and [19].

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), indicating some scope for improvement via selection. 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). This indicates that the traits are governed largely by additive gene action and genetic factors strongly control the trait with minimal environmental influence. The results obtained for the above characters are broadly in agreement with earlier reports in rice [15], [16], [20], [17], [21], [22], [18], [19] and [23].

**CONCLUSION**

The multi-seasonal evaluation of 21 rice genotypes for 14 yield and yield-attributing traits revealed substantial variability, heritability, and genetic advance. The presence of sufficient genetic variability among the traits, indicating a promising scope for genetic improvement 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.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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.

|  |  |  |
| --- | --- | --- |
| **Source of Variation** | **df** | **Mean sum of squares** |
| **Leaf Blade Length (cm)** | **Leaf Blade Width (cm)** | **Time of heading (50% of plants with panicles)** | **Stem: Length (cm)** | **Panicle: Length of main axis (cm)** | **Panicle: Number per plant** | **Panicle: length of longest awn** | **Time maturity (days)** | **Grain: weight of 1000 fully developed grains** | **Grain: length** | **Grain: width** | **Decorti-cated grain: length** | **Decorti-cated grain: width** | **Endosperm: content of amylose** |
| **Genotypes**  | 20 | 33.158 | 0.084 | 158.10 | 193.021 | 6.831 | 11.302 | 0.172 | 156.699 | 28.369 | 2.178  | 0.128 | 0.861 | 0.043 | 2.752 |
| **Replications**  | 1 | 2.325 | 0.001 | 149.33 | 3.751 | 1.412 | 0.820 | 0.000 | 3.048 | 0.001 | 0.001 | 0.000 | 0.015 | 0.004 | 0.009 |
| **Error**  | 20 | 1.729 | 0.050 | 138.52 | 3.927 | 0.536 | 2.465 | 0.000 | 1.385 | 0.016 | 0.019 | 35.10 | 0.004 | 0.004 | 0.048 |

**Table 2. Analysis of variance for quantitative parameters in twenty-one paddy genotypes**

\*, \*\*, \*\*\* Significance at 5%, 1% and 0.1% levels probability, respectively

**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.

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