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Assessment of genetic variability and selection parameters for yield improvement in rice (*Oryza sativa* L.)

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Abstract

An experiment was conducted to evaluate the genetic variability, heritability and genetic advance for yield and its component traits on 69 rice (*Oryza sativa* L.) genotypes including five checks. All the genotypes were evaluated in a Randomized Complete Block Design with three replications. The analysis revealed substantial genetic variability among the genotypes, with phenotypic coefficient of variation (PCV) slightly higher than genotypic coefficient of variation (GCV) for all the traits, indicating minimal environmental influence on the traits. Grain yield per plant exhibited the highest variability (GCV = 31.77%, PCV = 31.88%) followed by panicle weight per plant (30.33%, 30.45%), fertile spikelets per panicle (30.32%, 30.44%), spikelet density (28.23%, 28.46%) and total spikelets per panicle (27.08%, 27.18%). Similarly, high variability was also observed for the number of tillers per plant (24.49%, 24.64%), productive tillers (22.38%, 22.53%) and biological yield per plant (23.30%, 23.44%). In contrast, days to 50% flowering (7.36%, 7.71%) and days to maturity (4.42%, 5.11%) exhibited low variability. High heritability coupled with high genetic advance as percent of mean was recorded for grain yield per plant (89.37%, 65.21%), panicle weight (84.76%, 62.22%), fertile spikelets per panicle (77.55%, 62.19%), spikelet density (88.53%, 57.68%), biological yield per plant (88.90%, 47.70%) and number of tillers per plant, indicating the predominance of additive gene action for these traits. Moderate to high estimates were also observed for morphological traits, while phenological traits showed lower genetic advance. The study concludes that the traits with high heritability with high genetic advance can be effectively used for direct selection, providing a strong scope for developing high-yielding and stable rice genotypes.

Keywords: Rice (*Oryza sativa* L.), additive gene action, GCV, PCV, heritability, genetic advance as percent of mean

1. Introduction

Rice (*Oryza sativa* L.) is a self-pollinated, semi-aquatic cereal crop belonging to the genus *Oryza* under the family *Poaceae*, with a chromosome number of $2n = 24$. The plant is an annual grass characterized by round, hollow, and jointed culms, flat leaves and a terminal panicle inflorescence. Notably, rice is the only cultivated cereal adapted to thrive under both flooded and non-flooded conditions, enabling its cultivation across diverse agro-ecological environments worldwide (Lahre J. 2021) ^[14]. In a number of countries, rice fulfills more than 70% of human calorie needs and serves as the primary source of protein for the needy in developing nations (Singh *et al.*, 2025) ^[25]. Owing to its wide adaptability, rice is cultivated on all five continents and serves as a staple food for nearly 3 billion people, contributing approximately 700 calories per person per day.

From a nutritional standpoint, rice is predominantly a carbohydrate-rich food, with starch comprising amylose and amylopectin as its principal component. The grain typically contains about 75-80% starch, 7% protein with a balanced amino acid profile and minor quantities of fats. It also provides essential micronutrients and vitamins, particularly the B-complex vitamins thiamin, riboflavin and niacin. Additionally, minerals including calcium (Ca), magnesium (Mg) and phosphorus (P) are present, along with trace elements such as iron (Fe), zinc (Zn), copper (Cu) and manganese (Mn). However, conventional polished rice varieties exhibit relatively low micronutrient density, averaging around 2 mg/kg Fe and 16 mg/kg Zn, with substantial losses occurring during milling compared to brown rice levels (10-11 mg/kg Fe and 20-25 mg/kg Zn) (Trijatmiko *et al.*, 2016; Nathani *et al.*, 2023; Oko *et al.*, 2012) ^[29, 19, 20].

Due to its high digestibility and nutritional importance, rice is often referred to as the “queen of cereals” (Anjum *et al.*, 2007) ^[1].

Globally, rice production reached approximately 520 million tonnes (MT) in 2024, with India and China being the leading producers. India alone accounts for about 150.18 MT from 51.27 million hectares, with an average productivity of 2.93 t/ha during 2024-25 (Government of India, 2025) ^[7]. In Madhya Pradesh, rice production has shown a consistent upward trend, reaching 7.02 MT in 2023 from nearly 2.0 million hectares, with productivity levels around 3.5 t/ha (CEIC Data, 2023) ^[3]. Despite these achievements, the global demand for rice is projected to rise to 550-600 MT annually by 2050, driven by a growing population expected to reach 9.7 billion (USDA FAS, 2025) ^[31]. We have already been fulfilling the anticipated rice production demands to increase the production from 121.2 MT in 2030 to 137.3 MT in 2050 (CRRI, 2013) ^[4], through the development of high-yielding varieties in the year 2024-25 from the current productivity of 2.93 t/ha.

The challenge of meeting future demand is further compounded by climate change, which poses a serious threat to rice productivity. Projections indicate potential yield reductions of 3.5-5% in irrigated systems and 20-47% in rainfed systems in India by 2050 due to rising temperatures, erratic rainfall patterns and water scarcity (Li *et al.*, 2024; ICAR, 2023) ^[16, 4]. These challenges are particularly significant in states like Madhya Pradesh, where rice cultivation is largely under rainfed situation, underscoring the urgent need to develop climate-resilient, high-yielding genotypes rich in essential micronutrients especially zinc and iron contents.

In this context, the exploitation of genetic variability remains fundamental to crop improvement programs. Genetic variability provides the essential raw material for selection and recombination, enabling breeders to develop superior genotypes with enhanced yield potential and stability (Demeke *et al.*, 2023) ^[5]. Estimating genetic parameters, such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (broad sense) and genetic advance, is critical for understanding the inheritance of quantitative traits. These parameters facilitate the prediction of selection response and the design of effective breeding strategies (Umadevi *et al.*, 2023) ^[30].

Therefore, the present investigation was undertaken to evaluate the extent of genetic variability, heritability and genetic advance for yield and its component traits in a diverse set of rice genotypes. The outcomes of this study are expected to provide valuable insights for identifying promising genotypes and developing ideotypes suitable for the varied agro-climatic conditions of India, thereby contributing to sustainable genetic improvement and enhanced rice productivity.

2. Materials and Methods

The field experiment was conducted during *kharif* 2023 at the Seed Breeding Farm, Rice Improvement Project, Department of Genetics and Plant Breeding, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, Madhya Pradesh, India. The experimental site was characterized by medium-black soils with uniform topography, good drainage and no waterlogging, providing a conducive environment for optimal crop growth. Standard recommended agronomic

and plant protection practices were uniformly adopted throughout the cropping period to minimize environmental variation and ensure healthy crop establishment.

The experimental material comprised of 69 rice (*Oryza sativa* L.) genotypes, including five checks (JR 206, DRR 45, DRR 48, Kalanamak, and Chittimutayalu). All the experimental genotypes were sourced from the Rice Improvement Project, Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications to ensure precision and reliability of the results. Each genotype was grown in a four rows of four meter length, maintaining the recommended spacing 20 x 15cm between rows and within rows to ensure an optimum plant population and uniform crop geometry.

Observations were recorded on a set of agro-morphological and yield-related traits, including days to 50% flowering, days to maturity, number of total tillers per plant, number of productive tillers per plant, stem length (cm), panicle length of main axis (cm), plant height (cm), flag leaf length (cm), flag leaf width (cm), stem thickness (cm), stem weight per plant (g), panicle weight per plant (g), biological yield per plant (g), number of fertile spikelets per panicle, number of sterile spikelets per panicle, spikelet fertility (%), total spikelets per panicle, spikelet density, panicle index (%), harvest index (%), thousand-grain weight (g) and grain yield per plant (g). Observations were recorded on randomly selected five representative plants from each replication, except for traits measured on a plot basis.

To assess the extent of genetic variability among the genotypes, various genetic parameters were estimated. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following Burton (1952) ^[2], while variance components were estimated according to Burton and De Vane (1953) ^[2]. Broad-sense heritability (H^2) was computed using the method suggested by Hanson *et al.* (1956) ^[8]. The expected genetic advance (GA) and genetic advance as a percentage of the mean (GAM) were estimated as per Johnson *et al.* (1955) ^[12].

These parameters were utilized to quantify the magnitude of variability, determine the proportion of heritable variation and predict the potential response to selection. The combined analysis of GCV, PCV, heritability and genetic advance facilitated a comprehensive understanding of the genetic architecture of yield and its component traits, thereby aiding in the identification of traits with greater scope for improvement through selection in rice breeding programs.

3. Result and Discussion

3.1 Genotypic and phenotypic coefficient of variation

The present investigation revealed considerable genetic variability among the evaluated rice (*Oryza sativa* L.) genotypes for yield and its component traits. The estimates of phenotypic coefficient of variation (PCV) were consistently higher than the corresponding genotypic coefficient of variation (GCV) for all traits, indicating the influence of environmental factors on trait expression. However, the relatively narrow differences between PCV and GCV for most of the characters suggested that the environmental effects were minimal and that the observed variability was predominantly governed by genetic factors.

Similar trends have been reported in earlier studies (Hasan *et al.*, 2011; Patel *et al.*, 2025) ^[9, 21], supporting the reliability of selection based on phenotypic performance.

Among all the traits studied, grain yield per plant showed the greatest variability, with GCV and PCV values of 31.77% and 31.88%, respectively. The high variability observed for this complex quantitative trait indicates a broad genetic base and substantial scope for improvement through selection. These findings are in agreement with the previous reports by Pragya *et al.* (2018) ^[22], Tiwari *et al.* (2019), and Patel *et al.*, (2025) ^[21], who also reported high variability for grain yield and emphasized its importance as a primary selection criterion in rice breeding programmes.

High estimates of GCV and PCV were also recorded for panicle weight per plant (30.33% and 30.45%), number of fertile spikelets per panicle (30.32% and 30.44%), spikelet density (28.23% and 28.46%), and total spikelets per panicle (27.08% and 27.18%). The high variability observed for these traits underscores their significant contribution to yield determination and highlights their potential utility as effective selection indices. The close correspondence between GCV and PCV for these characters further indicates minimal environmental influence, thereby enhancing the efficiency of phenotypic selection. These results corroborate the findings of Lipi *et al.* (2021) ^[17], and Surjaye *et al.* (2022) ^[27], who also reported high variability for spikelet-related traits.

The number of tillers per plant (GCV = 24.49%, PCV = 24.64%) and the number of productive tillers per plant (GCV = 22.38%, PCV = 22.53%) showed high variability, underscoring their importance for yield improvement. Productive tillers directly influence sink capacity and grain number, and the substantial variability observed indicates ample opportunity for genetic enhancement through direct selection. These findings are consistent with earlier reports by Hasan *et al.* (2011) ^[9] and Pragya *et al.* (2018) ^[22], who highlighted the positive association of tillering traits with grain yield.

Biological yield per plant also showed high variability (GCV = 23.30%, PCV = 23.44%), indicating significant genetic differences in biomass production among genotypes. This suggests the potential to improve yield by selecting genotypes with superior biomass accumulation. In contrast, harvest index exhibited moderate variability (GCV = 19.24%, PCV = 19.60%), indicating that improvements in assimilate partitioning efficiency can be achieved alongside biomass enhancement.

Moderate variability was observed for the traits such as stem length (GCV = 20.15%, PCV = 20.52%), thousand-grain weight (GCV = 19.31%, PCV = 19.50%), stem thickness (GCV = 17.34%, PCV = 17.50%), plant height and flag leaf dimensions. The presence of moderate variability for thousand-grain weight is particularly advantageous, as it allows for genetic improvement while maintaining grain size stability, an important quality parameter during hulling, milling and head rice recovery. These findings are in agreement with Pragya *et al.* (2018) ^[22], and Sao *et al.* (2024) ^[26], who reported similar trends for these traits.

Low estimates of GCV and PCV were recorded for phenological traits such as days to 50% flowering (7.36% and 7.71%) and days to maturity (4.42% and 5.11%), as well as for panicle length of the main axis and panicle index. The low variability observed for these traits indicates a high degree of genetic uniformity, likely resulting from

prolonged selection for adaptation and stability under specific agro-climatic conditions. These results are in strong agreement with previous studies (Lamichhane and Mohini, 2015; Pragya *et al.*, 2018; Sao *et al.*, 2024) ^[15, 22, 26], which consistently reported low variability for flowering and maturity traits.

The overall pattern of variability observed in the present study aligns well with recent large-scale germplasm evaluations. Sao *et al.* (2024) ^[26], in a study involving 2879 rice accessions, reported moderate variability for traits such as plant height, seed weight and effective tillers, while most other traits exhibited low variability. Similarly, Umamaheswar *et al.* (2024) observed low to moderate GCV and PCV values with close correspondence between genotypic and phenotypic estimates, indicating stable genetic control and minimal genotype × environment interaction.

3.2 Heritability and Genetic advance as %age of mean

In the present investigation, most traits exhibited high broad-sense heritability coupled with high genetic advance, indicating the predominance of additive gene action and suggesting that genetic improvement through direct phenotypic selection would be highly effective. Grain yield per plant exhibited very high heritability (89.37%) and the highest genetic advance as a percentage of the mean (65.21%), indicating that phenotypic variation among genotypes is largely governed by additive genetic effects, with minimal environmental variance. This result strongly corroborates the findings of Kumar *et al.* (2018), Rahangdale *et al.* (2019) ^[24] and Demeke *et al.* (2023) ^[5], all of whom documented high heritability and high genetic advance for grain yield, thereby confirming its suitability as a primary selection criterion for effective phenotypic selection in breeding programmes.

Similarly, panicle weight per plant exhibited high heritability (84.76%) and genetic advance (62.22%), while fertile spikelets per panicle demonstrated heritability of 77.55% and genetic advance of 62.19%. These results indicate strong additive genetic control over panicle architecture and reproductive efficiency. Comparable observations were documented Gour (2015) ^[6] who emphasised the effectiveness of selecting spikelet- and panicle-related traits as indirect selection criteria to improve grain yield.

Biological yield per plant (heritability = 88.90%, genetic advance = 47.70%) and stem weight per plant (heritability = 86.44%, genetic advance = 59.01%), also exhibited a favourable combination of high heritability and high genetic advance. These findings indicate substantial additive genetic variance governing biomass accumulation and partitioning and are consistent with reports by Vinoth *et al.* (2016) ^[32], Rahangdale *et al.* (2019) ^[24] and Demeke *et al.* (2023) ^[5], who highlighted the importance of biomass-related traits in enhancing yield potential.

Spikelet density (heritability = 88.53%, genetic advance = 57.68%) and total spikelets per panicle (heritability = 78.53%, genetic advance = 55.58%) exhibited high values for both parameters, suggesting that sink size can be effectively enhanced through phenotypic selection. These results closely align with those of Gour (2015) ^[6] and Kumar *et al.* (2018) ^[13], who reported strong additive genetic control of spikelet number and density.

Number of tillers per plant (heritability = 75.44%, genetic advance = 50.15%) and number of productive tillers per plant (heritability = 72.64%, genetic advance = 45.81%) exhibited high heritability along with high genetic advance, indicating the predominance of additive gene action with minimal non-additive genetic variance. Similar conclusions were drawn by Narinder (2006) ^[18], Rahangdale *et al.* (2019) ^[24] and Demeke *et al.* (2023) ^[5], who consistently identified tillering traits as major contributors for enhance the grain yield.

Morphological traits such as stem length (heritability = 84.09%, genetic advance = 40.77%), plant height (heritability = 85.66%, genetic advance = 31.55%), stem thickness (heritability = 79.42%, genetic advance = 35.41%) and panicle length of the main axis (heritability = 84.03%, genetic advance = 18.55%) exhibited high heritability with moderate to high genetic advance. This pattern indicates that these traits are predominantly under genetic control but may involve both additive and non-additive gene effects, including dominance and epistatic interactions. Comparable trends were documented by Kumar *et al.* (2018) ^[13] and Sao

et al. (2024) ^[26].

Flag leaf length (heritability = 80.96%, genetic advance = 28.27%) and flag leaf width (heritability = 78.05%, genetic advance = 27.48%) also recorded high heritability coupled with high genetic advance, indicating sufficient additive genetic variance. These findings support the observations of Gour (2015) ^[6], who emphasized the role of flag leaf morphological traits in enhancing photosynthetic efficiency and yield.

Days to 50% flowering exhibited high heritability (81.96%) but moderate genetic advance (14.47%), indicating partial additive gene action with possible non-additive genetic components. Similar results were documented by Pratap *et al.* (2018) ^[23] and Sao *et al.* (2024) ^[26]. In contrast, days to maturity recorded medium heritability (67.22%) with low genetic advance (7.87%), suggesting limited scope for genetic improvement through direct phenotypic selection. This pattern is consistent with the findings of Narinder (2006) ^[18] and Pratap *et al.* (2018) ^[23], who attributed the low response to selection for maturity to genetic stabilization and greater relative environmental influence.

Table 1: Genetic parameters of variability for yield and its component traits

Characters	Grand Mean	Range		Coefficient of Variation		h ² (bs)	GAM at 5%
		Min	Max	GCV (%)	PCV (%)		
DTF	102.73	86.00	130.00	7.36	7.71	81.96	14.47
DTM	130.48	117.00	154.00	4.42	5.11	67.22	7.87
NOT	8.98	5.74	19.57	24.49	24.64	75.44	50.15
NOPT	7.83	5.03	16.06	22.38	22.53	72.64	45.81
SL	59.46	30.91	95.18	20.15	20.52	84.09	40.77
PL	23.78	19.25	29.87	9.32	9.65	84.03	18.55
PH	83.24	52.03	120.77	15.54	15.76	85.66	31.55
FLL	30.96	21.68	45.22	13.94	14.15	80.96	28.27
FLW	1.27	0.73	1.94	13.56	13.79	78.05	27.48
ST	5.38	3.79	9.47	17.34	17.50	79.42	35.41
SWPP	24.28	11.69	42.43	29.23	29.83	86.44	59.01
PWPP	24.05	8.05	53.52	30.33	30.45	84.76	62.22
BY	48.33	23.60	75.63	23.30	23.44	88.90	47.70
FS	163.43	81.73	335.36	30.32	30.44	77.55	62.19
SS	42.77	13.87	118.28	31.20	30.54	76.88	56.54
SF%	79.14	47.71	92.37	9.96	9.99	86.72	20.45
TSPP	206.20	95.83	371.05	27.08	27.18	78.53	55.58
SD	8.77	4.44	16.88	28.23	28.46	88.53	57.68
PI	82.02	60.39	93.99	7.44	8.27	72.97	13.81
HI	40.74	21.99	68.94	19.24	19.60	86.70	38.90
TGW	19.59	12.83	27.73	19.31	19.50	88.25	39.38
GYPP	19.71	6.51	46.97	31.77	31.88	89.37	65.21

Classes of Heritability (%): High >70.0%, Medium 50.0-70.0%, Low <50.0%

Classes of GAM (Genetic advance as a percentage of mean) at 5%: High>20.0%, Medium 10.0-20.0%, Low <10.0%

Where,

DTF-Days to 50% flowering; DTM-Days to maturity; NOT-Number of tillers per plant; NOPT-Number of productive tillers per plant; SL-Stem length (cm); PL-Panicle length of main axis (cm); PH-Plant height (cm); FLL-Flag leaf length (cm); FLW-Flag leaf width (cm); ST-Stem thickness (cm); SWPP-Straw weight per plant (g); PWPP-Panicle weight per plant (g); BY-Biological yield per plant (g); FS-Fertile spikelets per panicle; SS-Sterile spikelets per panicle; SF%-Spikelet fertility (%); TSPP-Total spikelets per panicle; SD-Spikelet density; PI-Panicle index (%); HI-Harvest index (%); TGW-Thousand grain weight (g); GYPP-Grain yield per plant (g).

4. Conclusion

The study revealed substantial genetic variability among rice genotypes, with PCV values slightly higher than GCV, indicating minimal environmental influence and strong genetic control. High GCV, heritability and genetic advance were observed for grain yield per plant, panicle weight, spikelets number, tillers number and biological yield, suggesting the predominance of additive gene action and high potential for improvement through direct selection. In contrast, phenological traits exhibited low variability and

limited scope for selection. Overall, the results highlight that yield and its major components can be effectively improved by selecting traits with high heritability and genetic advance, thereby facilitating the development of high-yielding and stable rice varieties. The traits governing yield traits identified as high heritable and high genetic advance must be considered for the designing of systematic breeding programme for the development of high yielding and desired maturity based lines for the further utilization under rice breeding.

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