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EVALUATION OF GENETIC VARIABILITY AND SELECTION POTENTIAL IN RICE (*ORYZA SATIVA* L.) GENOTYPES

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ABSTRACT

The study was conducted during *Kharif* 2024 and *Rabi* 2024–25 at ICAR–Indian Institute of Rice Research, Hyderabad, to assess genetic variability, heritability, and genetic advance in 80 rice hybrids, 42 parents, and 5 checks using an augmented randomized block design. Analysis of variance revealed highly significant ($P<0.01$) differences among genotypes for most of the 13 traits, confirming substantial genetic divergence. Phenotypic coefficients of variation slightly exceeded genotypic values, indicating minimal environmental influence. Wide variability was observed for filled grains, 1000-grain weight, productive tillers, and grain yield, whereas flowering and kernel traits showed lower variation. Broad-sense heritability estimates were high (68.04–95.82%), with kernel breadth (95.82%) and kernel length (92.52%) recording the maximum. The greatest genetic advance as percent of mean was noted for filled grains (38.83%), 1000-grain weight (31.21%), and grain yield (30.09%), suggesting predominance of additive gene action. Traits such as flowering time, plant height, and kernel dimensions showed high heritability with moderate advance, reflecting additive and non-additive effects. Overall, the findings demonstrate that direct selection for major yield-contributing traits can accelerate genetic improvement in rice breeding.

Key words: Rice, Genetic variability, Heritability, Genetic advance, Yield traits, Selection

Introduction

Rice (*Oryza sativa* L.) constitutes the principal staple food for more than half of the global population and is the foremost among the three major cereals, followed by wheat and maize. It represents one of the earliest domesticated crops and exhibits remarkable ecological adaptability, encompassing 22 wild relatives within the genus *Oryza*. Cultivation occurs across diverse ecosystems including irrigated lowlands, uplands, and rainfed environments and the crop continues to hold strategic importance in Indian agriculture. From a nutritional perspective, rice contributes approximately 20% of global caloric intake and 15% of protein, in addition to providing minerals and dietary fiber (Sao *et al*., 2024). Future projections indicate that global demand will reach 852 million tons by 2035; however, productivity increases over the last decade have remained modest, averaging only 1% annually (Khush, 2013). In India, demand is expected to rise to 130 million tons by 2030 and 168 million tons by 2050, while the area under cultivation is likely to remain restricted to around 42 and 40 million hectares, respectively (Gupta *et al*., 2020).

Rice productivity has increasingly been challenged by climatic variability, erratic rainfall, pest and disease epidemics, and genetic erosion associated with intensive developmental activities (Ali *et al*., 2017). Nonetheless,

Table 1: Analysis of Variance for yield and yield components.

Source	Block	Entries	Check	Treatments	Treatment Vs. Check	Residuals
Df	3	126	4	121	1	12
DFF	0.67	87.11**	700.3**	66.59**	117.43**	5
PH	6.93	90.66**	11.68	75.98**	2182.43**	16.27
NPTS	0.32	1.67*	1.82*	1.67*	0.69	0.53
PL	3.53	6.96**	11.1**	6.42**	55.85**	1.79
FG	540.8**	1941.24**	5347.84**	1327.54**	62571.83**	85.17
PF	10.76	39.35**	60.38**	38.98**	0.6	4.38
SF	55.21**	40.65**	18.16*	34.74**	845.68**	4.18
TGW	14.33**	11.34**	61.58**	9.3**	57.89**	0.9
KL	0.04*	0.16**	1.18**	0.11**	1.85**	0.01
KB	0	0.04**	0.06**	0.03**	0.25**	0
L*B	0.01	0.08**	0.03**	0.07**	1.41**	0
GYP	5.04	20.65**	66.94**	19**	34.38**	3.64

*at 5% level of significance; **at 1% level of significance

(DF- Degrees of freedom, DFF- Days to fifty percent flowering, PH- Plant height, NPTS- Number of productive tillers, PL- Panicle length, FG- Filled grains, PF-Pollen fertility, SF-Spikelet fertility, TGW- Thousand grain weight, KL- Kernal length, KB- Kernal breadth, L*B- Kernal length-to-breadth ratio, GYP-Grain yield per plant)

the crop still possesses considerable untapped yield potential. Several strategies have been proposed to exploit this potential, including molecular breeding, new plant type development, and hybrid rice technology. Among these, hybrid technology has been recognized as the most practical approach for large-scale yield enhancement. The success of this strategy has been clearly demonstrated in China, where hybrid rice increased yields from 35–40 q/ha in conventional cultivars to 65–70 q/ha, resulting in improved farmer incomes and a rapid shift from inbred varieties to hybrids (Anis GB *et al.*, 2017; Yuan *et al.*, 1989).

Genetic variability provides the foundation for crop improvement, offering opportunities to identify and combine desirable attributes. The assessment of genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance expressed as a percentage of the mean (GAM) is central to formulating effective selection strategies (Gupta *et al.*, 2020). GCV and PCV partition total variability into genetic and environmental components (Girma *et al.*, 2018), while heritability quantifies the proportion of genetic variance expressed phenotypically and the likelihood of its transfer across generations (Akter *et al.*, 2018; Saisupriya *et al.*, 2022). Genetic advance estimates the expected improvement under selection pressure. Notably, traits exhibiting both high heritability and high genetic advance are typically governed by additive gene action, thereby enhancing their amenability to direct selection (Lakshmi *et al.*, 2020; Pasha *et al.*, 2019).

In this context, the present investigation was undertaken to evaluate genetic variability, heritability, and genetic advance in rice hybrids and their parental lines, with the aim of identifying promising material and traits for hybrid rice breeding.

Materials and Methods

The experiment was conducted during *Kharif 2024* at the ICAR–Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana. Forty restorer lines and three stable CMS lines were crossed using a line × tester mating scheme, resulting in the development of 80 hybrids. Standard agronomic practices recommended for the region were followed. The hybrids, along with their 42 parental lines and five standard checks (US-314, US-312, 27P63, WGL-14, and NDR-359), were evaluated during *Rabi* 2024–25. Seedlings, 25 days old, were transplanted at a spacing of 20 × 15 cm in an augmented randomized block design. Recommended crop management practices were adopted to ensure a uniform and healthy crop stand.

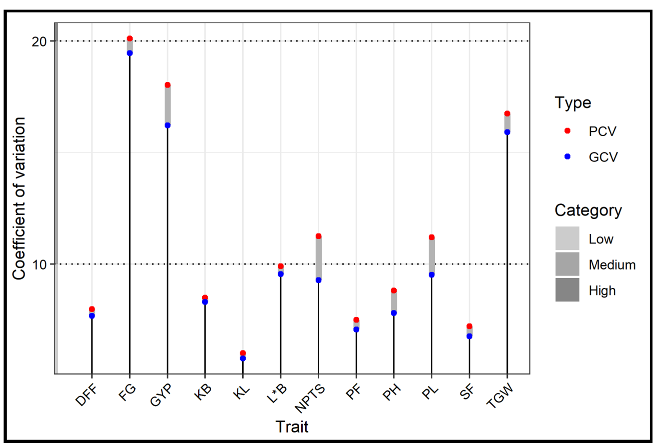

Fig. 1: Genotypic and phenotypic coefficients of variation.

Table 2: Mean, estimates of coefficient of variation, heritability, and genetic advance.

Trait	Mean	GCV	PCV	hBS	GAM
DFF	102.29	7.67	7.98	92.49	15.22
PH	98.94	7.81	8.81	78.59	14.28
NPTS	11.48	9.29	11.26	68.04	15.8
PL	22.61	9.52	11.2	72.15	16.67
FG	181.14	19.46	20.11	93.58	38.83
PF	83.15	7.07	7.51	88.77	13.75
SF	81.74	6.76	7.21	87.98	13.09
TGW	18.2	15.92	16.75	90.3	31.21
KL	5.63	5.78	6.01	92.52	11.47
KB	2.13	8.31	8.49	95.82	16.78
L*B	2.66	9.55	9.9	93.11	19.02
GYP	24.17	16.22	18.04	80.86	30.09

(DF- Degrees of freedom, DFF- Days to fifty percent flowering, PH- Plant height, NPTS- Number of productive tillers, PL- Panicle length, FG- Filled grains, PF-Pollen fertility, SF-Spikelet fertility, TGW- Thousand grain weight, KL- Kernal length, KB- Kernal breadth, L*B- Kernal length-to-breadth ratio, GYP-Grain yield per plant, GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, hBS -Broad sense heritability, GAM- Genetic advance as a percentage of mean)

Observations were recorded on five randomly selected plants per entry for 13 traits: days to 50% flowering, plant height, panicle length, number of productive tillers, filled grains, 1000-seed weight, spikelet fertility, pollen fertility, kernel length, kernel breadth, kernel length-to-breadth ratio, and grain yield per plant.

Statistical analyses were carried out using established biometrical procedures. Analysis of variance (ANOVA) for the experimental design was performed following Panse and Sukhatme (1967) and Federer (1956). Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated using the formulae of Burton and De Vane (1953). Broad-sense heritability (h^2) was computed as the ratio of genotypic variance ($\sigma^2 g$) to phenotypic variance ($\sigma^2 p$) on a mean basis (Allard, 1960).

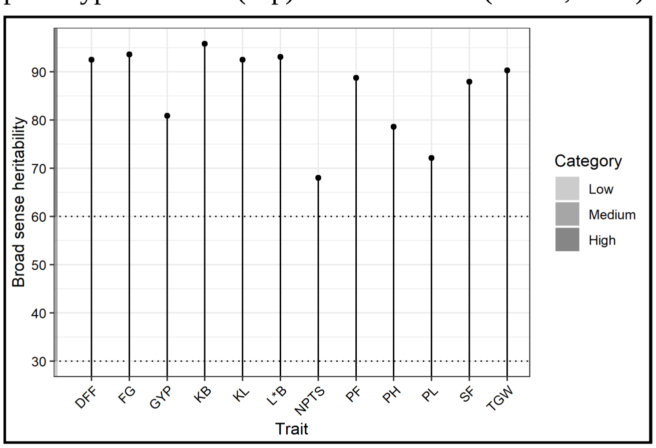

Fig. 2: Broad-sense heritability.

Genetic advance (GA) and genetic advance as a percentage of the mean (GAM) were calculated assuming 5% selection intensity, according to Johnson *et al.*, (1955).

Result and Discussion

Analysis of variance

The ANOVA revealed highly significant differences among treatments for all yield-related traits, confirming the presence of substantial genetic variability in the material studied. Results of the augmented block design are presented in Table 1. Block effects were not significant for traits such as days to 50% flowering, plant height, panicle length, number of productive tillers, pollen fertility, kernel breadth, kernel length-to-breadth ratio, and grain yield per plant. Similar findings of non-significant block variation have been reported earlier (Loitongbam *et al.*, 2019; Kumar *et al.*, 2024).

In contrast, treatment effects were significant for all traits examined, indicating considerable genetic differences among genotypes. Comparable results were also documented by Gebrie *et al.*, (2022) and Kumar *et al.*, (2024). Furthermore, significant differences were observed among standard checks for all traits except plant height, highlighting the genetic diversity present within the checks.

Mean performance

Wide variation was observed in mean values for several traits. Filled grains ranged from 95 to 239, plant height varied from 73.10 to 128.50 cm, and days to 50% flowering from 81 to 127. The number of productive tillers ranged between 9 and 15, 1000-seed weight between 12.20 and 26.16 g, and grain yield per plant between 16.54 and 36.50 g. This broad spectrum of variability suggests that these traits can serve as useful targets in selection and hybridization programs.

Genetic variability

For all traits, PCV estimates were consistently higher

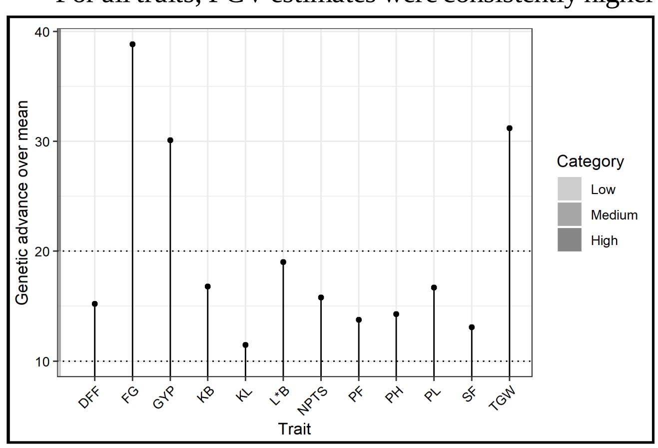

Fig. 3: Genetic advance expressed as a percentage of the mean.

than their corresponding GCV values, indicating environmental influence in addition to genetic control. Low variability (<10%) was recorded for traits such as days to 50% flowering (GCV = 7.67%, PCV = 7.98%), plant height (GCV = 7.81%, PCV = 8.81%), pollen fertility (GCV = 7.07%, PCV = 7.51%), spikelet fertility (GCV = 6.76%, PCV = 7.21%), kernel length (GCV = 5.78%, PCV = 6.01%), kernel breadth (GCV = 8.31%, PCV = 8.49%), and kernel length-to-breadth ratio (GCV = 9.55%, PCV = 9.90%). Moderate variation (10–20%) was recorded for number of productive tillers (GCV = 9.29%, PCV = 11.26%), grain yield per plant (GCV = 16.22%, PCV = 18.04%), and 1000-seed weight (GCV = 15.92%, PCV = 16.75%). Panicle length displayed low GCV (9.52%) but moderate PCV (11.20%), while filled grains exhibited moderate GCV (19.46%) along with high PCV (20.11%) (Table 2). These findings corroborate earlier reports in rice (Kumar *et al*., 2018; Debsharma *et al*., 2022; Lingaiah *et al*., 2022).

Heritability

Broad-sense heritability estimates ranged from 68.04% (productive tillers) to 95.82% (kernel breadth). High heritability was observed for all traits: days to 50% flowering (92.49%), plant height (78.59%), panicle length (72.15%), filled grains (93.58%), pollen fertility (88.77%), spikelet fertility (87.98%), 1000-seed weight (90.30%), kernel length (92.52%), kernel breadth (95.82%), kernel length-to-breadth ratio (93.11%), and grain yield per plant (80.86%) (Table 2). Such high estimates confirm that genetic factors play a predominant role in trait expression. These observations are in agreement with previous reports (Saha, 2019; Shivani *et al*., 2018).

Genetic advance

Genetic advance expressed as a percentage of the mean (GAM) was highest for filled grains (38.83%), 1000-seed weight (31.21%), and grain yield per plant (30.09%). Moderate GAM values were observed for days to 50% flowering (15.22%), plant height (14.28%), productive tillers (15.80%), panicle length (16.67%), pollen fertility (13.75%), spikelet fertility (13.09%), kernel length (11.47%), kernel breadth (16.78%), and kernel length-to-breadth ratio (19.02%)(Table 2).

Since heritability alone does not differentiate between additive and non-additive gene effects (Panse and Shukhatme, 1967), the combination of high heritability with high genetic advance provides more reliable guidance. In this study, such a pattern was recorded for filled grains, 1000-seed weight, and grain yield per plant, indicating predominance of additive gene action and suggesting that simple selection strategies may be effective. Similar conclusions were drawn by Dhurai *et al*., (2013) and Chandramohan *et al*., (2016). On the other hand, traits such as days to 50% flowering, plant height, number of productive tillers, panicle length, pollen fertility, spikelet fertility, kernel length, kernel breadth, and kernel length-to-breadth ratio exhibited high heritability coupled with moderate genetic advance, implying the involvement of both additive and non-additive gene actions. Improvement in these traits may therefore be achieved more efficiently through intermating of superior genotypes in segregating populations, as reported by Krishna *et al*., (2008) and Akinola *et al*., (2019).

Conclusion

The study revealed that phenotypic coefficient of variation (PCV) was generally higher than genotypic coefficient of variation (GCV), with high PCV observed only for filled grains. Heritability estimates were high for all traits, ranging from 68.04% (productive tillers) to 95.82% (kernel breadth). Genetic advance as percent of mean was high for filled grains, 1000-grain weight, and grain yield per plant. High heritability coupled with high genetic advance for these traits indicates additive gene action and the scope for direct selection, while traits showing high heritability with moderate genetic advance may be improved through intermating of superior genotypes.

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