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Genetic variability analysis in rice (*Oryza sativa* L.) genotypes based on quantitative traits

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Abstract

The present investigation involved an evaluation of the genetic variability, heritability and genetic advance of 42 (*Oryza sativa* L.) germplasm accessions for nine yield and yield attributing traits of rice during *Kharif* (wet) season of 2025. The differences among the different genotypes were highly significant ($P < 0.01$) for each of the studied traits, days to 50% flowering, days to maturity, plant height, seeds per panicle, panicle length, effective tillers, leaf width, test weight and grain yield per plant, which showed that there are significant differences between the different genotypes in terms of the studied parameters. The phenotypic coefficient of variation (PCV) was slightly greater than genotypic coefficient of variation (GCV) for all traits indicating a relatively low effect of environmental factors on expression of traits. The estimates for grain yield per plant, test weight, seeds per panicle, effective tillers, plant height and leaf width had high GCV and PCV values, which showed that these characters possess high variability. The broad-sense heritability values were very high for all traits from 74.6 to 98.1 with the maximum being observed in days to 50% flowering. Grain yield per plant, test weight, seeds per panicle, plant height, effective tillers and leaf width were highly heritable with a high genetic advance as percent of mean, suggesting a strong tendency of the additive gene action and that direct phenotypic selection was effective.

Keywords: Variability, heritability, genetic advance, GCV, PCV

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world and has been called the Global Grain as it is the staple food of almost half the world's population. It is an important crop for global food and nutritional security. Rice production, as one of the staple crops, would need to grow by about 2 million tonnes annually in India to meet the food demand of the growing population, which is expected to reach around 121 million tonnes by 2050. (Buelah *et al.*, 2022). Rice is a self-pollinated crop. It is a semi-aquatic plant composed of aerenchymatous tissues. The aerenchymatic cells found in the leaves, culm and roots which facilitates the diffusion of oxygen from the aerial parts down to the roots (Steffens *et al.*, 2011). More than ninety percent of the global rice is consumed as well as cultivated in Asia. Rice and its derivatives contribute to 35 to 75% of the calorie's intake for over 3 billion Asians, while approximately 20% of the global calorie supply is derived from rice, as it serves as a primary source of nutrition. The versatility, availability and adaptability of rice to any flavour and seasoning is over 50% of the world's population has made it a staple food. Rice normally contains 80% carbohydrates, 7-8% protein, 3% fat, and 3% fibre (Juliano, 1985). Vitamin B3 is lost at 67%, B1 lost at 80%, B6 lost at 90%, manganese lost at 50%, phosphorus lost at 50%, iron lost at 60% and all dietary fibre and essential fatty acids are lost when milling and polishing. Rice is an excellent food to include in a balanced diet. Rice has no fat, no cholesterol and is sodium free. (Dinesh *et al.*, 2009). The improvement of a crop is largely dependent on the nature and the amount of genetic variation available, heritability and introgression of desirable traits to new varieties. The success of breeding programmes can be enhanced when variability within the existing germplasm is high, thus the plant breeder can rapidly produce new varieties or improve existing ones (Meena and Bahadur, 2013, 2014; Ranganatha *et al.*, 2013; Yared and Misteru 2016) [2, 5, 7, 9, 14, 17].

Material and Methods

A field experiment was conducted during the *Kharif* 2025 with 42 accessions of rice at Crop Research Centre-1, Department of Genetics and Plant Breeding, School of Agriculture, ITM University, Sithouli, Gwalior (M.P.). Germplasms received from the Fuliya Indigenous Aromatic Rice Research Station, Nadia (W.B), ICAR-IARI, New Delhi, through the material transfer agreement (MTA). Each accession was planted in five rows with three replications using a randomized block design (RBD). Observations were recorded on five selected (tagged) plants of each accession except days to 50% flowering, days to maturity and 1000 seed weight (g) which were recorded on plot basis. Seed per panicle, plant height, leaf length, leaf width, grain yield per plant.

The statistical package used for analysis was R studio and the statistical methods to calculate the genetic components of variances used for the current study was given by Burton (1952) and Panse and Sukhatme (1985). The genotypic variations (GCV) were estimated using the formula recommended by Burton (1952). Phenotypic coefficient of variation (PCV), was estimated by the formula suggested by Burton (1952). The percentage of heritability was calculated as in Burton (1952) and Johnson *et al.* (1955a) gave the formula for calculating the genetic advance ^[3, 4].

Result and Discussion

The analysis of variance of 9 quantitative yield and yield attributing traits of rice germplasm accessions presented in

Table 1: ANOVA for 9 yield and yield attributing traits during wet season *Kharif* 2025

Source	Df	DF	DM	PH	SPP	PL	ET	LW	TSW	GYPP
Replication	2	21.93	23.15	106.69	812.7	0.54	1.86	0.014	0.53	23.37
Genotype	41	676.85**	655.54**	2133.49**	7969.6**	34.2**	32.91**	0.37**	109.93**	793.65**
Error	82	4.29	5.06	30.37	282.5	1.81	3.35	0.035	2.65	20.47

According to table 1 for analysis of variance (ANOVA) showed highly significant differences ($P < 0.01$) among the 42 rice genotypes for all the nine quantitative traits evaluated including days to 50% flowering, days to maturity, plant height, seeds per panicle, panicle length,

effective tillers, leaf width, test weight and grain yield per plant. These differences are highly significant which suggest a relatively high degree of genetic variability within the genotypes and thus a good opportunity for selection and genetic improvement.

Table 2: Mean, GCV, PCV, Heritability and Genetic Advance

Character	Mean	GCV (%)	PCV (%)	h^2 (bs)	GAM (%)
DF	103.43	14.48	14.61	98.1	29.54
DM	135.54	10.86	10.99	97.7	22.12
PH	129.75	20.41	20.84	95.9	41.16
SPP	212.66	23.8	25.08	90.1	46.54
PL	25.03	13.13	14.19	85.7	25.03
ET	13.38	23.45	27.15	74.6	41.74
LW	1.65	20.37	23.3	76.4	36.68
TSW	21.72	27.53	28.53	93.1	54.72
GYPP	57.97	27.69	28.77	92.6	54.91

Coefficient of variation was calculated at phenotypic and genotypic levels as analysis of variance permits estimation of phenotypic, genotypic and environmental coefficient of variation (Burton, 1952).

Phenotypic coefficient of variation: In Table 2. The magnitude of GCV and PCV of the quantitative characters are displayed in the data revealed that, in both the magnitude of PCV, falls higher than GCV. The value of PCV in season are 14.61, 10.99, 20.84, 25.08, 14.19, 27.15, 23.30, 28.53 and 28.77. (Fig.1) ^[3].

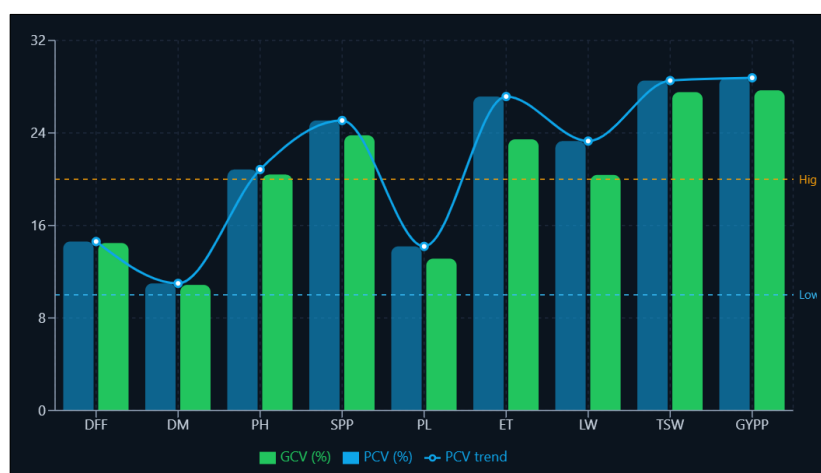


Fig 1: Comparison between GCV% and PCV% for various traits

Genotypic coefficient of variation

The magnitude of GCV and PCV of the quantitative characters are displayed in the data revealed that, in both the magnitude of PCV, falls higher than GCV. The value of GCV is 14.48, 10.86, 20.41, 23.80, 13.13, 23.45, 20.37, 27.53 and 27.69.

The present study showed that the phenotypic coefficient of variation (PCV) was consistently greater than genotypic coefficient of variation (GCV) for all the nine quantitative traits which show that the expression of traits is influenced by environmental factors. The mean of PCV ranged from 10.95% (for panicle length) to 40.17% (for grain yield per plant) and the mean of GCV ranged from 10.45% (for panicle length) to 39.15% (for grain yield per plant). A significant genetic variability was observed in some characters, namely, grain yield per plant (40.17% and 39.15%), test weight (29.41% and 29.28%), seeds per panicle (28.11% and 26.85%), effective tillers (24.33% and 22.34%) and plant height (22.21% and 22.07%), thus suggesting a higher potential for improvement by selection. In contrast, days to maturity (13.14% and 12.87%) and panicle length (10.95% and 10.45%) displayed relatively low variations.

Narrow differences in PCV and GCV of all the studied traits suggested that the expression of the traits has low environmental component and the differences that occurred were mostly genetic. Johnson *et al.* (1955) and Burton (1952) also reported similar results and gave a plausible explanation for the higher level of PCV as a result of the environmental effects on phenotypic expression. The present findings corroborate those of Babu *et al.* (2012), Sumanth *et al.* (2017), Srujana *et al.* (2017), Rukmini Devi *et al.* (2017) and Tuhina-Khatun *et al.* (2015) who also observed higher PCV than GCV and high variability in grain yield, test weight, number of productive tillers and number of seeds per panicle in rice. In the same way, Sabesan *et al.* (2009) recorded relatively low values for GCV and PCV for flowering and maturity characteristics, similar to those recorded in the present study. The high

genetic variation in grain yield and its associated traits, therefore, suggests that these traits could be successfully utilized in rice breeding programmes by selecting directly for yield in the field. Heritability As given by Johnson *et al.* (1955) heritability values are categorised as low (<30%), medium (30-60) and high (>60). In the present study heritability was estimated for nine quantitative traits under investigation. All the traits have been shown high estimates of broad sense heritability. days to 50% flowering 98, days maturity 98, plant height 96, seed per panicle 90, panicle length 86, effective tillers 75, leaf width 76, test weight 93, grain yield per plant 93% respectively.

In the present investigation, high estimates of broad-sense heritability were obtained for all the nine quantitative traits (>60%) which showed that all these characters were mainly subjected to genetic control with comparatively low environmental influence. Days to maturity (96%), leaf width (94), grain yield per plant (95) and seed per panicle and panicle length (91) also had high heritability. The same conclusion was reached by Johnson *et al.* (1955) who proposed that traits of high heritability are subject to lesser environmental influence and would be more amenable to selection for improvement. Rice grain yield and various yield contributing traits were found to be highly heritable by Sumanth *et al.* (2017), Srujana *et al.* (2017), Rukmini Devi *et al.* (2017), Babu *et al.* (2012) and Tuhina-Khatun *et al.* (2015) [1, 3, 4, 13, 15, 16].

Genetic advance: Genetic advance is an increase in a mean genotypic value relative to its parental population. The method recommended by Johnson *et al.*, (1955) was used to calculate expected genetic advancement. (Fig.2) [4].

In the present study highest genetic advance as a percent of mean was recorded for all nine characters. The genetic advance percent of mean for days to 50% flowering 29.54, days to 22.12, plant height 41.16, seed per panicle 46.54, panicle length 25.03, effective tillers 41.74, leaf width 36.68, test weight 54.72 and grain yield per plant 54.91% [10].



Fig 2: Comparison between heritability and genetic advance for various traits

The genetic advance expressed as percent of mean (GAM) was also high for all the studied traits ranging from 20.55% for panicle length to 78.61% for grain yield per plant. The

highest genetic advance was recorded for grain yield per plant (78.61%), followed by test weight (60.06%), seed per panicle (52.82%), plant height (45.16%), effective tillers

(42.26%), leaf width (41.45%), days to 50% flowering (39.37%), days to maturity (25.96%), and panicle length (20.55%). High heritability and high genetic advance values for most of the traits reflect highly additive gene action and direct phenotypic selection will be effective to improve these characters. Johnson *et al.* (1955), Burton (1952), Sumanth *et al.* (2017), Sabesan *et al.* (2009), Anis *et al.* (2016) and Rukmini Devi *et al.* (2017) reported that high heritability combined with high genetic advance is a good parameter for identification of superior genotypes for rice breeding programmes [3, 4, 9, 10, 15].

Conclusion

The present study has shown a high degree of genetic variability in all forty -two rice genotypes for the 9 yield and yield-attributing traits which was substantiated by highly significant ANOVA results. Assessments of the environmental influences on trait expression were made by comparing the high correlation between GCV and PCV for most traits. The high broad-sense heritability together with the high genetic advance per unit of mean for these characteristics indicated the predominant additive gene action and the effectiveness of selection among these traits for grain yield per plant, test weight, seeds per panicle, plant height and effective tillers.

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