

#### **RESEARCH ARTICLE**

## Studies on Genetic Variability, Heritability, Genetic Advance for Yield, and Yield Components in Rice Landraces

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### Abstract

An investigation was carried out to study the variability, heritability, and genetic advance as per cent of mean for yield and yield components in 100 rice landraces along with four checks at Regional Agricultural Research Station, Maruteru during *Kharif*, 2021. Analysis of variance revealed significant differences among the landraces for all the characters indicating sufficient genetic variation in the experimental material under study. The studies on variability, heritability, and genetic advance as per cent mean revealed small differences between GCV and PCV that were recorded for all the characters studied, indicating less environmental influence on these characters. Moderate levels of PCV and GCV, high heritability coupled with high genetic advance as per cent of mean were recorded for plant height, panicle length, grain yield, plant, and test weight indicating the effectiveness of simple selection in the improvement of these traits.

Keywords: Variability, Heritability, Rice, Landraces

### Introduction

Rice (*Oryza sativa* L.) is an important cereal crop belonging to the Gramineae family and serves as a staple food for more than 60% of the world's population (Singh and Singh, 2008). Landraces harbour the great genetic potential for rice improvement. Landraces maintained by farmers are enriched with tremendous genetic variability when compared with high-yielding varieties (whose variability is constrained due to homozygosity) since they are not subjected to subtle selection over a long period. This aids in the adaptation of landraces to wide agroecological niches and they contain qualitative traits. It is, however, necessary to know the extent, magnitude, and pattern of rice diversity for a successful rice-breeding programme (Singh *et al.*, 2016).

Grain yield is a complex quantitative character that is governed by polygenes. While making a selection, it is essential to take into account genotypic variation in yield and its component traits. Heritability is the measure of transmission of characters from generation to generation and the estimates of heritability will be of great use to the breeder in choosing superior individuals for a desired trait. Genetic advance measures the difference between the mean genotypic values of the selected population over the original population from which these were selected. Johnson et al., (1955) proposed that heritability coupled with genetic advance would be more useful than heritability estimates alone in predicting genetic gain under selection. Keeping in view the above prospects, the present investigation is carried out with the objective of estimating the genetic variability for yield, yield components, heritability, and genetic advance which would help in the selection and further improvement of rice genotypes.

### **Material and Methods**

#### Experimental material and experimental design

The present investigation was carried out using 100 rice landraces along with four checks (BM 71, TN 1,

Chandra, and Sri Dhruthi) grown in augmented block design during *Kharif*, 2021 at Regional Agricultural Research Station, Maruteru. Each genotype was grown in a single row of 3.75 m in length with a spacing of 20 cm between rows and 15 cm between plants within the row. Observations were recorded on five randomly selected plants in each genotype for days to 50% flowering, plant height (cm), number of ear bearing tillers/m<sup>2</sup>, panicle length (cm), number of grains/panicle, spikelet fertility%, grain yield/plant (g) and test weight (g).

#### Statistical analysis

Analysis of variance was worked out by the method suggested by Federer (1956, 1961) and was elaborated by Federer and Raghavarao (1975) and Peterson (1985). Genotypic and phenotypic variances were estimated by the method suggested by Burton and Devane (1953) and heritability (broad sense) as the ratio of genotypic to phenotypic variance by Allard (1960). The genetic advance was estimated as per the formula proposed by Lush (1940). The data analysis was carried out using the software, Windostat version 4.2.0 from R Studio.

The GCV and PCV are classified as low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Madhavamenon (1973). Heritability was estimated by the formula given by Johnson *et al.* (1955) and they classified the heritability as low (below 30%), moderate (30-60%), and high



(more than 60%). The range of genetic advance as per cent of the mean was classified as low (<10%), moderate (10-20%), and high (>20%) as suggested by Johnson *et al.* (1955).

### **Results and Discussion**

The ANOVA for augmented design consisting of 100 landraces along with four checks pertaining to eight quantitative characters was shown in **Table 1**. The results showed significant differences among the entries, genotypes, and checks for eight characters *viz.*, days to 50% flowering, plant height (cm), number of ear-bearing tillers/m<sup>2</sup>, panicle length (cm), number of grains/panicle, spikelet fertility (%), grain yield/ plant (g) and test weight (g) except the number of squares for checks vs genotypes showed significant differences for all the traits except the number of ear-bearing tillers/m<sup>2</sup> and grain yield/plant. Thus, the results revealed the presence of significant variability among the landraces.

The PCV estimates were slightly higher than the corresponding GCV estimates for the characters studied (**Table 2** and **Figure 1**) indicating that the characters were less influenced by the environment. Therefore, phenotypic selection would be effective for the improvement of these traits. Low PCV and GCV values were recorded for the traits *viz.*, days to 50% flowering (7.39, 7.32), number of ear bearing tillers/ $m^2$  (9.45, 8.33) number of grains/panicle (8.87, 7.22)

Source of	d.f.	Days	Plant	Number of	Panicle	Number	Spikelet	Grain	Test		
variation		to 50%	height (cm)	ear bearing	length	of grains/	fertility%	yield/	weight (g)		
		flowering		tillers/m <sup>2</sup>	( <b>cm</b> )	panicle		plant (g)			
		Sum of squares									
Block	4	5.12 *	56.01	243.25	2.96 *	127.43	4.33 *	7.08 **	1.16*		
Entries	103	59.78 **	384.71 **	816.76 **	9.74 **	627.82 **	65.25 **	12.52 **	12.41**		
Genotypes	99	50.87 **	292.35 **	830.34 **	9.49 **	243.73 *	37.4 **	12.86 **	12.55 **		
Checks	3	311.25 **	245.34 **	556.18	11.48 **	1222.93 **	11.58 **	5.45 *	8.28 **		
Checks vs genotypes	1	188.16 **	9947.08 **	254.8	29.28 **	3870.96 **	2984.1 **	0.72	10.72 **		
Error	12	0.96	17.26	184.18	0.7	82.06	1.29	1.26	0.28		

 Table 1. Analysis of variance for yield and yield components

\* Significant at 5% level; \*\* Significant at 1% level



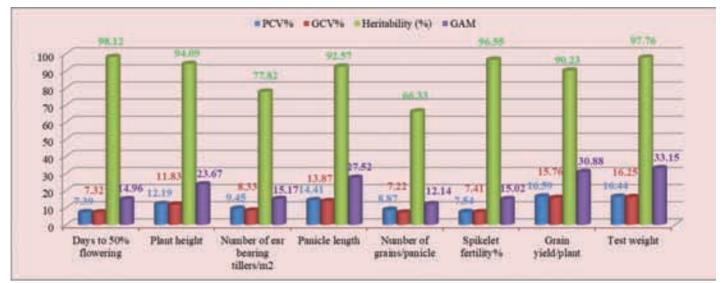


Figure 1: Variability, heritability, and GAM for eight characters in 100 landraces along with four checks

S.		Coefficient	of variation	Heritability	Genetic	Genetic advance	
No.	Character	PCV (%)	GCV (%)	(%) ·	advance	as per cent of mean	
1.	Days to 50% flowering	7.39	7.32	98.12	14.44	14.96	
2.	Plant height (cm)	12.19	11.83	94.09	33.19	23.67	
3.	Number of ear bearing tillers/m <sup>2</sup>	9.45	8.33	77.82	46.26	15.17	
4.	Panicle length (cm)	14.41	13.87	92.57	5.88	27.52	
5.	Number of grains/panicle	8.87	7.22	66.33	21.36	12.14	
6.	Spikelet fertility%	7.54	7.41	96.55	12.18	15.02	
7.	Grain yield/plant (g)	16.59	15.76	90.23	6.67	30.88	
8.	Test weight (g)	16.44	16.25	97.76	7.14	33.15	

 Table 2. Variability, heritability and GAM for yield and yield components

and spikelet fertility% (7.54, 7.41) indicating presence of less variability among the landraces for these traits. Similar findings were reported by Sudeepthi *et al.*, (2020) and Gbenga *et al.*, (2021) for days to 50% flowering; Singh *et al.*, (2018) and Devi *et al.*, (2019) for the number of ear-bearing tillers/m<sup>2</sup>; Bhim *et al.*, (2018) and Swapnil *et al.*, (2020) for number of grains/panicle and Lamichhane *et al.*, (2021) for spikelet fertility%. Moderate levels of PCV and GCV were recorded for plant height (12.19, 11.83), panicle length (14.41, 13.87), grain yield/plant (16.59, 15.76) and test weight (16.44, 16.25) indicating the existence of comparatively moderate variability for these traits and provide scope for improvement through selection in further generations. The results are similar to the findings of Edukondalu *et al.*, (2017) and Rachana *et al.*, (2018) for plant height; Anup *et al.*, (2020) and Bhor *et al.*, (2020) for panicle length; Bhor *et al.*, (2020) and Sudeepthi *et al.*, (2020) for grain yield/ plant and Lakshmi *et al.*, (2021) and Lamichhane *et al.*, (2021) for the test weight.

High heritability coupled with moderate genetic advance as per cent of mean for days to 50% flowering (98.12%, 14.96), number of ear bearing tillers/m<sup>2</sup> (77.82%, 15.17) number of grains/panicle (66.33%, 12.14) and spikelet fertility% (96.55%, 15.02) indicating the presence of additive and non-additive gene action in the expression of these traits. Hence, the improvement of these characters



would be easier through mass selection, varietal or hybrid development, or any other modified selection procedure aiming to make use of additive gene effects rather than simple selection. Similar results were reported by Lamichhane et al., (2021) and Nihad et al., (2021) for days to 50% flowering; Parimala et al., (2019) and Bhor et al., (2020) for the number of earbearing tillers/m<sup>2</sup>; Nayak et al., (2016) and Hari et al., (2018) for the number of grains/panicle and Sudeepthi et al., (2020) and Swapnil et al., (2020) for spikelet fertility%. High heritability coupled with high genetic advance as per cent of mean for plant height (94.09%, 23.67), panicle length (92.57%, 27.52), grain yield/ plant (90.23%, 30.88), and test weight (97.76%, 33.15) indicating the presence of additive gene action in the inheritance of these traits and effectiveness of simple selection for improvement of these characters. The results are similar to the findings of Lakshmi et al., (2021) and Lamichhane et al., (2021) for plant height; Parimala et al., (2019) and Anup et al., (2020) for panicle length; Sudeepthi et al., (2020) and Lakshmi et al., (2021) for grain yield/plant; Nihad et al., (2021) for the test weight.

# Conclusion

Moderate PCV, GCV, and high heritability coupled with high genetic advance as per cent mean were observed by plant height, panicle length, test weight, and grain yield/plant indicating the effectiveness of simple selection in the inheritance of these traits.

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