

Genetic variability studies for yield and yield component characters of landraces of rice (*Oryza sativa* L.)

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ABSTRACT

In the present study 36 landraces along with four checks were evaluated in alpha lattice design (ALD) for yield and yield component traits at Agricultural College Farm, Bapatla, Andhra Pradesh during *kharif*, 2023 to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as per cent of mean. The analysis of variance revealed significant variability for all the characters studied. Among the traits studied, high phenotypic and genotypic coefficients of variation were recorded for number of tillers per plant, ear bearing tillers per plant, test weight, number of filled grains per panicle, L/B ratio and grain yield/plant (g) indicating large amount of variation among the genotypes included in the study. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height (cm), number of tillers per plant, ear bearing tillers per plant, test weight (g), number of filled grains per panicle, L/B ratio and grain yield per plant (g) indicating that these traits governed by additive gene effects and hence direct phenotypic selection may be rewarding for improvement of these traits in rice.

Keywords: *Genetic advance, GCV, Heritability, PCV and Variability*

Rice (*Oryza sativa* L.) is one of the most significant cereal food crops in the world which fulfills the nutritional requirements of half of the world's population belonging to the family Poaceae ($2n=24$). It accounts for around 45 per cent of India's cereal production occupies a pivotal place in Indian agriculture as it is a staple food for more than 70% of population. About 90% of the world's rice is grown and consumed in Asia. Its versatility and nutritional value make it an indispensable part of daily meals for millions. The world's second most important cereal crop, rice plays a crucial role in global food security. In India, rice is cultivated over an area of 46.38 m ha with total production of about 130.29 mt and productivity of 2809 kg ha⁻¹ and in A.P, it occupied an area of 2.25 m ha with the production of 7.79 mt and productivity of 3470 kg ha⁻¹ during 2021-22 (Directorate of Economics and Statistics, 2022). Traditional cultivars are still grown by farmers because of their ethnic preferences and unique indigenous applications. With the introduction of contemporary high-yielding semi-dwarf varieties, efforts to develop these land races have also been severely constrained. Therefore, it is imperative to assess yield for the

traditional cultivars. Rice production and productivity are modulated by an array of biotic and abiotic factors. Major diseases like blast, sheath blight and bacterial blight pose substantial obstacles to rice production among biotic factors. Indigenous folk rice cultivars often exhibit incredible but untapped potential for nutritional qualities and biotic stress resistance. In rice breeding programs, increasing yield is one of the main breeding goals. Any crop improvement program must have sufficient genetic variability in order to be launched, and the degree of genetic variability within a species determines how successful the program will be. The degree of genetic variability can be determined by the genotypic coefficient of variation. Because it depicts the heritable component of variability. It is imperative to include genotypic variation in yield and its component qualities throughout the selection process. Characters like yield and its components being polygenic in nature, the breeder has to select desired genotypes from the knowledge of components of variation. For this the basis is to partition the total variation into phenotypic and genotypic components and to study the extent of these components for various traits which aids to

know the type of gene action and helps in deciding breeding procedure for the genetic improvement of particular trait. The nature and extent of variability is the basis for all crop improvement programmes. According to Allard (1960), yield is polygenically controlled quantitative character and is highly influenced by environment. Partitioning of observed variability into heritable and non-heritable components is very much essential to get a true indication of the genetic coefficient of variability as a useful measure of the magnitude of genetic variance present in the population. Assessment of variability for morphological and yield related traits is essential in planning of appropriate breeding strategy for genetic improvement of the crop. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. 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 selected population over the original population from which these were selected. Heritability coupled with genetic advance is more reliable and useful genetic parameters in predicting the genetic gain under selection than heritability values alone (Bhargavi *et al.*, 2021).

MATERIAL AND METHODS

The present investigation was carried out using 36 landraces along with four checks grown in alpha lattice design with two replications during late *kharif*, 2023 at Agricultural College Farm, Bapatla. Each genotype was grown in three rows of 3.0 m length with a spacing of 20 cm between rows and 15 cm between plants, within the row. The data was recorded on five competitive plants taken from each replication on days to 50 per cent flowering, plant height (cm), number of tillers per plant, ear bearing tillers per plant, panicle length (cm), test weight (g), number of filled grains per panicle, L/B ratio and grain yield/plant (g). Analysis of variance was worked out by the method suggested by Panse and Sukhatme (1964) and the genotypic and phenotypic coefficients of variations were estimated by the method suggested by Burton and Devane (1953). The data analysis was carried out with INDOSTAT software. 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). The range of genetic advance as per cent of mean was classified as low ($< 10\%$), moderate (10-20%) and high ($> 20\%$) as suggested by Johnson *et al.* (1955). Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance. Heritability provides information on magnitude of inheritance of quantitative characters while genetic advance helps in formulating suitable selection procedure.

RESULTS AND DISCUSSION

Analysis of variance for nine characters, revealed significant differences among the genotypes for all the characters included under study indicating the presence of greater variability among the genotypes. (Table 1). Low GCV and PCV ($< 10\%$) values were recorded for the traits *viz.*, days to 50 per cent flowering and panicle length (cm) indicating that the variability for these characters among the genotypes was meagre. Similar findings were reported for these characters by Bandi *et al.* (2018), Devi *et al.* (2022) and Manivelan *et al.* (2022).

Moderate GCV and PCV (10-20%) values were recorded for the trait *viz.*, plant height (cm). This result is in agreement with the earlier reports of Nath and Kole (2021), Faysal *et al.* (2022), Demeke *et al.* (2023), Kumar *et al.* (2024) and Sao *et al.* (2024). The characters, number of tillers per plant, ear bearing tillers per plant, test weight (cm), number of filled grains per panicle, L/B ratio, grain yield/plant (g) registered higher GCV and PCV ($> 20\%$) values indicating that large amount of variation is present among the genotypes for these characters. Similar results were obtained by Bandi *et al.* (2018), Saha *et al.* (2019), Patel *et al.* (2021), Deepthi *et al.* (2022), Faysal *et al.* (2022), Manivelan *et al.* (2022), Demeke *et al.* (2023), Agalya *et al.* (2024). High heritability coupled with high genetic advance as per cent of mean (Table 2) was reported for plant height (cm), number of tillers per plant, ear bearing tillers per plant, test weight (g), number of filled grains per panicle, L/B ratio and grain yield/plant (g)

Table 1. Analysis of variance for yield and yield component traits in rice (*Oryza sativa* L.)

Source of variation	Degrees of freedom	Days to 50 per cent flowering	Plant height (cm)	Number of tillers per plant	Ear bearing tillers per plant	Panicle length (cm)	Test weight (g)	Number of filled grains per panicle	L/B ratio	Grain yield/plant (g)
Mean sum of squares										
Replication	1	0.16	15	6.823	7.079	0.408	0.08	57.9	0.1083	10.98
Treatments	39	67.86**	901.8**	31.249**	26.311**	9.115**	36.04**	2622.8**	1.7286**	124.27**
Blocks (b)	18	1.89	2.6	2.734	1.005	1.019	1.05	47	0.0458	5.78
Error	20	1.22	3.5	2.929	2.239	1.094	0.77	33	0.0332	4.78
Total	78	71.13	922.9	43.735	33.634	11.636	37.94	2760.7	1.9159	145.81

* Significance at 5% level, ** Significance at 1% level

Table 2. Estimates of genetic parameters for grain yield and yield component traits in rice (*Oryza sativa* L.)

S.No.	Characters	Mean	Range		GCV (%)	PCV (%)	Genetic Advance	Heritability (Broad Sense) (%)	Genetic Advance as % of Mean
			Minimum	Maximum					
1	Days to 50 per cent flowering	88.95	80	114	6.51	6.66	11.59	95.53	13.11
2	Plant height (cm)	142.86	81	177.35	14.91	14.96	43.72	99.31	30.6
3	Number of tillers per plant	16.83	9	25	22.49	24.62	7.12	83.41	42.31
4	Ear bearing tillers per plant	14.39	7.5	24.5	24.5	26.07	6.83	88.33	47.44
5	Panicle length (cm)	22.29	17.91	27.42	9.02	10	3.69	79.56	16.57
6	Test weight (g)	19.37	13.8	29.45	21.91	22.46	8.53	95.14	44.02
7	Number of filled grains per panicle	119.1	49.3	192.1	30.37	30.81	73.67	97.14	61.66
8	L/B ratio	3.52	2	5.51	26.22	26.8	1.86	95.7	52.84
9	Grain yield per plant (g)	27.93	15.4	55.95	27.79	28.97	15.34	92	54.91

PCV-Phenotypic Coefficient of Variation; GCV-Genotypic Coefficient of Variation

indicating that these traits mostly under the control of additive gene action and hence direct phenotypic selection of these traits would be effective for crop improvement. Similar findings were earlier reported for these characters by Rao *et al.* (2020) for ear bearing tillers per plant; Devi *et al.* (2022) for test weight, number of filled grains per panicle and grain yield per plant; Saha *et al.* (2019) and Faysal *et al.* (2022) for panicle length (cm). High heritability coupled with moderate genetic advance as per cent of mean was observed for the traits viz., days to 50 per cent flowering and panicle length (cm) indicating the presence of both additive and non-additive genetic effects and genetic improvement of these characters can be exploited through heterosis breeding. Similar findings were earlier reported by Manivelan *et al.* (2022), Sao *et al.* (2024) for days to 50 per cent flowering; Sudeepthi *et al.* (2020a), Bhargavi *et al.* (2021), Deepthi *et al.* (2022), Demeke *et al.* (2023) and Pranaya *et al.* (2024) for panicle length.

CONCLUSION

High PCV and GCV were recorded for the traits viz., number of tillers per plant, ear bearing tillers per plant, test weight (cm), number of filled grains per panicle, L/B ratio and grain yield/plant (g) indicating that the large amount of variation included in study among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for yield contributing traits like plant height (cm), number of tillers per plant, ear bearing tillers per plant, test weight (g), number of filled grains per panicle, L/B ratio and grain yield/plant (g) indicating that these traits are under the control of additive gene action and hence direct phenotypic selection of these traits would be effective for crop improvement.

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Received on 03.02.2024 and Accepted on 20.03.2024