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ASSESSMENT OF GENETIC VARIABILITY IN RICE (*ORYZA SATIVA* L.) FOR YIELD AND NUTRITIONAL TRAITS

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ABSTRACT

The present study was conducted using 144 rice genotypes including five checks (BPT 5204, BPT 2841, Chittimuthyalu, Kalanamak, DRR DHAN 45) evaluated for 12 traits at Agricultural College Farm, Bapatla during *kharif,* 2024-25 using augmented block design. Analysis of variance revealed significant differences among genotypes for 12 traits, indicating substantial genetic variability with in the experimental material and hence can be exploited for future crop improvement programme. High genotypic and phenotypic coefficients of variation was observed for protein content (%), antioxidant activity (mgAAE/100g), Fe content (ppm), Zn content (ppm) and grain yield per plant (g), while plant height (cm), number of tillers per plant, number of productive tillers per hill and test weight (g) showed moderate GCV and PCV values. The PCV estimates were higher than GCV for all the characters indicating that substantial variation for these characters was contributed by environmental components. High heritability coupled with high genetic advance as percent of mean was recorded for plant height (cm), number of tillers per plant, number of productive tillers per hill, test weight (g), protein content (%), antioxidant activity (mgAAE/100g), Fe content (ppm), Zn content (ppm) and grain yield per plant (g) indicating that these traits are largely governed by additive gene action and hence direct selection of these traits for improvement of dependent variable (yield) may be rewarding.

Keywords: GCV, Genetic Advance, Heritability, PCV and Rice

INTRODUCTION

Rice (*Oryza sativa* L.; 2n = 24) is a self-pollinated cereal crop belonging to the family Poaceae and order Poales. It is one the most widely consumed cereals across the world and plays a major role in the global food supply. As the global population continues to rise, the demand for rice is anticipated to escalate correspondingly (Sujarwo Putra *et al.,* 2022). It provides essential micronutrients in addition to being the main source of carbohydrate. Next to China, India is the world's second-largest producer of rice, grown in an area of 51.42 mha with production and productivity of 14.90 mt and 2899 kg ha^{-1} respectively. In Andhra Pradesh, it occupies an area of 2.07 mha with production and productivity of 8.01 mt and 3863 kg ha^{-1} respectively (*www.Indiastat.com,* 2024-25).In addition to efforts to achieve yield gains, improving the nutritional value of rice has gained global interest. Further, micronutrient studies in rice grain also help

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address the problem of malnutrition among rice consumers particularly in developing nations which cannot afford dietary diversity. The immune system, enzymatic processes, and cognitive development all depend on micronutrients like iron (Fe) and zinc (Zn). So the deficiencies in these micronutrients might impact countries especially where rice is consumed as staple food crop. The low levels of essential nutrients in conventional rice, particularly when polished, causes hidden hunger in populations as they rely on rice as a primary diet.

Genetic variability serves as a critical resource for the effective improvement of crop species.Genetic variability provides extent of variation and the role of environment in trait expression. Heritability indicates the proportion of genetic contribution to phenotypic variation, while genetic advance as percent of mean reflects the expected improvement under selection. Together, these parameters guide effective selection in crop improvement programs. Hence, in the present studyan attempt was made to study variability among 144 rice genotypes.

MATERIAL AND METHODS

The present study was conducted at Agricultural College Farm, Bapatla during 2024-25 *kharif* season. The experimental material comprised of 144 rice genotypes including five checks (BPT 5204, BPT 2841, Chittimuthyalu, Kalanamak, DRR DHAN 45)

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

Source of variation	D.F	Days to 50 per cent flowering	Plant height (cm)	Number of tillers per plant	Number of productive tillers per hill	Panicle length (cm)	Number of filled grains per panicle
Block	6	361.71**	460.44**	10.62**	7.07**	6.46**	2503.93**
Treatments	143	80.15**	157.18**	2.50**	1.76**	5.73**	1658.43**
Checks	4	362.69**	1162.43**	10.59**	5.83**	10.97**	11577.09**
Treatment: Test and Test vs. Check	139	72.02**	128.25**	2.27**	1.65**	5.58**	1373.00**
Error	24	1.75	1.26	0.37	0.33	0.96	198.81

Source of variation	D.F	Test weight (g)	Protein content (%)	Antioxidant activity (mgAAE/100g)	Fe content (ppm)	Zn content (ppm)	Grain yieldper plant (g)
Block	6	23.32**	11.34**	620.47**	1.85**	74.04*	374.91**
Treatments	143	10.81**	22.16**	375.14**	6.30**	20.36**	87.05**
Checks	4	51.60**	391.15**	5927.40**	128.80**	4.05**	391.79**
Treatment: Test and Test vs. Check	139	9.63**	11.54**	215.37*	2.77**	20.82**	78.28**
Error	24	0.63	0.03	1.50	0.01	0.09	3.14

* Significance at 5 % level and ** Significant at 1 % level

Table 2. Estimates of genetic parameters for morphological and nutritional traits in rice (*Oryza sativa* L.).

S.No.	Character	Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as % of mean
		PCV (%)	GCV (%)		
1	Days to 50 percent flowering	8.97	8.88	97.95	18.13
2	Plant height (cm)	10.16	10.11	99.11	20.77
3	Number of tillers pr plant	16.30	15.08	85.63	28.79
4	Number of productive tillers per hill	15.74	14.28	82.35	26.74
5	Panicle length (cm)	10.24	9.35	83.46	17.63
6	Number of filled grains per panicle	20.41	18.96	86.24	36.32
7	Test weight (g)	18.42	17.81	93.50	35.54
8	Protein content (%)	25.58	25.49	99.35	52.42
9	Antioxidant activity (mgAAE/100g)	26.23	26.14	99.36	53.76
10	Fe content (ppm)	62.32	62.03	99.08	127.38
11	Zn content (ppm)	27.27	27.22	99.62	56.05
12	Grain yield per plant (g)	35.61	35.01	96.62	70.99

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

using augmented block design. The experimental material including advanced breeding lines 127, released varieties 18 and land races 9 from ARS, Bapatla and ICAR-IIRR, Hyderabad. Each genotype was planted in 3 rows with 3 m length, with a spacing of 20×15 cm. The crop was cultivated following all recommended agricultural practices. Observations were recorded for 12 traits *viz.,* days to 50% flowering, plant height (cm), number of tillers per plant, number of productive tillers per hill, panicle length (cm), number of filled grains per panicle, test weight (g), protein content (%), antioxidant activity (mgAAE/100g), Fe content (ppm), Zn content (ppm) and grain yield per plant (g). Heritability in the broad sense $h^2_{(b)}$and genetic advance was calculated using the formula provided by Johnson *et al*. (1955). The genotypic and phenotypic coefficients of variation were determined according to the methods described by Burton (1952).The estimates of PCV and GCV were categorized as low (0-10%), moderate (10-20%), and high (>20%) based on the classification by Sivasubramanian and Madhavamenon (1973). The analysis was carried using R Studio version R.4.4.2.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among all the genotypes for all the 12 characters studied (Table 1), indicating the presence of sufficient variability for exploitation. The PCV estimates were higher than GCV for all the characters indicating that substantial variation for these characters was contributed by environmental components. Further, the significance of ANOVA for checks reflected that each check performed differently than the other (including yield and micronutrient checks) indicating that the experiment is sensitive enough to detect treatment differences.

The variability parameters for 12 traits was discussed under (Table 2). In the study, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters (Table 2). High phenotypic and genotypic coefficients of variations (PCV and GCV) was observed for protein content (%), antioxidant activity (mgAAE/100g), Fe content (ppm), Zn content (ppm) and grain yield per plant (g) which indicated the presence of sufficient genetic variability in the material included. These results are consistent with the experimental findings of Singh *et al*. (2020). Moderate GCV and PCV values was observed for plant height (cm), number of tillers per plant, number of productive tillers per hill and test weight (g). These results were in confirmity with the reports of Sao *et al*. (2024), Usha *et al*. (2024) and Kerketta *et al*. (2024). Low GCV and PCV were observed for the traits of days to 50% flowering. Similar results were reported by Usha *et al*. (2024).

In the present study, high heritability coupled with high genetic advance as percent of mean was observed for traits like plant height, number of tillers per plant, number of productive tillers per hill, number of filled grains per panicle, test weight (g), protein content (%), antioxidant activity (mgAAE/100g), Fe content (ppm), Zn content (ppm) and grain yield per plant (g). These findings are consistent with the previous experimental results of Kerketta *et al*. (2024) and Sridevi (2018).High heritability combined with moderate genetic advance as percent of mean was observed for days to 50% flowering and panicle length. These results are in agreement with the experimental findings of Usha *et al*. (2024).

CONCLUSION

The analysis of variance indicated the significant variation among all the genotypes included in the study. Further the significance of ANOVA for checks reflected that each check performed differently than the other (including yield and micronutrient checks) indicating that the experiment is sensitive enough to detect treatment differences. In the present study, the characters *viz.,* plant height (cm), number of tillers per plant, number of productive tillers per hill, test weight (g),protein content (%), antioxidant activity (mgAAE/100g), Fe content (ppm), Zn content (ppm) and grain yield per plant (g), all recorded moderate to high variability and high heritability coupled with high genetic advance as percent mean indicating the predominance of additive gene action. Hence, direct simple selection of yield traits may be rewarding for overall improvement of dependent variable yield.

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