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Assessment of genetic variability for yield and its components across multiple locations in rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was undertaken to estimate genetic variability parameters for yield and quality traits using pooled data across three environments in Andhra Pradesh *viz.,* RARS, Maruteru; ARS, Ragolu and ARS, Bapatla, during *kharif* 2024-25. The experimental material consisted of 28 medium-duration genotypes along with two checks (MTU 1224 and MTU 1239), evaluated in a randomized block design with two replications. Analysis of variance revealed significant differences among genotypes for all traits, confirming ample genetic variability. Moderate genotypic and phenotypic coefficients of variation were recorded for filled grains per panicle, 1000-seed weight, grain yield per plant, head rice recovery, kernel L/B ratio, protein, and zinc content. High heritability coupled with high genetic advance as a percent of mean was recorded for filled grains per panicle, 1000-seed weight, grain yield per plant, head rice recovery, kernel L/B ratio, protein, iron, and zinc content indicating the predominance of additive gene action, and hence simple phenotypic selection would be effective for improvement of this traits. The results are also useful for identification of potential donor genotypes for developing high-yielding and nutritionally enriched rice varieties adaptable to diverse agro-environments.

Keywords: *Genetic advance, Genetic variability and Heritability*

Rice (*Oryza sativa* L., 2n = 24) is one of the world's most vital cereal crops and the principal source of dietary energy for nearly half of the global population. Asia accounts for approximately 90% of global rice production and consumption, underscoring its central role in ensuring food and nutritional security (FAO, 2023). Besides globally, more than 3 billion people depend on rice as their staple food, and in countries such as India, Bangladesh and China, it contributes over 50% of daily caloric intake. With the rapid rise in population and changing dietary preferences, the demand for rice continues to grow. However, increasing population density, shrinking arable land, climate variability and stagnant yield trends have become major constraints in meeting the projected food demand by 2050 (Subbaiah *et al.,* 2011). Consequently, genetic improvement of rice remains a priority for ensuring sustainable production.

In addition to yield, grain quality traits such as head rice recovery, grain shape, protein content, and micronutrient density are gaining importance. Modern consumers prefer fine-grained, aromatic and nutrient-rich rice. Biofortification, which involves enhancing micronutrient content in staple crops, has emerged as a promising strategy to address hidden hunger, particularly iron and zinc deficiencies prevalent in developing countries. Thus, breeding programmes must simultaneously address both yield potential and grain quality improvement.

Assessing genetic variability, heritability and genetic advance provides critical insight into the nature and magnitude of variation available for selection and the effectiveness of various breeding methods. The success of crop improvement largely depends on the presence of sufficient genetic diversity, which determines the potential for selection and hybridization Rice yield and quality traits are complex, polygenic and influenced by environmental fluctuations. Therefore, evaluation under multiple environments provides more reliable estimates of the genetic parameters. Understanding the contribution of additive and non-additive gene effects helps breeders design efficient selection strategies. Considering these aspects, the present study aimed to assess the magnitude of genetic variability, heritability and genetic advance for yield and quality traits among 30 rice genotypes evaluated across three agro-ecologically distinct environments in Andhra Pradesh.

MATERIAL AND METHODS

The experiment comprised 30 medium-duration rice genotypes from RARS, Maruteru, ARS, Ragolu, ARS, Bapatla and ARS, Nellore, along with two widely grown checks (MTU 1224 and MTU 1239). The genotypes represent diverse pedigrees with varying genetic backgrounds (Table 1). The trial was conducted at multi locations during *kharif* of 2024-25 at RARS, Maruteru; ARS, Ragolu and ARS, Bapatla. The experiment was laid out in randomized block design (RBD) with two replications. Observations were recorded on five randomly selected competitive plants per replication. Data was collected on the following eight yield traits and seven quality traits *viz.,* days to 50 per cent flowering (DFF), days to maturity (DM), plant height (PH), number of productive tillers per hill (NPT), panicle length (PL), number of filled grains per panicle (FGPP), 1000-seed weight (TSW) and grain yield per plant (GYPP), head rice recovery (HRR), kernel length (KL), kernel breadth (KB), kernel L/B ratio, protein content, iron (Fe) content, and zinc (Zn) content. Post-harvest grain samples were analyzed at the Rice Quality Laboratory,

Table 1. List of genotypes and their parents used in the study

S.No.	Genotype	Cross combination/ Pedigree
1	RGL 7047	(MTU 1210/ MTU 1224)/ RP Bio 226
2	BPT 3468	BPT 2231/ MTU 1140
3	MTU 2869-17-2-1-1	BPT 5204/MTU 1210
4	RGL 7034	NLR 34449/ Chittimuthyalu
5	MTU 1239 (Check)	MTU 1075 / BM71
6	BPT 3456	BPT 2270/ MTU 1166
7	MTU2861-1-1-2	MTU 1075/ NLR 34449
8	MTU2776-29-1-1-1-2	MTU 1121/ SM 12
9	RGL7045	(MTU 1210/ MTU 1224)/ RP Bio 226
10	RGL 7048	MTU 1262/RNR 15048
11	MTU 2823-23-1-1	MTU 1121 / MTU 1061
12	MTU 2854-9-1-1-1-1	APMS 8B/ APMS 12B
13	MTU 2855-6-2-1-1	APMS 9B/ APMS 12B
14	MTU 2861-1-1-1-1-1	MTU 1075/ NLR 34449
15	MTU 2837-56-1-1-1	(MTU 1075/ Chittimuthyalu)/ MTU 1075
16	BPT 3451	BPT 2270/ BPT 2605
17	MTU 2851-19-1-1-1	MTU 1187/ RP Bio 226
18	RGL 7036	MTU 1210/ MTU 1224
19	NLR 3895	BPT 3291/ MTU 1010
20	RGL 7038	MTU 1262/ MTU 1075
21	MTU 1224	(JGL 3844 / NLR 34449) / BPT 5204
22	RGL 7046	(MTU 1210/ MTU 1224)/ RP Bio 226
23	BPT3250	MTU 7029 / IRGC 18193 / MTU 1081
24	NLR3893	BPT 3291 / MTU 1081
25	RGL7051	DRR Dhan 45 / RGL 1880
26	BPT3354	BPT 3291 / BPT 2411
27	MTU2878-13-1-1	MST 15/ CSR 27
28	RGL 7039	MTU 1262/ MTU 1075
29	MTU 1310	MTU 1075 / CR 3598-1-4-2-1
30	MTU 2716	BPT 5204 / MTU 5249

Department of Genetics and Plant Breeding, RARS, Maruteru, for quality parameters. The data was subjected to analysis of variance (ANOVA) as per Fisher (1935) to test the significance of differences among genotypes. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated following Burton (1953). Broad-sense heritability (h^2) was calculated according to Hanson *et al.,* (1956), and genetic advance as a percent of mean (GAM) was computed as per Johnson et al. (1955).

RESULTS AND DISCUSSION

Analysis of variance

The ANOVA revealed highly significant differences among the genotypes for all traits studied, indicating the presence of considerable genetic variability (Table 2). This variability provides ample scope for selection and genetic improvement of yield and quality traits.

Estimates of Genetic Variability

The magnitude of GCV and PCV reflects the extent of genetic variability available for selection. In this study, GCV values were lower than PCV values, indicating the influence of environmental factors on trait expression (Table 3).

Low GCV and PCV (<10%) were recorded for days to 50 per cent flowering (3.15%, 3.29%), days to maturity (2.40%, 2.52%), plant height (7.30%, 7.69%), productive tillers per hill (4.75%, 6.32%), panicle length (6.75%, 7.46%), kernel length (9.36%) and kernel breadth (9.13%). These results indicate limited variability and, consequently, a narrow scope for genetic improvement through direct selection. Comparable results were observed by Kishore *et al.* (2015) and Lingaiah *et al.* (2018).

Moderate GCV and PCV (10–20%) were observed for filled grains per panicle (12.57%, 14.97%), 1000-seed weight (12.25%, 13.89%), grain yield per plant (12.90%, 14.73%), head rice recovery (14.25%, 14.33%), kernel L/B ratio (11.02%), protein content (13.66%), and zinc content (16.76%), implying moderate variability and the possibility of improvement through selection. Similar results were reported by Harsharaj *et al.* (2024) and Behera *et al.* (2020).

High GCV and PCV (>20%) were observed for iron content (57.46%, 57.48%), suggesting substantial variability and a high potential for selection gain. This aligns with reports by Hasan *et al.* (2020) and Ullah *et al.* (2023).

Heritability and Genetic Advance

High heritability values in general indicate the reliability of phenotypic selection. In the present study, high heritability (>70%) was recorded for most traits, signifying the predominance of genetic factors over environmental influence (Fig.1). High heritability coupled with high genetic advance as a percent of

Table 2. Analysis of Variance for yield and quality traits in rice genotypes

S.No.	Traits	MSS Replication df = 1	TSS Treatments df = 29	ESS error df =29
1	Days to 50 per cent flowering	4.27	36.20**	9.96
2	Days to maturity	11.58	40.32**	3.27
3	Plant height	0.29	296.89**	9.75
4	Productive tillers per hill	1.32	1.67**	0.35
5	Panicle length	0.02	12.52**	2.15
6	Filled grains per panicle	331.35	4162.36**	159.83
7	1000 seed weight	3.67	26.26**	2.29
8	Grain yield per plant	1.27	49.99**	4.06
9	Head rice recovery	1.67	146.55**	11.74
10	Kernel length	0.001	0.46**	0.001
11	Kernel breadth	0.0001	0.05**	0.001
12	Kernel L/B ratio	0.0001	0.18**	0.003
13	Protein content	0.007	1.99**	0.006
14	Iron content	0.004	0.65**	0.002
15	Zinc content	0.6	12.24**	0.77

Table 3. Estimates of variability, heritability and genetic advance as percentage of mean

S. No.	Character	Coefficient of variation		Heritability (%)	Genetic advance as per cent of mean
		PCV (%)	GCV (%)		
1	Days to 50 per cent flowering	3.29	3.15	91.25	6.19
2	Days to maturity	2.52	2.4	90.37	4.7
3	Plant height (cm)	7.69	7.3	90.24	14.29
4	Productive tillers per hill	6.32	4.75	56.33	7.34
5	Panicle length (cm)	7.46	6.75	81.91	12.59
6	Filled grains per panicle	14.97	12.57	70.45	21.73
7	1000 seed weight (g)	13.89	12.25	77.81	22.26
8	Grain yield per plant (g)	14.73	12.9	76.76	23.29
9	Head rice recovery (%)	14.33	14.25	98.84	29.18
10	Kernel length (mm)	9.36	9.36	99.96	19.27
11	Kernel breadth (mm)	9.13	9.11	99.54	18.72
12	Kernel L/B Ratio	11.02	11.01	99.78	22.65
13	Protein content (%)	13.66	13.65	99.93	28.12
14	Iron content (ppm)	57.48	57.46	99.94	98.33
15	Zinc content (ppm)	16.76	16.65	98.76	34.09

mean was observed for filled grains per panicle (70.45%, 21.73%), 1000-seed weight (77.81%, 22.26%), grain yield per plant (76.76%, 23.29%), head rice recovery (98.84%, 29.18%), kernel L/B ratio (99.78%, 22.65%), protein (99.93%, 28.12%), iron (99.94%, 98.33%), and zinc (98.76%, 34.09%). These results suggest the predominance of additive gene action, allowing for effective improvement through simple phenotypic selection. High heritability with moderate genetic advance as percent of mean was observed for plant height, kernel length, and kernel breadth, suggesting the involvement of both additive and non-additive gene effects. High heritability with low genetic advance as percent of mean was observed for days to flowering and days to maturity, which reflects the influence of non-additive gene effects and environmental factors, implying limited scope for selection.

CONCLUSION

The pooled genetic analysis across three distinct agro-environments demonstrated significant genetic variability among the evaluated rice genotypes. The high variability in micronutrient content suggests that biofortification breeding for iron and zinc can be accelerated using the identified donor genotypes. Furthermore, the consistency of these traits across multiple environments highlights the stability and adaptability of certain genotypes such as MTU 2823-23-1-1, RGL 7039, and RGL 7048, which may serve as potential parents in hybridization programs aimed at improving both yield and nutritional quality. Moderate to high genotypic and phenotypic coefficients of variation, combined with high heritability and high genetic advance as percent of mean for filled grains per panicle, 1000-seed weight, grain yield per plant, head rice recovery, kernel L/B ratio, protein, iron, and zinc contents, confirm the predominance of additive gene action. These findings indicated the potential of direct phenotypic selection for these traits in rice improvement programs. Genotypes exhibiting both high yield potential and superior grain quality can serve as promising donors for breeding nutritionally rich, high-yielding, and widely adaptable rice varieties, contributing to the goals of sustainable production and nutritional security.

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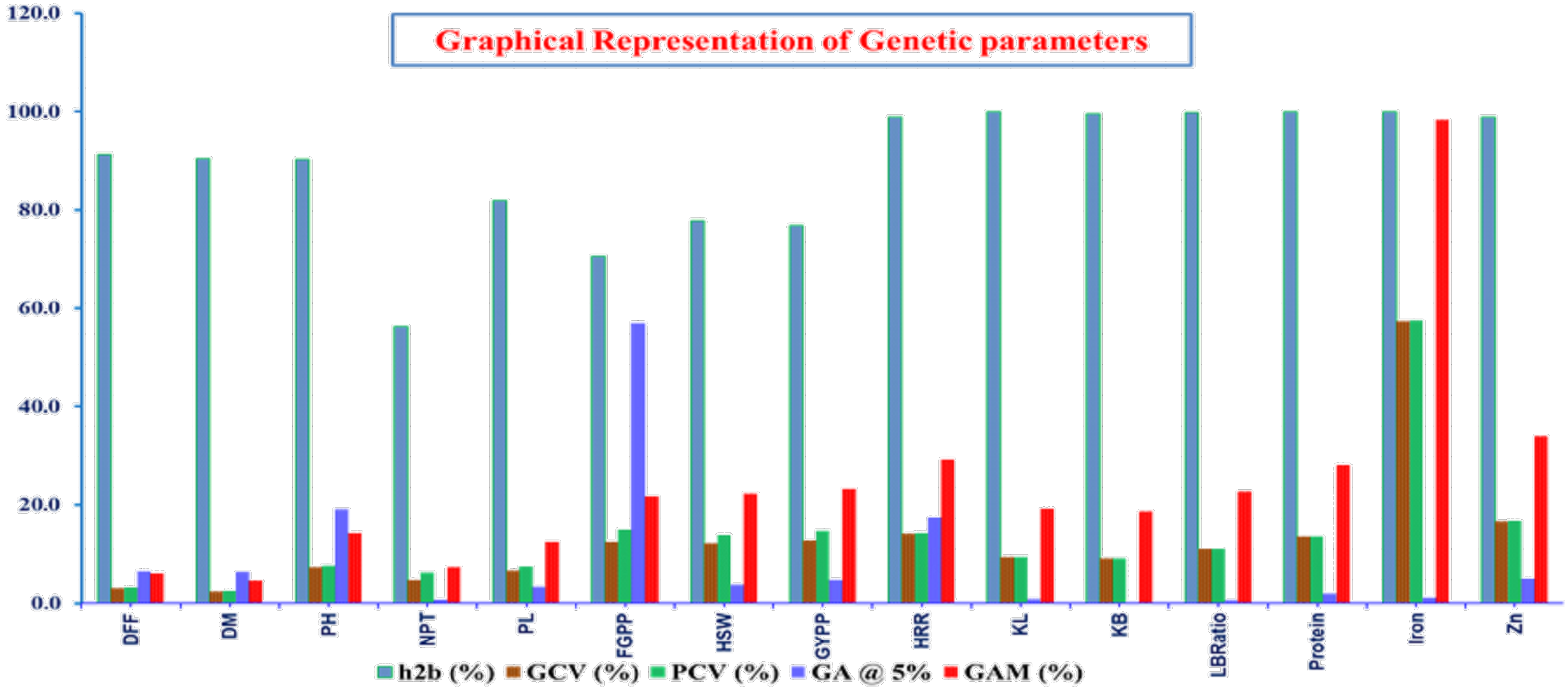
Fig 1: Variability parameters for grain yield and quality traits studied in rice genotypes



Labels: DFF= Days to 50 per cent flowering, DM= Days to maturity, PH= Plant height, NPT= Productive tillers per plant, PL= Panicle length, FGPP= Filled grains per panicle, HSW= 1000-seed weight, GYPP= Grain yield per plant, HRR= Head rice recovery %, KL = Kernel length, KB = Kernel breadth, LB ratio =kernel L/B ratio, Protein=Protein content, Iron = Iron content, Zn = Zinc content.

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