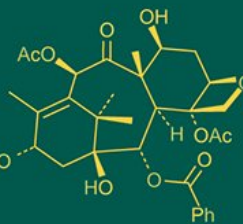


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Genetic variability and selection prospects among upland rice genotypes under Kharif conditions in peninsular India

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Abstract

A field experiment was conducted to quantify genetic variability and selection prospects for yield and associated traits in 40 upland rice (*Oryza sativa* L.) genotypes. The material, comprising EDS, CR Dhan, aerobic rice and CRR lines, was evaluated in a randomized block design with three replications at the Experimental Farm of Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, during Kharif 2025. Genotype effects were highly significant for all 11 traits analyzed, with F-ratios ranging from 3.943 for tillers plant⁻¹ to 192.979 for plant height. Grain yield plant⁻¹ ranged from 2.09 to 5.94 g, and R-IR17A2891 was the best-performing entry. Grain yield showed the highest genotypic coefficient of variation (25.084%), broad-sense heritability (0.969) and genetic advance as percent of mean (50.857%). High heritability coupled with high expected gain was also observed for plant height, test weight, grain length, grain breadth and length/breadth ratio. By contrast, tiller number had moderate heritability (0.455) and the largest GCV–PCV gap, indicating stronger environmental sensitivity. The results demonstrate substantial exploitable variation, but they should be interpreted as single-season, single-location evidence. R-IR17A2891, Hazaridhan and CRR-433-1-1 are proposed as priority entries for multi-environment validation, while selection should emphasize yield itself and complementary traits with stable expression. These findings provide a focused genetic-variability basis for improving upland rice under moisture-limited production conditions.

Keywords: Upland rice; genetic variability; GCV; PCV; broad-sense heritability; genetic advance; grain yield; selection

Introduction

Upland rice is cultivated without standing water and therefore experiences greater dependence on rainfall distribution, soil-water storage and the duration of the effective growing season than irrigated lowland rice. In such environments, breeding progress depends on identifying germplasm with sufficient genetic variation and on distinguishing traits whose phenotypic expression reliably reflects inherited differences. Genetic variability, broad-sense heritability and expected genetic advance are consequently used together to assess the likely response to selection rather than relying on mean performance alone (Seyoum *et al.*, 2012; Demeke *et al.*, 2023) [3, 6]. Grain yield is a complex quantitative character influenced by several component traits and by genotype × environment interaction. A diverse germplasm set can provide alternative combinations of flowering duration, plant stature, panicle architecture and grain attributes from which selection indices may be constructed. Studies in upland and transplanted rice have similarly demonstrated that significant genotype effects and coordinated estimates of variance, heritability and genetic advance are useful for identifying selection targets (Seyoum *et al.*, 2012; Faysal *et al.*, 2022) [4, 6]. The present paper therefore isolates the genetic-variability objective of the thesis and asks: how much variation exists among the 40 entries, which traits are predominantly genetic in expression, and which genotypes merit further validation?

2. Materials and methods

The experiment was conducted during Kharif 2025 at the Experimental Farm of the Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra, India. Forty upland rice genotypes obtained from CRRUS, Hazaribagh, and ICAR-IRRI, Hyderabad, were evaluated in a randomized block design with three replications. Each entry occupied two rows in a 4.5 m × 1.20 m plot, with 30 cm × 5 cm row-to-plant spacing. Recommended agronomic practices were followed throughout the crop season. Five competitive plants per genotype per replication were sampled for observations. This manuscript analyzes the 11 traits for which complete numerical summary tables were available: days to 50% flowering, days to maturity, plant height, tillers plant-1, panicle length, total spikelets panicle-1, test weight, grain length, grain breadth, length/breadth ratio and grain yield plant-1. The thesis methods chapter also describes filled and unfilled spikelets; because complete numerical estimates for those traits were not supplied in the summary tables, they were not reconstructed or included here. The randomized-block model was used to test genotype effects. Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic and phenotypic coefficients of variation (GCV and PCV), broad-

sense heritability (h^2_b) and genetic advance as percent of mean (GA%) were interpreted using the frameworks of Burton and DeVane (1953) [2] and Johnson *et al.* (1955) [5]. In broad-sense form, $h^2_b = \sigma^2_g/\sigma^2_p$. GCV and PCV were calculated as $100\sqrt{\sigma^2_g}/\text{mean}$ and $100\sqrt{\sigma^2_p}/\text{mean}$, respectively. The estimates reported here are transcribed from the thesis summary tables; no raw-plot reanalysis was performed.

3. Results and discussion

3.1 Genotypic differentiation and experimental precision

Genotype mean squares were highly significant for all 11 traits, establishing broad differentiation within the evaluated germplasm. The largest F-ratio occurred for plant height (192.979), followed by grain length (172.910), while tiller number showed the smallest but still highly significant F-ratio (3.943). Grain yield plant-1 had an F-ratio of 93.824. Replication effects were reported as non-significant, supporting the interpretation that the observed differences were primarily associated with genotype rather than block heterogeneity. Similar genotype-level differentiation has been reported in upland rice collections by Seyoum *et al.* (2012) and Demeke *et al.* (2023) [3, 6].

Table 1: Genotype mean squares and F-ratios for the evaluated traits

Trait	Genotype MS	F-ratio	Interpretation
Days to 50% flowering	93.462	89.048	Highly significant
Days to maturity	166.642	71.294	Highly significant
Plant height (cm)	304.738	192.979	Highly significant
Tillers plant-1	3.367	3.943	Highly significant
Panicle length (cm)	22.837	22.585	Highly significant
Total spikelets panicle-1	442.176	74.003	Highly significant
Test weight (g)	92.514	68.329	Highly significant
Grain length (mm)	11.516	172.910	Highly significant
Grain breadth (mm)	0.513	49.290	Highly significant
L/B ratio	1.094	35.059	Highly significant
Grain yield plant-1	3.406	93.824	Highly significant

3.2 Magnitude and nature of variability

The PCV exceeded the GCV for every trait, as expected when environmental variance contributes to phenotypic expression. The GCV–PCV difference was smallest for grain yield, plant height, grain length, flowering time and maturity, suggesting comparatively limited environmental masking at the genotype-mean level. The largest gap occurred for tillers plant-1, for which GCV was 14.416% and PCV was 21.382%; this pattern is consistent with the thesis interpretation that tillering should be selected using replicated progeny means rather than a single observed

value. Grain yield plant-1 had the largest GCV (25.084%), followed by test weight (20.950%) and grain length (20.765%). In practical breeding terms, high GCV indicates substantial relative dispersion, but it does not by itself prove that selection will be effective. The more informative combination is high heritability with high expected gain. In the present population, grain yield, grain length, test weight, plant height, grain breadth and length/breadth ratio met that combined criterion, whereas tiller number combined high GA% with only moderate heritability.

Table 2: Genetic variability parameters and selection interpretation.

Trait	GCV (%)	PCV (%)	h^2_b	GA (% mean)	Selection interpretation
Days to 50% flowering	6.376	6.484	0.967	12.916	High h^2 ; moderate gain
Days to maturity	7.000	7.148	0.959	14.122	High h^2 ; moderate gain
Plant height (cm)	15.228	15.347	0.985	31.127	High h^2 + high gain
Tillers plant-1	14.416	21.382	0.455	30.499	Moderate h^2 ; replicated selection
Panicle length (cm)	11.700	12.486	0.878	22.582	High h^2 + high gain
Total spikelets panicle-1	5.370	5.797	0.858	22.754	High h^2 + high gain
Test weight (g)	20.950	21.412	0.957	42.227	High h^2 + high gain
Grain length (mm)	20.765	20.946	0.983	42.408	High h^2 + high gain
Grain breadth (mm)	14.854	15.309	0.942	29.689	High h^2 + high gain
L/B ratio	17.230	17.971	0.919	34.023	High h^2 + high gain
Grain yield plant-1	25.084	25.486	0.969	50.857	High h^2 + high gain

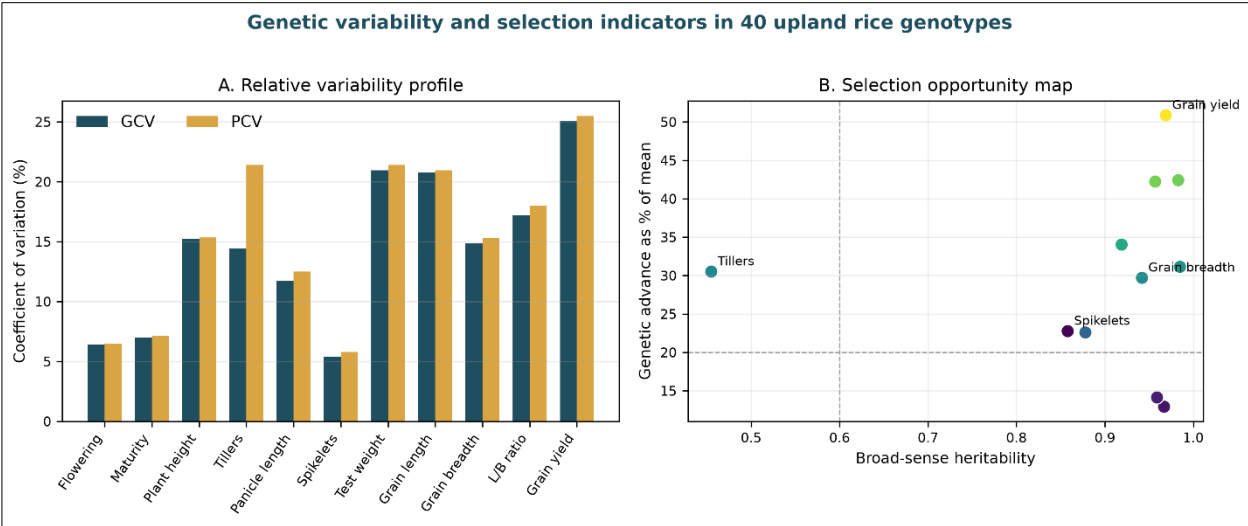


Fig 1: Original visualization derived from the reported thesis summary statistics. Panel A compares GCV and PCV; Panel B maps broad-sense heritability against genetic advance as percent of mean.

3.3 Genotype performance and breeding utility

The genotype means indicated meaningful contrasts for phenology, architecture, grain attributes and yield. Gangavati Ageti was earliest for flowering (71.00 days) and maturity (87.67 days), whereas Sanchuriya Mutant-15 was latest for flowering (97.33 days) and CR Dhan-415 was

latest for maturity (121.67 days). R-IR17A2891 had the highest total spikelet number (124.00) and grain yield (5.94 g plant⁻¹). Hazaridhan combined high yield (5.84 g plant⁻¹) with the longest and broadest grain, while CRR-433-1-1 was among the high-yielding entries and shared the highest mean tiller number with Hazaridhan.

Table 3: Priority genotypes identified from reported genotype means

Genotype	Yield (g plant-1)	Breeding-relevant feature
R-IR17A2891	5.94	Highest yield; highest spikelets (124.00)
Hazaridhan	5.84	High yield; 6.67 tillers; broadest grain (3.55 mm)
CRR-433-1-1	5.82	High yield; 6.67 tillers
CRR-747-3-B	5.51	High-yielding entry
IR19A8130	5.45	High-yielding entry
CR 4437-7-4-4	5.44	High-yielding entry
Gangavati Ageti	5.40	Early flowering and maturity
CR Dhan-808	5.30	High-yielding entry
NDR 2025-3-CP-01	5.27	High-yielding entry
IR24IN1199	5.23	High-yielding entry

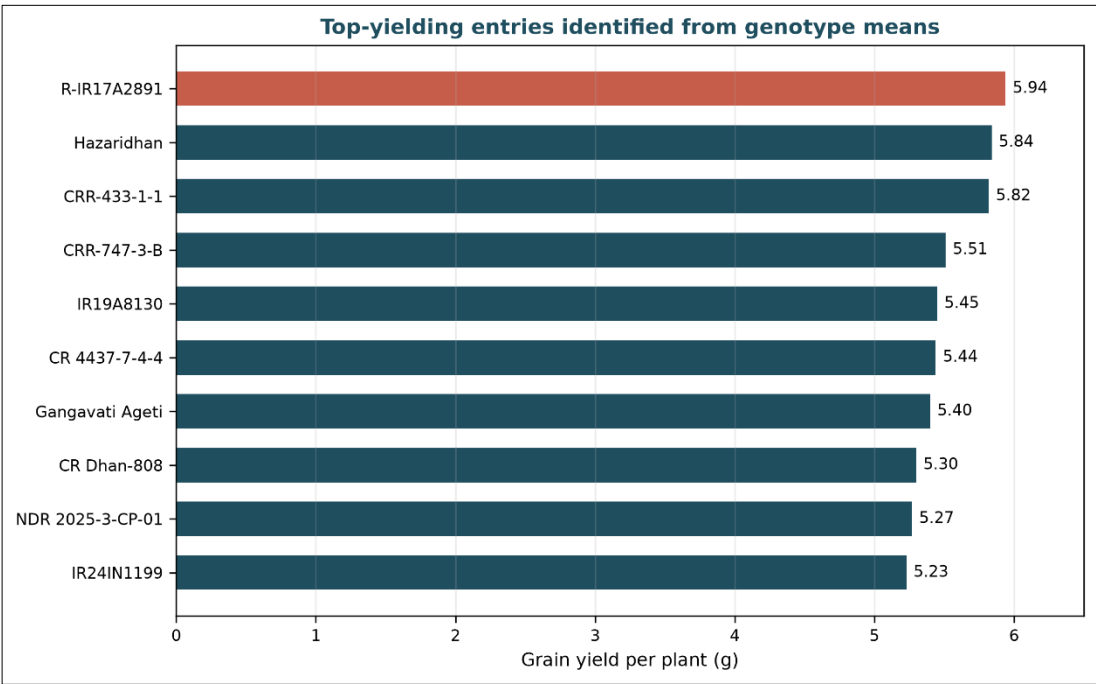


Fig 2: Original ranking visualization of the ten highest-yielding entries reported in the thesis summary. Values are genotype means in g plant⁻¹.

4. Conclusions and breeding implications

The 40-genotype upland rice set contained substantial exploitable variability for all 11 analyzed traits. Grain yield plant⁻¹ was especially promising as a direct selection target because it combined the highest GCV (25.084%), high broad-sense heritability (0.969) and the highest GA% (50.857%). Plant height, grain length, test weight, grain breadth and length/breadth ratio also showed high heritability with high expected gain, although each must be balanced against agronomic and market requirements.

Tiller number requires a different selection strategy: its high GA% should not be interpreted as evidence of stable single-plant expression because heritability was only 0.455 and the PCV–GCV difference was large. In the next breeding cycle, selection should prioritize productive panicles and yield-related sink traits, with tiller number evaluated across replications and environments. R-IR17A2891, Hazaridhan and CRR-433-1-1 should be advanced to multi-location upland trials, but none should be recommended for release or broad cultivation solely on the basis of this one-season experiment.

References

1. Brar DS, Khush GS. Biotechnology for rice breeding: progress and potential impact. In: Plant Breeding Reviews. 2003;24:43-101.
2. Burton GW, DeVane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45:478-481.
3. Demeke B, Dejene T, Abebe D. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza sativa* L.) genotypes at Pawe, northwestern Ethiopia. Cogent Food Agric. 2023;9(1):2157099. doi:10.1080/23311932.2022.2157099.
4. Faysal ASM, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, *et al.* Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. Plants. 2022;11(21):2952. doi:10.3390/plants11212952.
5. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47:314-318. doi:10.2134/agronj1955.00021962004700070009x.
6. Seyoum M, Alamerew S, Bantte K. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). J Plant Sci. 2012;7:13-22. doi:10.3923/jps.2012.13.22.