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ASSESSMENT OF GENETIC VARIATION IN A SUBSET OF 3K PANEL OF DIVERSE RICE ACCESSIONS FOR YIELD AND YIELD RELATED TRAITS

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ABSTRACT

A subset of 3k rice genome panel consisting of 200 accessions was evaluated in an augmented design at Zonal Agricultural and Horticultural Research Station, College of Agriculture, Shivamogga during summer 2023 and at Agricultural and Horticultural Research Station, Kathalagere, Davanagere during Kharif 2024 to analyze genetic variability for yield and yield related traits. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for traits such as single plant yield, number of tillers per plant, number of productive tillers per plant and number of spikelets per panicle in both the environments. Moderate GCV and PCV were recorded for all other traits such as, days to fifty percent flowering, plant height, panicle length, test weight and length-breadth-ratio except spikelet fertility in both the environments. The narrow difference between GCV and PCV for all the traits indicates minimal environmental influence on trait expression. High heritability in association with high genetic advance as a percentage of the mean was observed for all the traits except for spikelet fertility, indicating the predominance of additive gene action and the effectiveness of simple phenotypic selection for these traits. Conversely, low heritability combined with low genetic advance for limited potential for improvement through individual plant selection. Overall, the findings indicate that the experimental material possesses substantial genetic variability, which can be effectively utilized in future crop improvement programs.
***Keywords*:** Variability; rice; 3 k panel; PCV, GCV, heritability.

Introduction

Rice (*Oryza sativa* L.) is a staple starchy cereal that holds a vital role in global diets, particularly across Asia. It serves as a primary food source for nearly half of the world's population, meeting between 40 to 80 % of daily caloric needs in Asian countries, often consumed in 2–3 meals per day. Beyond being a crucial dietary component, rice is also a significant livelihood source for small and marginal farmers. Archaeological evidence suggests rice cultivation in India dates back to 1500–1000 B. C., highlighting its long-standing historical presence. Additionally, rice is deeply rooted in Indian culture, playing a role in traditional festivals and religious practices (Vijay and Roy, 2013). The importance of rice is reflected in its association with the name of the goddess

Annapoorneshwari, who symbolizes nourishment and abundance.

Rice is the third most produced cereal crop globally, following maize and wheat. It is grown on approximately 165.47 million hectares worldwide, resulting in around 515.82 million metric tonnes of milled rice, with over 90 *per cent* of this amount being consumed (Anon., 2024a). The average global per capita rice consumption stands at 53.9 kg annually (Anon., 2024b). China leads in rice consumption with 154.99 million metric tonnes, which surpasses its domestic production of 145.95 million metric tonnes. India ranks as the second-largest rice producer, yielding 135.76 million metric tonnes from 47.83 million hectares. Additionally, India holds the position of the world's top rice exporter, followed by Thailand and Vietnam (Anon., 2024a; Anon., 2024c). But, the demand for rice continues to rise across Asia, where consumption accounts for nearly 90% of global intake. Worldwide projections suggest that rice demand may reach about 650 million tons by 2050 (Chukwu *et al.*, 2019). In India, with the rapidly increasing population, rice production must increase to approximately 121.2 million tons by 2030).

Grain yield, being a complex quantitative trait, is controlled by multiple genes. Although average rice yields have improved over time, the rate of yield increase has recently stagnated. Therefore, enhancing productivity through the effective use of genetic variability within rice germplasm is essential (Islam *et al*., 2025). Sufficient genetic variability is a key requirement for any crop improvement program. Relying solely on phenotypic performance may not yield effective results, as some genotypes might underperform in later segregating generations. Hence, selecting genotypes based on heritability and genetic advance becomes crucial. The genotypic coefficient of variation (GCV) indicates the extent of genetic diversity and represents the heritable fraction of total variability. Combined estimates of genetic variability and heritability help to predict the potential genetic gain achievable through selection (Burton, 1952). Therefore, evaluating variability for yield traits and yield attributes among rice germplasm is vital for developing efficient selection strategies aimed at yield improvement (Akshay *et al*., 2022).

The 3,000 Rice Genomes Project (3K RGP) is a significant global initiative aimed at understanding the genetic diversity of rice (*Oryza sativa* L.) and enhancing rice breeding programs to meet future food demands. The project's importance lies in its comprehensive approach to sequencing 3,024 rice accessions from 89 countries, providing a detailed view of rice genetic diversity and potential for crop improvement. To carry out any plant breeding activity, it should meet two criteria *viz.,* existence of sufficient variability and it should be heritable.

In this context, the present study was carried out on a sub set of 3k RGP comprising of 200 rice accessions to assess variability, heritability and genetic advance for enhancing grain yield and yield related traits.

Materials and Methods

Experimental material and location

The experimental material used was comprised of a subset of 200 diverse rice accessions of 3k panel obtained from Division of Crop Improvement, ICAR-CSSRI, Karnal, Haryana. Germplasm association subset comprised of indica (135), aus (26), trophical (18), aro (8), japonica (6), temperate (5) and admixture (2) rice accessions. Five checks namely, Swarna sub-1, Sahyadri Jalamukthi, Jyothi, Sahyadri Jyothi (Advanced breeding line of Tunga × Jyothi, present in varietal release pipeline) and Sahyadri Kempumukthi. The experiment was laid out for evaluation of yield and yield related traits in two environments viz., Environment-1; ZAHRS Shivamogga, Karnataka, during summer 2024 (E1) and Environment-2; AHRS Kathalagere, Davanagere, Karnataka during Kharif 2024 (E2).

Experimental design and layout

The nursery was established by sowing the seeds of accessions from the association panel. After 25 days, seedlings were manually transplanted into the main field, placing one seedling per hill. The experiment followed an augmented design with ten blocks, each consisting of 20 test entries and five check varieties. Transplanting was done with a spacing of 25 cm between rows and 15 cm between individual plants. Standard agronomic practices and recommended fertilizer doses were followed to ensure healthy crop growth.

Data collection

Days to fifty percent flowering recorded as the number of days taken by each accession from sowing to opening of the first flower in 50 per cent of the plant population. The average value of five randomly selected plants were taken for calculation of nine yield related traits, such as plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, spikelet fertility, test weight and single plant yield. Grain length to breadth ratio was assessed using rice analyser.

Statistical analyses

The analysis of variance for both summer and kharif 2024 for ten traits was carried out using R programme (Version 4.5.1). The mean data of each character was used to partition the variability due to different sources. To assess and quantify the variability among the accessions for the characters under study, estimation of parameters such as the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability in broad sense (h^2), genetic advance as per cent of mean (GAM) were estimated using R Studio (Version 4.5.1).

Structure of ANOVA for Augmented design (Federer, 1956):

Source of variation	Degree of freedom	Mean sum of squares	'F' ratio
Blocks (b)	b-1	$MSS_{(b)}$	$MSS_{(b)}$ /EMSS
Entries(e) (Inbred lines + checks)	e-1	$MSS_{(e)}$	$MSS_{(e)}$ /EMSS
Checks (c)	c-1	$MSS_{(c)}$	$MSS_{(c)}$/EMSS
Inbred lines (i)	g-1	$MSS_{(i)}$	$MSS_{(i)}$ /EMSS
Inbred lines vs checks (ic)	1	$MSS_{(ic)}$	$MSS_{(ic)}$/EMSS
Error	(b-1) (c-1)	EMSS	

Where,

Total Sum of Squares (TSS) = Σ (Observation) ^{2} - CF

Treatments Sum of Squares unadjusted (SST_U) = $[\Sigma Ti^2] /m – CF$

Blocks Sum of Squares unadjusted (SSB_U) = $[\Sigma Bj^2] / s – CF$

Treatments Sum of Squares adjusted (SST_A) = $\Sigma T_i Q_i$

Error SS (SSE) = $TSS - SSB_U - SST_A$

Blocks Sum of Squares adjusted (SSB_A) = $SST_A + SSB_U – SST_U$

Estimation of mean and variability parameters

The following descriptive statistics were computed.

$$\text{Mean} = \Sigma x_i/n$$

Where, x_i = i^{th} observation of a population

n = number of observations

Range: Range was calculated as difference between minimum and maximum value recorded for each character on individual plant. Absolute range and standardized range were calculated using the following formulae.

Absolute range (AR) = Maximum value – Minimum value.

$$\text{Standardized range (SR)} = \frac{\text{Maximum value- Minimum value}}{\text{Mean}}$$

The genotypic and phenotypic coefficients of variation were estimated following the procedures outlined (Lush, 1940)

Genotypic co-efficient of variation (GCV): $\sigma_g/\bar{x} \times 100$

Phenotypic co-efficient of variation (PCV): $\sigma_p/\bar{x} \times 100$

Where,

σ_p = phenotypic standard deviation

σ_g = genotypic standard deviation

$\bar{x}$ = mean

The GCV and PCV values were classified as low (0–10%), moderate (10–20%) and high (>20%).

Heritability in broad sense (h2 (bs)) (Lush, 1945) was calculated by the formula:

$$h^2_{(bs)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 (bs) = heritability (Broad sense) expressed in per cent

σg^2 = genotypic variance

σp^2 = phenotypic variance

The percentage of heritability was classified following the criteria proposed by Robinson *et al.* 1949, where values between 0–30% were considered low, 30–60% as moderate and above 60% as high.

Falconer and Mackay () proposed the formula for estimating genetic advance as a percentage of the mean (GAM) as follows:

$$\text{GAM (\%)} = \frac{\text{Genetic advance (GA)}}{\text{Grand mean (GM)}} \times 100$$

The genetic advance as a percentage of the mean (GAM) was classified according to the criteria proposed by Johnson *et al.* 1955, as low (0–10%), moderate (10–20%) and high (>20%).

Results and Discussion

Analysis of variance

The analysis revealed that, the mean sum of squares (MSS) associated with genotypes were

statistically significant in both the environments, reflecting a strong genetic impact on phenotypic trait expression. This indicates that phenotypic selection could be an effective approach in breeding programs. The studied accessions exhibited substantial variability across the assessed traits. Analysis of variance for ten traits under two environments are presented in Table 1 and Table 2, respectively. Similarly, Adjah *et al*., 2020, Sravani *et al*, 2022 and Ali *et al*., 2025 also reported the similar pattern

Variability parameters

Genetic variability plays a fundamental role in the success of any plant breeding program (Khan *et al*., 2023). Key genetic variability parameters, such as the mean, range (absolute range and standardized range), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2) and genetic advance as a per cent of the mean (GAM) were estimated for ten agronomic traits of both the environments. These results are summarized in Tables 3 and 4, respectively.

Significant variations were observed among all the evaluated lines for the traits studied. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) showed low to high levels across different characters. Among the yield-related traits, single plant yield exhibited the highest PCV (36.53 % in Environment 1 and 32.57 % in environment 2) and GCV (35.98 % in environment 1 and in environment 2) values in both the environments, followed by number of productive tillers per plant and number of tillers per plant, number of spikelets per panicle indicating substantial genetic variability for the above traits among the evaluated rice accessions. Moderate GCV and PCV were recorded for days to fifty percent flowering, plant height, panicle length, test weight and length-breadth-ratio in both the environments, indicating the moderate level of variability existing in this population for these traits. Other traits showed minimal variation. It was observed that there was a narrow or little difference between the PCV and GCV for all traits indicating least effect of environment on these traits of the population studied. These findings are in accordance with the many scientists, who reported high GCV and PCV for various traits in their population such as number of grains per panicle (Ahamed *et al*., 2021), for number of tillers, productive tillers and single plant yield (Demeke *et al*., 2023; Khanal *et al*., 2025), for plant height, number of productive tillers per plant, panicle length and grain yield per plant (Meena *et al*., 2025).

Heritability and genetic advance are crucial factors in selecting desirable traits in rice. While heritability estimates the proportion of total variation that is genetic in origin, genetic advance indicates the potential improvement achievable through selection. These parameters together help to predict the effectiveness of selection for a given trait (Rezk *et al*., 2024; Sao *et al*., 2024; Singh *et al* 2024). Genetic advance serves as an important indicator of the expected progress from selection within a population (Akshay *et al*., 2022; Satturu *et al* 2022; Khan *et al*., 2023; Ali *et al*., 2025). The combination of heritability and genetic advance thus provides valuable insight into the efficiency of selection.

Broad-sense heritability (h^2bs) values were found to be high across all the evaluated traits except for number of spikelets per plant under both the environments. High heritability indicates that selecting superior genotypes based on their phenotypic performance would be effective. Both heritability and genetic advance as a percentage of the mean were high for traits all traits except for number of spikelets per plant. This suggests that additive gene effects play a major role in the inheritance of these traits, making direct selection an efficient approach. Generally, traits showing high heritability coupled with high genetic advance are primarily governed by additive genes and can be improved through simple or progeny selection methods (Roy and Shil, 2020). Whereas, number of spikelets per plant showed low heritability and also low GAM, indicating the trait is under the influence of non-additive and non-fixable part of variation, hence could not poses any opportunity for improvement of this trait in this population.

Conclusion

The analysis of genetic parameters revealed that single plant yield, number of tillers per plant, number of productive tillers per plant and number of spikelets per panicle. Which showed high estimates of GCV, PCV, heritability and genetic advance as a percentage of the mean, indicating that selection for these traits could be highly effective. Other traits except spikelet fertility exhibited moderate GCV and PCV values coupled with high heritability and genetic advance, indicating existence of limited but reasonable opportunity for improvement of these traits.

Table 1: ANOVA for yield and yield attributing traits in association panel in Environment-1 (summer 2024 at Shivamogga)

Source of variation	df	DFF	PH	NT	NPT	PL	NSPP	SF
Entries (Genotypes + Checks)	204	213.67 **	567.51 **	33.54 **	33.35 **	12.11 **	1013.54 **	20.23
Checks	4	858.82 **	2283.78 **	10.45 **	17.78 **	24.01 **	476.40 **	5.80
Genotypes	199	129.71 **	424.10 **	34.11 **	33.83 **	11.28 **	948.95 **	20.51
Genotypes vs. Checks	1	14341.4 **	22241 **	12.32 **	0.05	130.07 **	16015.70 *	22.21
Blocks	9	3.84	5.11	1.36	0.82	0.90	63.08	5.28
Residuals	36	3.65	10.95	1.47	1.48	1.34	136.20	14.89

Source of variation	df	TW	SPY	LBR
Entries (Genotypes + Checks)	204	23.67**	154.75**	0.34**
Checks	4	140.62**	109.47**	0.81**
Genotypes	199	21.30**	145.96**	0.32**
Genotypes vs. Checks	1	26.58**	2085.51**	2.23**
Blocks	9	1.62	1.97	0.01
Residuals	36	1.26	4.41	0.01

Note:
DFF= Days to 50% flowering (days) PH= Plant height (cm) NT= Number of tillers (No.)
NPT= Number of productive tillers (No.) PL= Panicle length (cm) NSPP= Number of spikelets per plant (No.)
SF= Spikelet fertility (%) TW= Test weight (g) SPY= Single plant yield (g)
LBR= Length to breadth ratio

Table 2: ANOVA for yield and yield attributing traits in association panel in Environment-2 (*Kharif* 2024 at Kathalagere)

Source of variation	df	DFF	PH	NT	NPT	PL	NSPP	SF
Entries (Genotypes + Checks)	204	199.52**	523.46**	32.23**	32.06**	23.47**	1112.88**	11.70
Checks	4	849.53**	2338.79**	13.27**	19.33**	19.45**	572.14*	5.93
Genotypes	199	121.90**	402.90**	32.76**	32.39**	20.81**	1027.84**	11.48
Genotypes vs. Checks	1	13046.54**	17254.17**	2.86	16.27**	567.99**	20198.19**	79.50*
Blocks	9	7.28	8.66	1.42	1.56	2.10	61.52	2.71
Residuals	36	4.03	15.36	1.68	1.78	1.62	157.12	12.44

Source of variation	df	TW	SPY	LBR
Entries (Genotypes + Checks)	204	24.47**	123.32**	0.37**
Checks	4	133.68**	112.74**	0.80**
Genotypes	199	22.29**	120.73**	0.34**
Genotypes vs. Checks	1	21.29**	681.15**	5.52**
Blocks	9	1.43	4.58	0.10
Residuals	36	0.96	5.69	0.01

* P <= 0.05; ** P <= 0.01

Note:
DFF= Days to 50% flowering (days) PH= Plant height (cm) NT= Number of tillers (No.)
NPT= Number of productive tillers (No.) PL= Panicle length (cm) NSPP= Number of spikelets per plant (No.)
SF= Spikelet fertility (%) TW= Test weight (g) SPY= Single plant yield (g)
LBR= Length to breadth ratio

Table 3: Descriptive statistics for yield and yield attributing traits of association panel in Environment-1 (summer 2024 at Shivamogga)

SL. No.	Trait	Mean±SE	Range		Standardized range (SR)	Absolute range (AR)	GCV (%)	PCV (%)	h^2(bs)	GAM (%)
			Minimum	Maximum						
1	DFF	82.71±0.81	57.98	116.6	0.71	58.62	13.58	13.77	97.18	27.61
2	PH	114.2±1.45	65.67	193.4	1.12	127.73	17.8	18.03	97.42	36.24
3	NT	18.17±0.41	6.31	34.04	1.53	27.73	31.44	32.14	95.69	63.45
4	NPT	17.22±0.4	5.79	32.66	1.56	26.87	33.02	33.77	95.62	66.61
5	PL	25.32±0.23	14.21	36.61	0.88	22.4	12.45	13.27	88.10	24.11
6	NSPP	105.74±2.15	56.20	282.27	2.14	226.6	26.96	29.13	85.65	51.47
7	SF	92.11±0.32	67.58	99.82	0.35	32.24	2.57	4.92	27.40	2.78
8	TW	25.01±0.33	12.89	34.86	0.88	21.97	17.9	18.45	94.10	35.82
9	SPY	33.07±0.84	8.06	68.46	1.83	60.4	35.98	36.53	96.98	73.09
10	LBR	3.05±0.04	2.06	4.86	0.92	2.8	18.49	18.58	99.03	37.96

Note:
DFF= Days to 50% flowering (days) PH= Plant height (cm) NT= Number of tillers (No.)
NPT= Number of productive tillers (No.) PL= Panicle length (cm) NSPP= Number of spikelets per plant (No.)
SF= Spikelet fertility (%) TW= Test weight (g) SPY= Single plant yield (g)
LBR= Length to breadth ratio

Table 4: Descriptive statistics for yield and yield attributing traits of association panel in Environment-2 (*Kharif* 2024 at Kathalagere)

Sl. No.	Trait	Mean±SE	Range		Standardized range (SR)	Absolute range (AR)	GCV (%)	PCV (%)	h^2(bs)	GAM (%)
			Minimum	Maximum						
1	DFF	84.23±0.79	63.44	117.3	0.64	53.86	12.89	13.11	96.69	26.15
2	PH	113.49±1.41	51.83	191.12	1.23	139.29	17.35	17.69	96.19	35.1
3	NT	18.81±0.39	7.44	32.64	1.35	25.30	29.74	30.43	94.88	59.57
4	NPT	17.15±0.4	6.01	32.31	1.53	26.30	32.26	33.18	94.50	64.69
5	PL	24.28±0.32	15.05	34.72	0.81	19.67	18.04	18.79	92.19	35.74
6	NSPP	105.26±2.23	52.46	290.12	2.25	237.66	28.00	30.46	84.71	53.23
7	SF	92.94±0.24	71.24	98.73	0.30	27.49	2.36	3.65	28.99	2.07
8	TW	25.29±0.33	14.25	36.03	0.86	21.78	18.26	18.67	95.69	36.85
9	SPY	33.75±0.76	9.76	68.14	1.73	58.38	31.79	32.57	95.29	64.02
10	LBR	3.06±0.04	2.05	5.02	0.97	2.97	18.73	18.92	98.03	38.26

Note:
DFF= Days to 50% flowering (days) PH= Plant height (cm) NT= Number of tillers (No.)
NPT= Number of productive tillers (No.) PL= Panicle length (cm) NSPP= Number of spikelets per plant (No.)
SF= Spikelet fertility (%) TW= Test weight (g) SPY= Single plant yield (g)
LBR= Length to breadth ratio

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