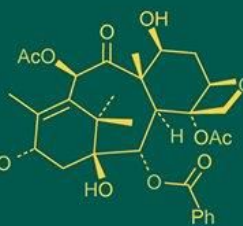


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Genetic variability, correlation and diversity analysis for yield and related traits among advanced breeding lines of rice (*Oryza sativa* L.)

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Abstract

A field experiment was conducted during *Rabi* 2024-25 at the Agricultural Research Station, Kampasagar, to evaluate 126 rice genotypes along with six checks under irrigated conditions using an augmented block design. Observations were recorded for days to 50% flowering, plant height, panicle length, number of productive tillers, and grain yield. Analysis of variance revealed significant differences among genotypes, indicating substantial genetic variability. High heritability coupled with high genetic advance was observed for grain yield, plant height, and number of productive tillers, suggesting the predominance of additive gene action and the effectiveness of direct selection. Correlation analysis showed a significant positive association of days to flowering with plant height and panicle length, while grain yield exhibited non-significant relationships with other traits, indicating its complex nature. Cluster analysis grouped genotypes into six distinct clusters, reflecting considerable genetic diversity. Cluster III recorded the highest grain yield, whereas cluster VI showed balanced performance across traits. The results highlight the presence of exploitable genetic variability and emphasize the potential for selecting superior genotypes for yield improvement and future breeding programs.

Keywords: Correlation, diversity, yield, rice

Introduction

Rice (*Oryza sativa* L.) belongs to the Poaceae family, tribe Oryzae, and genus *Oryza*. It is a diploid species ($2n = 24$) with a genome size of 430 Mb and is widely recognized as the most important cereal crop (Devi *et al.*, 2025) ^[9]. As a predominant staple food, more than half of the world's population consumes rice daily (Ngangkham *et al.*, 2018) ^[19]. In developing countries, rice contributes 27% of dietary calories, 20% of dietary protein, and 3% of dietary fats. Rice is prone to a range of abiotic stresses like drought, salinity, flooding, temperature extremes and heavy metal stress; to name a few and all of these have an impact on plant growth and yield (Bindu *et al.*, 2022) ^[4].

Climate change and abiotic stresses are further reshaping agricultural landscapes (Kylash *et al.*, 2023) ^[15] and even conversion of highly productive rice lands for industrial and residential purposes has forced cultivation into less favorable areas such as saline, drought-prone, and flood-prone regions (Kylash *et al.*, 2025) ^[14]. To meet the challenges of population growth, climate change, and limited arable land, rice production must be expanded by increasing yield potential. Yield in rice is a complex quantitative trait governed by genotype, environment, management practices, and their interactions (Chandramohan *et al.*, 2025) ^[7].

Genetic variation is important for any breeding material, as it not only provides selection, but also valuable information on the selection of different parents for hybridization programs. Phenotypic variability refers to the observed differences among individuals for a trait, arising from both genetic variation and environmental factors. In breeding programs, the genotypic coefficient of variation and phenotypic coefficient of variation quantify this variability: GCV reflects the genetic portion, while PCV captures the total observed variation, including environmental influences. Understanding grain yield's heritability and genetic variability is a prerequisite for successful breeding. High heritability suggests that genetic factors strongly

influence the trait, making selection more reliable; conversely, low heritability indicates that environmental effects have a greater impact (Chacko *et al.*, 2023) ^[6]. Traits that exhibit high heritability coupled with substantial genetic advance are most likely governed by additive gene action and are strong candidates for effective selection. Such knowledge broadens the gene pool and guides breeders in efficiently transferring desirable traits to future generations (Islam *et al.*, 2025) ^[13].

To accelerate rice improvement, it is crucial to examine phenotypic variation in exotic and native germplasms. Identifying new genes and assessing morphological traits are essential for evaluating genetic variability and trait associations, particularly for developing varieties suited to coastal and stress-prone regions (Alam *et al.*, 2025) ^[2]. The presence of sufficient genetic variability, coupled with knowledge of character associations and relative contributions to yield, forms the foundation of any breeding program. Heritability and genetic advance are key selection parameters, offering predictive value for genetic gain under effective selection (Bisne *et al.*, 2009) ^[5].

Therefore, the present investigation was undertaken to estimate genetic parameters, character associations, in a set of 126 genotypes with 6 checks, with the goal of developing high-yielding, stress-tolerant rice varieties.

Materials and Methods

This study evaluated 126 promising rice lines, with 6 checks KPS-2874, DRR Dhan 44, US 312, Sambha mahsuri, IR 64, and KNM-118 under irrigated conditions at Agricultural Research Station, Kampasagar during *Rabi*, 2024-25. The experiment was conducted using an Augmented Block Design (ABD) with a plant spacing of 20 × 15 cm. Check varieties were replicated across blocks to control for environmental variation, while test genotypes were unreplicated. Standard crop management practices and necessary precautions were followed to ensure optimal crop growth. Observations were taken on traits such as days to

50% flowering, plant height, panicle length, number of productive tillers, and grain yield. Phenotypic and genotypic correlation coefficients among traits were calculated following Falconer (1981) ^[11]. Direct and indirect effects of yield components on single plant yield were estimated through path coefficient analysis based on methods by Wright (1921) ^[28] and Dewey and Lu (1959) ^[8], using grain yield as the dependent variable. Genetic divergence was estimated by Mahalanobis’ D2 statistics (1936) on 10 quantitative traits. The genotypes were grouped into a number of clusters by Tocher’s method described by Rao (1952) ^[23].

All statistical analyses were performed in R statistical software (Posit Team, 2025) utilizing packages such as ' augmented RCBD ' for analysis of variance, ‘metan’ for correlation, and path coefficient calculations.

Results and Discussion

The augmented design ANOVA revealed highly significant differences across most sources of variation. Block effects were highly significant for all traits, indicating strong environmental heterogeneity across blocks. Treatment effects were also highly significant, confirming substantial genetic variability among the entries. The checks showed very high significance across traits, reflecting consistent differences among the standard checks (Table 1). Test entries and their comparison with checks were significant for most traits, with particularly strong effects for days to flowering (DFF), plant height (PH), panicle length (PL), and grain yield (GY), while number of productive tillers (NPT) showed moderate significance. The significance of test entries and their comparison with checks indicates that several test genotypes performed differently from the standard checks, especially for yield-related traits, suggesting potential for selection Residual variance was very low across traits, suggesting high precision of the experiment and reliable estimates of treatment differences.

Table 1: ANOVA-Based Assessment of Genotypic Performance of for test entries studied

Source	DF	DF	PH	PL	NPT	GY
Block (ignoring Treatments)	2	51.98**	430.46**	1.54**	10468.20**	18294774.22**
Treatment (eliminating Blocks)	131	38.68**	184.64**	2.27**	3578.72**	2114519.55**
Treatment: Check	5	126.19**	431.55**	1.07**	17415.53**	1342506.00**
Treatment: Test and Test vs. Check	126	35.21**	174.85**	2.32**	3029.64*	2145155.01**
Residuals	10	0.74	2.23	0.17	784.41	38812.80

Table 2: Genetic Parameter Estimates for Yield and Yield-Related Traits

Trait	Mean	GCV	PCV	ECV	hBS	GA	GAM
DFF	109.4	5.23	5.28	0.79	97.78	11.66	10.66
PH	109.85	12.13	12.21	1.36	98.76	27.32	24.87
PL	22.54	6.54	6.79	1.82	92.82	2.93	13
NPT	364.57	13.2	15.27	7.68	74.7	85.81	23.54
GY	4232.5	36.72	37.01	4.65	98.42	3180.86	75.15

Table 3: Trait Associations Based on Correlation Analysis for Yield and Yield-Related Traits

	DFF	NPT	PH	PL	GY
DFF	1 ***	-0.011 ns	0.209 *	0.182 *	0.137 ns
GY	0.137 ns	0.112 ns	0.057 ns	-0.01 ns	1 ***
NPT	-0.011 ns	1 ***	0.066 ns	0.1 ns	0.112 ns
PH	0.209 *	0.066 ns	1 ***	0.026 ns	0.057 ns
PL	0.182 *	0.1 ns	0.026 ns	1 ***	-0.01 ns

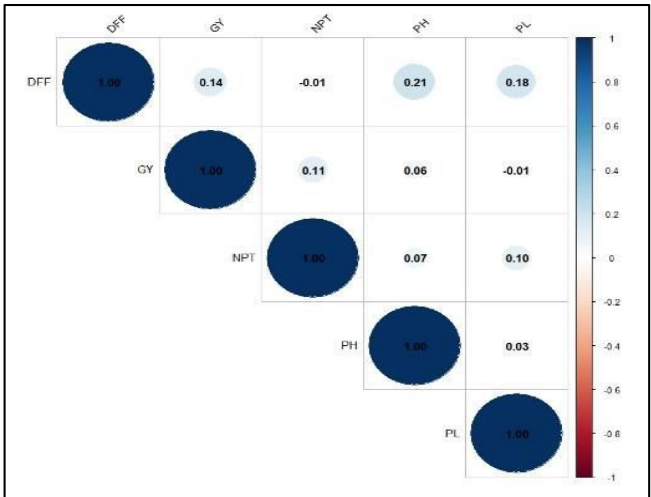


Fig 1: Heatmap of Correlation coefficients for test entries studied

Heritability is the ratio of genotypic variance to total or phenotypic variance (Broad sense) and the ratio of additive genetic variance to phenotypic variance (Narrow sense). Genetic advance is the improvement in the mean genotypic value of selected plants over the parental population. A character's heritability tells us how easily it can be passed down to subsequent generations. The reliability of phenotypic value is expressed using heritability estimates as a forecasting tool. This term "genetic advance" refers to the amount of genetic gain that has occurred as a result of selection. The heritability for which traits was under examination determines the effectiveness of genetic advances under selection. Even when the feature is lesser impacted with environmental influences, selection for enhancement of such characters could not be successful since heredity is based on total genetic variation, which comprises fixable (additive) and non-fixable (dominance and epistatic) variation.

Genetic parameter estimates revealed considerable variability among traits. GY recorded a mean of 4232.5 kg/ha with high GCV (36.72%), PCV (37.01%), coupled with high h^2 (98.42%) and GAM (75.15%), indicating strong selection potential (table 2). NPT showed moderate GCV (13.2%) and PCV (15.27%) with high h^2 (74.7%) and GAM (23.54%), suggesting additive gene action. PH also exhibited moderate variability (GCV = 12.13%, PCV = 12.21%) with very high h^2 (98.76%) and high GAM (24.87%), indicating reliable selection. PL and DFF showed low GCV and PCV but high h^2 (>90%) with moderate GAM, suggesting limited variability but effective selection due to high heritability. The close correspondence between GCV and PCV across traits indicates minimal environmental influence, further strengthening the reliability of genetic estimates.

Similar findings of variability were reported by Nithya *et al.*, (2020) [20] and Akhil *et al.*, (2025) [1] for plant height. Akhil *et al.*, (2025) [1] and Saha *et al.*, (2019) [24] for panicle length, Sharmila *et al.*, (2025) [25] for number of productive tillers and days to 50% flowering. High heritability coupled with high genetic advance as percent of mean was reported by Dhruv *et al.*, (2025) [10] for plant height, Shashidhara *et al.*, (2025) [26] for plant height, and number of productive tillers and grain yield, high heritability with moderate genetic advance as percent of mean by Gupta *et al.*, (2021) [12] for panicle length, and High heritability coupled with moderate genetic advance as percent of mean for days to 50% flowering by Shashidhara *et al.*, (2025) [26].

The high heritability coupled with high GAM observed for grain yield, number of productive tillers, and plant height suggests that these traits are predominantly governed by additive gene effects, making them highly amenable to direct selection in breeding programs. Grain yield, in particular, demonstrated substantial genetic variability, indicating that significant genetic gains can be achieved through selection. The medium GAM values for panicle length and days to flowering, despite their high heritability, imply that non-additive gene action may play a role, and selection for these traits may require larger populations or multiple cycles to achieve meaningful improvement.

The correlation analysis revealed varying degrees of association among the studied traits. Days to flowering (DFF) showed a significant positive correlation with plant height (PH, $r = 0.209$) and panicle length (PL, $r = 0.182$), suggesting that later flowering genotypes tend to be taller

and have longer panicles (table 3; Figure 1). However, DFF had no significant relationship with grain yield (GY) or number of productive tillers (NPT). The significant positive associations of DFF with PH and PL suggest that genotypes with delayed flowering may allocate more time to vegetative growth, resulting in taller plants and longer panicles. Muthuvijayaragavan and Murugan (2020) [17] Shrivatsav *et al.* (2020) [27] reported a positive significant association of days to flowering with plant height, while Narayanan *et al.* (2019) [18] Shrivatsav *et al.* (2020) [27] reported it with panicle length. This relationship can be useful in breeding programs where plant architecture traits are considered alongside flowering behavior. However, the absence of significant correlation between GY and other traits indicates that yield is influenced by complex interactions beyond these individual parameters, possibly involving physiological efficiency, stress tolerance, or other yield components not captured here. The weak and non-significant correlations among NPT, PH, and PL imply that these traits vary independently, offering opportunities for simultaneous improvement without strong trade-offs.

Table 4: Intra and Inter-cluster distances for the genotypes studied

	C1	C2	C3	C4	C5	C6
C1	0.50	6.26	5.19	5.80	4.78	5.76
C2		4.83	2.67	2.38	2.55	2.01
C3			4.79	2.41	2.33	1.71
C4				4.75	2.12	2.05
C5					4.81	1.58
C6						4.83

Table 5: Cluster mean values for the genotypes studied

Cluster	DFF	GY	NPT	PH	PL
1	124.6667	5070.833	427.3628	109.1422	29.49944
2	102.9598	3650.506	343.9538	95.09728	22.30674
3	111.559	5626.389	435.0325	109.3798	22.31227
4	108.4042	2318.633	396.0948	119.5942	22.28144
5	114.9444	3971.543	321.2528	113.1468	23.25432
6	108.5611	5134.867	341.9229	115.084	22.03191

Diversity is an effective tool which aids in the selection of genetically divergent parents to be used in hybridization programme for obtaining high heterosis and superior segregants. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. The cluster analysis grouped the genotypes into six distinct clusters with varying sizes (figure 2). Cluster 1 was the smallest, containing only 2 genotypes, while Cluster 6 was the largest with 30 genotypes. Clusters 2, 3, and 5 were moderately sized, comprising 29, 24, and 27 genotypes respectively, whereas Cluster 4 included 20 genotypes. The presence of both small and large clusters suggests considerable genetic variability within the population. The small Cluster 1 may represent highly distinct genotypes with unique trait combinations, making them potential candidates for use in breeding programs to broaden the genetic base. Larger clusters such as Cluster 6 and Cluster 2 indicate groups of genotypes with similar characteristics, which could be useful for identifying stable and consistent performers.

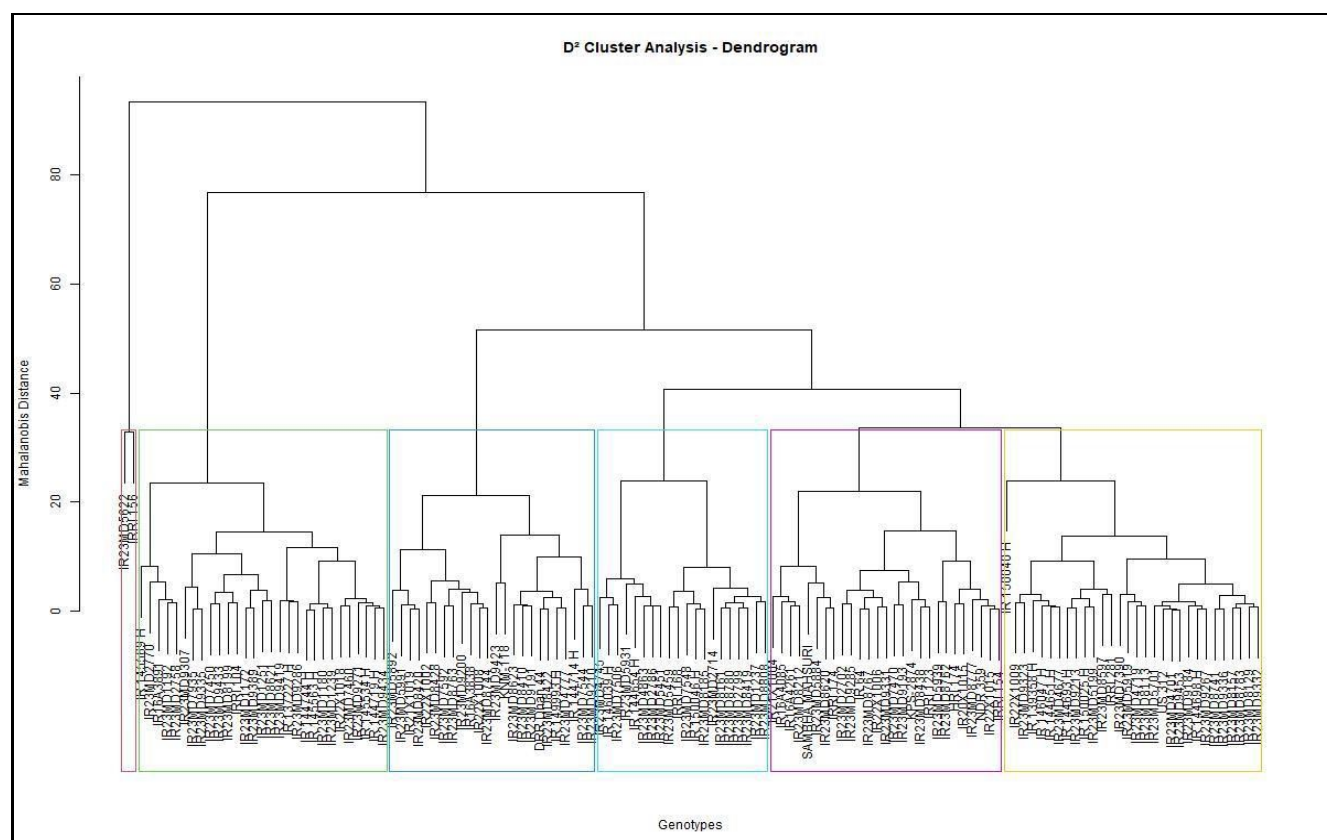
The cluster means (table 5) highlights that cluster 3 has the highest grain yield and strong productivity traits, making it the best performer. Cluster 1 shows late maturity and the longest panicle length, while cluster 4 has the tallest plants

and cluster 2 with shortest plants but with lowest yield. Cluster 2 consistently records the lowest values, suggesting weaker performance. Cluster 5 has the lowest number of productive tillers, and cluster 6 demonstrates balanced traits with high yield and good plant height. Together, these results suggest cluster 3 as the most promising for yield, cluster 6 as a balanced central group, and cluster 1 as structurally advantageous but distinct. Shashidhara *et al.*, (2025) also reported a similar clustering pattern into 6 clusters while studying advanced breeding lines.

This study revealed substantial variation across all the traits examined in the advanced breeding lines of rice. The presence of wide genetic diversity indicates that these lines

hold considerable potential for improvement. Importantly, most traits exhibited high heritability coupled with a high genetic advance as a percentage of the mean, suggesting that the observed differences are largely due to additive genetic effects rather than environmental influence.

Such a genetic pattern implies that these traits are stable and can be effectively fixed through selection. In other words, the inheritance of these characteristics is reliable, and breeders can expect consistent improvement when selecting for them. Therefore, focusing on these traits in breeding programs would be highly beneficial, as it would accelerate genetic gain and contribute to the development of superior rice varieties.



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