



Multivariate Genetic Diversity, Morphological Characterization, Correlation and Path Coefficient Analysis of Rice (*Oryza sativa* L.) Germplasm

Dhamarasingu Gayathri ^{a*}, Ayodhya Prasad Pandey ^a,
Madduri Usha Sri ^a, Guntupalli Akhilesh ^a, Rajbeer Singh Gaur ^a
and Bineeta Singh ^a

^a Department of Genetics and Plant Breeding, AKS University, Satna, MP 485001, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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Abstract

Rice (*Oryza sativa* L.) improvement depends on the effective utilisation of diverse germplasm and the identification of key yield-contributing traits. The present study evaluated 25 genetically diverse rice germplasm accessions during *Kharif* 2025 using multivariate genetic diversity, DUS-based morphological characterisation, correlation, and path coefficient analyses. The experiment was conducted in a CRBD with three replications, and observations were recorded for 10 qualitative and 11 quantitative traits. Analysis of variance revealed highly significant differences among the genotypes for all quantitative traits, indicating substantial genetic variability. Grain yield per plant exhibited a strong positive association with biological

*Corresponding author: E-mail: dhamarasingugayathri@gmail.com;

yield per plant ($r = 0.99$) at both the genotypic and phenotypic levels. Path coefficient analysis identified biological yield per plant (0.92) as the most influential trait, with the highest positive direct effect on grain yield. Mahalanobis D^2 analysis grouped the genotypes into six distinct clusters, with the maximum inter-cluster distance observed between Clusters II and VI (44.21), indicating their potential value in hybridisation programmes. DUS characterisation revealed considerable qualitative variation that facilitated varietal identification and germplasm differentiation. The findings identified promising and genetically diverse germplasm accessions that may provide useful parental material for yield improvement and the broadening of the genetic base of future rice-breeding populations.

Keywords: Rice (*Oryza sativa* L.); genetic diversity; Mahalanobis' D^2 ; DUS characterization; correlation analysis; path coefficient analysis; grain yield.

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops and serves as the staple food for more than half of the world's population. It plays a crucial role in global food and nutritional security by providing a substantial proportion of dietary energy and protein. In India, rice is cultivated across diverse agro-climatic regions and contributes significantly to agricultural production and rural livelihoods. Despite remarkable progress in rice improvement, increasing food demand, climate change, and the narrowing genetic base of modern cultivars necessitate the continuous exploration and utilisation of diverse rice germplasm for sustainable yield enhancement (Fukagawa & Ziska, 2019; Department of Agriculture & Farmers Welfare, 2026).

Rice germplasm is an important source of genetic variability for yield, adaptation, and other agronomic traits. Morphological characterisation is the first step in germplasm evaluation because it facilitates the identification, conservation, and effective utilisation of genetically diverse accessions. Likewise, estimating genetic variability through parameters such as GCV, PCV, heritability, and genetic advance provides valuable information on the extent of heritable variation and the effectiveness of selection for crop improvement (Burton & DeVane, 1953; Johnson *et al.*, 1955).

Recent investigations have shown that combining agro-morphological characterization with estimates of genetic variability and multivariate diversity can improve the identification of promising parental material and yield-associated traits in rice germplasm (Parikh *et al.*, 2025; Sar *et al.*, 2024; Pathak *et al.*, 2024).

Grain yield is a complex quantitative trait governed by several interrelated characters. Therefore, understanding the associations between grain yield and its component traits is essential for developing efficient selection strategies. Correlation coefficient analysis reveals the strength and direction of relationships among characters, whereas path coefficient analysis partitions these relationships into direct and indirect effects, thereby identifying the traits with the greatest influence on grain yield (Dewey & Lu, 1959). Furthermore, multivariate genetic diversity analysis using Mahalanobis' D^2 statistic provides an effective approach for identifying genetically divergent parents that can be used in hybridisation programmes to generate superior recombinants and broaden the genetic base of breeding populations. Evidence from traditional rice landraces also indicates that correlation and path coefficient analyses can distinguish yield components with meaningful direct and indirect effects, thereby supporting trait-based selection in breeding programmes (Deepika *et al.*, 2026).

Although recent studies have reported genetic variability, trait association, path analysis, genetic divergence, and DUS characterization in rice, these approaches are often evaluated separately. Recent reports have demonstrated the usefulness of variability and correlation analyses for identifying yield-related traits, multivariate approaches for quantifying genetic divergence, and DUS descriptors for distinguishing rice germplasm. However, an integrated evaluation combining DUS-based qualitative characterization, genotypic and phenotypic correlation, path coefficient analysis, and Mahalanobis' D^2 -based diversity assessment in a common set of improved cultivars, breeding derivatives, and aromatic landraces under the agro-climatic conditions of Central India remains limited. Such integration is useful because it simultaneously identifies phenotypically distinct germplasm, important yield-contributing traits, and genetically divergent parental combinations. The present study was therefore designed to address this gap and provide a unified basis for parental selection and rice improvement.

Therefore, the present investigation was undertaken with the following objectives: (i) to characterise 25 rice germplasm accessions using DUS-based qualitative morphological descriptors; (ii) to assess the extent of variation and relationships among yield and yield-contributing traits through ANOVA, genotypic and phenotypic correlation, and path coefficient analyses; and (iii) to quantify multivariate genetic divergence using Mahalanobis' D^2 statistic and identify genetically diverse and agronomically promising parental lines for future rice improvement programmes.

2. Materials and Methods

The present investigation was conducted during the *Kharif* 2025 season at the Research Farm, Department of Genetics and Plant Breeding, AKS University, Satna, Madhya Pradesh, India. The experiment was laid out in a Complete Randomised Block Design (CRBD) with three replications. The experimental material consisted of 25 genetically diverse rice (*Oryza sativa* L.) germplasm accessions representing improved cultivars, advanced breeding lines, and indigenous aromatic landraces. The genotypes originated from major rice-breeding programmes in India, including ANGRAU, Andhra Pradesh; Professor Jayashankar Telangana State Agricultural University (JTSAU), Telangana; Indira Gandhi Krishi Vishwavidyalaya (IGKV), Chhattisgarh; and traditional landraces collected from Chhattisgarh and Central India. The collection represented a broad genetic background comprising indica rice cultivars, high-yielding breeding derivatives (e.g., the MTU, WGL, RNR, JGL, NLR, and RDR series), and locally adapted aromatic landraces such as Dubraj, Nagri Dubraj, Dev Bhog, and Jeera Sankar. This diverse genetic constitution was selected to maximise phenotypic variation and facilitate a comprehensive evaluation of morphological diversity, trait associations, and genetic divergence among rice genotypes.

Observations were recorded for 10 qualitative morphological descriptors and 11 quantitative agronomic traits. Morphological characterisation of the rice germplasm was performed using DUS (Distinctness, Uniformity, and Stability) descriptors for rice, following the PPV&FRA Test Guidelines, which are primarily based on the standardised descriptors developed by the International Board for Plant Genetic Resources (IBPGR). Quantitative observations comprised days to 50% flowering, plant height, effective tillers per plant, days to maturity, spikelets per panicle, panicle length, test weight, grain length, biological yield per plant, harvest index, and grain yield per plant. Five randomly selected competitive plants from each genotype in every replication were used to record quantitative observations, whereas days to 50% flowering and days to maturity were recorded on a plot basis.

Analysis of variance (ANOVA) was performed following Panse and Sukhatme (1967). Genotypic and phenotypic correlation coefficients were computed following Searle (1961), whereas path coefficient analysis was conducted using the method proposed by Dewey and Lu (1959), with grain yield per plant as the dependent variable. Genetic diversity among the genotypes was estimated using Mahalanobis' D^2 statistic (Mahalanobis, 1936), and the genotypes were clustered using Tocher's method (Rao, 1952). All statistical analyses were performed using INDOSTAT software.

3. Results and Discussion

3.1 Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) revealed highly significant ($P \leq 0.01$) differences among the 25 rice genotypes for all 11 quantitative traits, demonstrating substantial genetic variability in the experimental material (Table 1). Treatment mean squares were consistently greater than the corresponding error mean squares for all characters, indicating that the observed variation was predominantly attributable to genetic differences rather than environmental influences. Among the evaluated traits, the highest treatment mean square was recorded for the number of spikelets per plant (1721.46), followed by plant height (700.74 cm), biological yield per plant (553.68 g), days to maturity (394.94), days to 50% flowering (340.69), and grain yield per plant (155.96 g), indicating exploitable genetic variability for these traits.

The highly significant variation among genotypes for all quantitative traits suggests that the evaluated germplasm possesses a broad genetic base, which is essential for effective selection and genetic improvement. Similar findings were reported by Bhargava *et al.* (2021), Demeke *et al.* (2023), Singh *et al.* (2024), and Islam *et*

al. (2025), who also observed highly significant differences among rice genotypes for yield and yield-contributing traits, indicating substantial genetic variability for crop improvement.

3.2 Genotypic and Phenotypic Correlation Analyses

The genotypic and phenotypic correlation coefficients among the 11 quantitative traits are presented in Tables 2 and 3, respectively. The direction of association for most characters was similar at both the genotypic and phenotypic levels; however, the magnitudes of the genotypic correlations were generally higher than those of the corresponding phenotypic correlations, indicating that environmental factors reduced the expression of the underlying genetic relationships among the traits. This pattern suggests that the observed associations were predominantly under genetic control and could therefore be effectively exploited in selection programmes.

Grain yield per plant, the principal economic trait, exhibited a highly significant and strong positive correlation with biological yield per plant at both the genotypic ($r = 0.99$) and phenotypic ($r = 0.99$) levels, indicating that biomass production was the major determinant of grain yield in the present investigation. In addition, grain yield showed positive associations with grain length (0.22 and 0.22), number of effective tillers per plant (0.18 and 0.16), test weight (0.17 and 0.14), panicle length (0.06 and 0.07), plant height (0.06 and 0.08), and days to maturity (0.05 and 0.04) at the genotypic and phenotypic levels, respectively. Although these associations were non-significant, they suggest that the simultaneous improvement of these component traits may contribute favourably to grain-yield enhancement. Conversely, grain yield exhibited highly significant negative genotypic associations with harvest index (-0.87) and number of spikelets per plant (-0.45); the corresponding phenotypic correlations were 0.55 and -0.39 , respectively. The generally greater magnitudes of the genotypic correlations than of the phenotypic correlations further indicated that these associations were largely governed by genetic factors rather than environmental influences, thereby increasing the potential effectiveness of indirect selection for grain-yield improvement.

The findings of the present investigation are broadly consistent with previous reports. Chamar *et al.* (2021) reported significant positive associations among grain-quality traits in rice. Faysal *et al.* (2022) identified plant height, productive tillers, filled spikelets, and harvest index as major contributors to grain yield. Sheena and Lavanya (2023) reported significant positive associations of grain yield with biological yield, productive tillers, panicle length, and test weight. More recently, Singh *et al.* (2024), Islam *et al.* (2025), and Modarresi (2026) also reported strong positive relationships between grain yield and important yield-contributing characters, particularly biological yield, grain size, test weight, and productive tillers. The agreement between the present findings and earlier reports indicates that biological yield per plant, effective tillers per plant, test weight, grain length, and panicle length may serve as useful selection criteria for the simultaneous improvement of grain yield in rice breeding programmes.

3.3 Genotypic and Phenotypic Path Coefficient Analyses

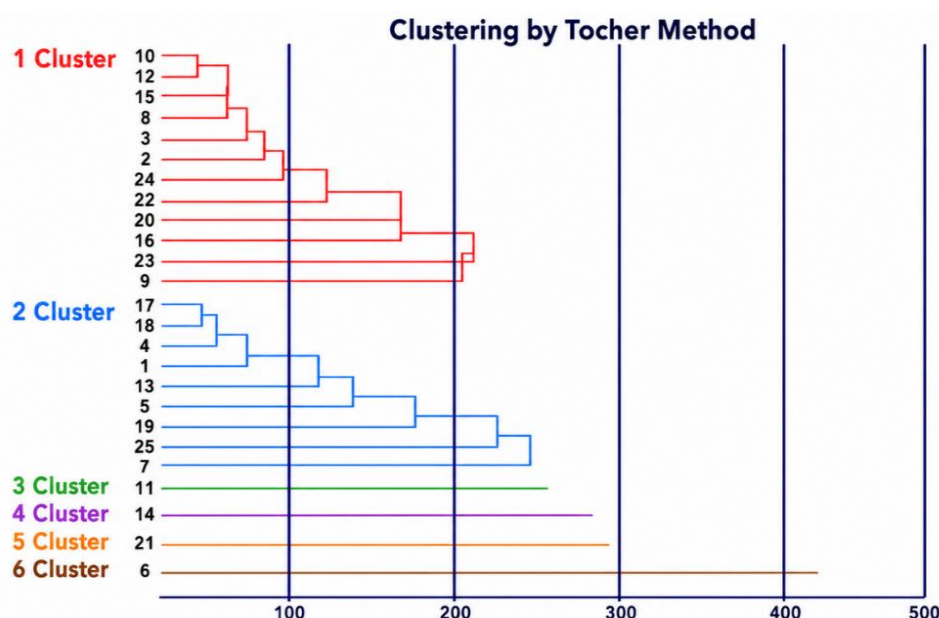
Path coefficient analysis was performed to partition the correlation coefficients into the direct and indirect effects of component traits on grain yield per plant (Tables 4 and 5). At the genotypic level, biological yield per plant exhibited the highest positive direct effect (0.92) on grain yield per plant, followed by grain length (0.10), number of spikelets per plant (0.08), plant height (0.07), days to maturity (0.03), and days to 50% flowering (0.02). In contrast, harvest index (-0.11), number of effective tillers per plant (-0.03), panicle length (-0.02), and test weight (-0.02) exerted negative direct effects. The coefficient of determination ($R^2 = 0.9933$) and the low residual effect (0.0820) indicated that the selected traits explained 99.33% of the variation in grain yield.

At the phenotypic level, biological yield per plant again recorded the highest positive direct effect (0.960), followed by harvest index (0.077), test weight (0.017), panicle length (0.016), number of spikelets per plant (0.010), and grain length (0.010). The high coefficient of determination ($R^2 = 0.9982$) and the low residual effect (0.0426) supported the reliability of the path model. The predominance of biological yield per plant at both the genotypic and phenotypic levels indicates that it was the most important trait governing grain yield in rice. The positive direct effects of grain length, harvest index, test weight, and number of spikelets per plant further suggest that these traits may be used as effective selection criteria for yield improvement. Similar findings were reported by Naik *et al.* (2021), Kayastha *et al.* (2022), Madishetty *et al.* (2023), Singh *et al.* (2024), and Islam *et al.* (2025), who also identified biological yield and other yield-contributing traits as major determinants of grain yield in rice.

Table 1. Eleven Quantitative Traits of Paddy were Subjected to an Analysis of Variance

S.No.	Traits	Replicate (df=2)	Treatments (df=24)	Error (df=48)
1	Days to 50% flowering	55.45	340.69**	7.22
2	Plant Height [cm]	912.67**	700.74	64.39
3	Number of Effective Tillers per Plant	0.37	6.19**	0.61
4	Days to maturity	41.88	394.94**	4.85
5	Number of Spikelet per Plant	734.64	1721.46**	45.83
6	Panicle Length [cm]	0.61	8.35**	0.33
7	Test Weight [g]	0.20	51.48**	0.21
8	Grain Length [cm]	0.00	0.06**	0.01
9	Biological Yield per Plant	102.34	553.68**	104.99
10	Harvest Index [%]	8.77	9.86**	11.79
11	Grain Yield per Plant	30.07	155.96**	32.65

*Significant at 5% probability level, **Significant at 1% probability level

**Fig. 1. Grouping of genotypes by dendrogram**

3.4 Genetic Diversity Analysis (Mahalanobis D²)

Mahalanobis' D² analysis grouped the 25 rice genotypes into six distinct clusters (Table 6 and Fig. 1), indicating substantial genetic diversity within the experimental material. Cluster I was the largest, comprising 12 genotypes, followed by Cluster II with nine genotypes, whereas Clusters III, IV, V, and VI were monogenotypic, each containing a single genotype. The clustering pattern was independent of geographical origin, suggesting that genetic divergence was governed primarily by genetic constitution rather than geographical distribution.

The intra-cluster distance ranged from 0.00 to 17.75, with the highest value recorded for Cluster II (17.75), followed by Cluster I (12.29) (Table 7), indicating greater genetic variability within these clusters. The four remaining monogenotypic clusters exhibited intra-cluster distances of 0.00. Inter-cluster distances varied considerably, with the maximum distance observed between Clusters II and VI (44.21), followed by Clusters V and VI (36.26) and Clusters IV and VI (30.33), whereas the minimum inter-cluster distance (9.95) was recorded between Clusters III and IV. High inter-cluster distances indicate greater genetic divergence and suggest that crosses between these clusters are likely to produce greater heterosis and wider segregation in subsequent generations. The presence of four monogenotypic clusters further indicates the uniqueness of these genotypes, making them valuable parental sources for hybridisation. Similar findings were reported by Sharma *et al.* (2021), Tarunum *et al.* (2023), Lodhi *et al.* (2023), Singh *et al.* (2024), and Islam *et al.* (2025), who also reported that hybridisation between genetically distant clusters enhances heterosis, broadens genetic variability, and facilitates the development of superior recombinants in rice breeding programmes.

Table 2. Genotypic correlation coefficient among different traits of paddy

Characters	Days to 50% flowering	Plant Height [cm]	Number of Effective Tillers per Plant	Days to maturity	Number of Spikelet per Plant	Panicle Length [cm]	Test Weight (1000 seeds) [g]	Grain Length [cm]	Biological Yield per Plant	Harvest Index [%]	Grain Yield per Plant
Days to 50% flowering	1.00	-0.03	0.36**	0.52**	0.20	0.14	-0.44**	-0.32*	-0.18	0.53**	-0.21
Plant Height [cm]		1.00	0.26	-0.17	-0.37**	0.44**	0.16	0.12	0.08	0.32*	0.06
Number of Effective Tillers per Plant			1.00	0.47**	-0.03	0.35**	-0.48**	-0.02	0.22	0.29*	0.18
Days to maturity				1.00	0.36**	0.31*	-0.38**	-0.10	0.08	0.54**	0.05
Number of Spikelet per Plant					1.00	-0.05	-0.21	-0.37**	-0.44**	0.80**	-0.45**
Panicle Length [cm]						1.00	-0.02	0.27	0.07	0.35**	0.06
Test Weight (1000 seeds) [g]							1.00	0.69**	0.14	-0.11	0.17
Grain Length [cm]								1.00	0.21	0.14	0.22
Biological Yield per Plant									1.00	-0.96**	0.99**
Harvest Index [%]										1.00	-0.87**
Grain Yield per Plant											1.00

*Significant at 5% probability level. **Significant at 1% probability level

Table 3. Phenotypic Correlation Coefficient Among Different Traits of Paddy

Characters	Days to 50% flowering	Plant Height [cm]	Number of Effective Tillers per Plant	Days to maturity	Number of Spikelet per Plant	Panicle Length [cm]	Test Weight (1000 seeds) [g]	Grain Length [cm]	Biological Yield per Plant	Harvest Index [%]	Grain Yield per Plant
Days to 50% flowering	1.00	-0.03	0.33**	0.50**	0.19	0.13	-0.44**	-0.30*	-0.17	-0.21	-0.19
Plant Height [cm]		1.00	0.25*	-0.16	-0.33**	0.43**	0.15	0.12	0.09	-0.15	0.08
Number of Effective Tillers per Plant			1.00	0.44**	-0.01	0.34**	-0.45**	-0.01	0.20	-0.15	0.16
Days to maturity				1.00	0.35**	0.31*	-0.38**	-0.09	0.07	-0.27	0.04
Number of Spikelet per Plant					1.00	-0.04	-0.21	-0.33**	-0.38**	-0.34**	-0.39**
Panicle Length [cm]						1.00	-0.02	0.25	0.07	-0.13	0.07
Test Weight (1000 seeds) [g]							1.00	0.64**	0.12	0.03	0.14
Grain Length [cm]								1.00	0.21	0.00	0.22
Biological Yield per Plant									1.00	0.50**	0.99**
Harvest Index [%]										1.00	0.55**
Grain Yield per Plant											1.00

*Significant at 5% probability level. **Significant at 1% probability level

Table 4. Direct and indirect effects of different characters on seed yield per plant at the genotypic level in paddy

Characters	Days to 50% flowering	Plant Height [cm]	Number of Effective Tillers per Plant	Days to maturity	Number of Spikelet per Plant	Panicle Length [cm]	Test Weight (1000 seeds) [g]	Grain Length [cm]	Biological Yield per Plant	Harvest Index [%]	Grain Yield per Plant
Days to 50% flowering	0.02	0.00	0.01	0.01	0.00	0.00	-0.01	-0.01	0.00	0.01	-0.21
Plant Height [cm]	0.00	0.07	0.02	-0.01	-0.03	0.03	0.01	0.01	0.01	0.02	0.06
Number of Effective Tillers per Plant	-0.01	-0.01	-0.03	-0.01	0.00	-0.01	0.01	0.00	-0.01	-0.01	0.18
Days to maturity	0.02	-0.01	0.02	0.03	0.01	0.01	-0.01	0.00	0.00	0.02	0.05
Number of Spikelet per Plant	0.01	-0.03	0.00	0.03	0.08	0.00	-0.02	-0.03	-0.03	0.06	-0.45
Panicle Length [cm]	0.00	-0.01	-0.01	-0.01	0.00	-0.02	0.00	0.00	0.00	-0.01	0.06
Test Weight (1000 seeds) [g]	0.01	0.00	0.01	0.01	0.00	0.00	-0.02	-0.02	0.00	0.00	0.17
Grain Length [cm]	-0.03	0.01	0.00	-0.01	-0.04	0.03	0.07	0.10	0.02	0.01	0.22
Biological Yield per Plant	-0.17	0.07	0.20	0.07	-0.40	0.06	0.13	0.19	0.92	-0.88	0.99
Harvest Index [%]	-0.06	-0.04	-0.03	-0.06	-0.09	-0.04	0.01	-0.02	0.11	-0.11	-0.87
Partial R ²	-0.01	0.00	-0.01	0.00	-0.03	0.00	0.00	0.02	0.92	0.10	

*R Square = 0.9933, Residual effect = 0.0820**Note: Diagonal Bold =Direct path & Red Color = Correlation Coefficient***Table 5. Direct and indirect effects of different characters on seed yield per plant at the phenotypic level in paddy**

Characters	Days to 50% flowering	Plant Height [cm]	Number of Effective Tillers per Plant	Days to maturity	Number of Spikelets per Plant	Panicle Length [cm]	Test Weight (1000 seeds) [g]	Grain Length [cm]	Biological Yield per Plant	Harvest Index [%]	Grain Yield per Plant
Days to 50% flowering	0.004	0.000	0.002	0.002	0.001	0.001	-0.002	-0.001	-0.001	-0.001	-0.187
Plant Height [cm]	0.000	-0.003	-0.001	0.000	0.001	-0.001	0.000	0.000	0.000	0.000	0.075
Number of Effective Tillers per Plant	-0.005	-0.004	-0.014	-0.006	0.000	-0.005	0.006	0.000	-0.003	0.002	0.164
Days to maturity	0.001	0.000	0.001	0.002	0.001	0.001	-0.001	0.000	0.000	0.000	0.045
Number of Spikelets per Plant	0.002	-0.003	0.000	0.004	0.010	0.000	-0.002	-0.003	-0.004	-0.003	-0.386
Panicle Length [cm]	0.002	0.007	0.005	0.005	-0.001	0.016	0.000	0.004	0.001	-0.002	0.073
Test Weight (1000 seeds) [g]	-0.008	0.003	-0.008	-0.007	-0.004	0.000	0.017	0.011	0.002	0.001	0.145
Grain Length [cm]	-0.003	0.001	0.000	-0.001	-0.003	0.002	0.006	0.010	0.002	0.000	0.222
Biological Yield per Plant	-0.164	0.086	0.190	0.066	-0.365	0.071	0.118	0.202	0.960	0.479	0.997
Harvest Index [%]	-0.017	-0.012	-0.011	-0.021	-0.026	-0.010	0.003	0.000	0.039	0.077	0.553
Partial R ²	-0.001	0.000	-0.002	0.000	-0.004	0.001	0.003	0.002	0.957	0.043	

*R Square = 0.9982, Residual effect = 0.0426**Note: Diagonal Bold =Direct path & Red Color = Correlation Coefficient*

Table 6. Distribution of 25 Genotypes of Paddy in Six Clusters

Group	Number of genotypes	Name of Genotypes
Group 1	12	KNM 118, VIKRAM TCR, JGL 24423, SUJALA, RDR 1140, NLR, WGL 3228, WGL 18833, BONITA, NP 1248, RNR 15459, MTU 1001.
Group 2	9	MTU 1032, SIDDHA SANNALU, DEV BHOG, CG DHAN 1919, DUBRAJ, SWARNA, MTU 1075, JEERA SANKAR, NAGRI DUBRAJ.
Group 3	1	DHAN MADHU RAJ 55
Group 4	1	MTU 1010
Group 5	1	MTU 1190
Group 6	1	DIHULA

Table 7. Inter and intra cluster distance between six groups of paddy genotypes

Clusters	Group. 1	Group. 2	Group. 3	Group. 4	Group. 5	Group. 6
Group. 1	12.29	27.00	16.89	17.08	18.11	23.93
Group. 2		13.40	17.75	18.24	19.04	44.21
Group. 3			0.00	9.95	16.03	29.58
Group. 4				0.00	20.02	30.33
Group. 5					0.00	36.26
Group. 6						0.00

Table 8. Frequency distribution of qualitative characterization of paddy

S.No.	Trait	Category	Frequency	Percent
1	Culm - attitude	Erect	3	12
		Semi-erect	11	44
		Open	7	28
		Spreading	4	16
2	Flag leaf: Attitude of blade	Erect	9	36
		Semi-erect	16	64
3	Leaf -Collar	Absent	6	24
		Present	19	76
4	Leaf - Ligule	Absent	1	4
		Present	24	96
5	Leaf - Shape of Ligule	Absent	26	24
		Present	19	76
6	Leaf: Anthocyanin	Truncate	1	4
		Acute	8	32
		Split	16	64
7	Panicle - Distribution of Awns	Tip only	20	80
		Upper half only	3	12
		Whole length	2	8
8	Panicle - Curvature of Main axis	Straight	1	4
		Semi-Straight	7	28
		Deflexed	13	52
		Dropping	4	16
9	Panicle - Secondary branching presence	Absent	0	0
		Present	25	100
10	Panicle - Attitude of Branches	Erect	1	4
		Erect to Semi-erect	10	40
		Semi-erect	10	40
		Semi-erect to Spreading	4	16

3.5 Morphological Characterisation Based on DUS Descriptors

Morphological characterisation of the 25 rice genotypes using 10 DUS descriptors revealed considerable qualitative variation, indicating appreciable phenotypic diversity among the evaluated germplasm. Among the culm-attitude classes, the semi-erect type was predominant and was observed in 11 genotypes (44%), followed by open (28%), spreading (16%), and erect (12%) types. A semi-erect flag-leaf attitude was also predominant, occurring in 16 genotypes (64%), whereas nine genotypes (36%) exhibited erect flag leaves. Most genotypes

possessed a leaf collar (76%) and leaf ligule (96%), whereas the split ligule was the most common ligule type, recorded in 16 genotypes (64%), followed by acute (32%) and truncate (4%) types (Table 8). These qualitative traits effectively differentiated the rice genotypes and provided useful descriptors for varietal identification and germplasm characterisation.

The observed qualitative diversity demonstrates substantial morphological variation among the rice genotypes and highlights the usefulness of DUS descriptors for varietal identification, maintenance of genetic purity, germplasm conservation, and parental selection in breeding programmes. Similar observations were reported by Lavanya *et al.* (2021), Gayathri *et al.* (2023), Prasanna *et al.* (2024), and Sen *et al.* (2026), who demonstrated that qualitative DUS descriptors are reliable tools for distinguishing genetically diverse rice genotypes and facilitating crop-improvement programmes.

4. Limitations of the Study

The present investigation was conducted during a single Kharif season at one location using 25 rice genotypes; therefore, genotype $\times$ environment interactions and the stability of trait expression across environments could not be assessed. The genetic diversity inferred in this study was based primarily on morphological and quantitative traits, which may be influenced by environmental conditions. Further validation across multiple locations and seasons, together with molecular-marker or genomic characterisation, would strengthen the assessment of genetic relationships and the identification of stable parental lines for rice improvement.

5. Conclusion

The evaluation of 25 rice germplasm accessions demonstrated substantial variability across the quantitative and qualitative traits examined. Biological yield per plant showed the strongest positive association with grain yield and the largest positive direct effect at both genotypic and phenotypic levels, indicating its relevance as a selection criterion. Effective tillers per plant, grain length, panicle length, and test weight also showed favourable associations with grain yield and may support selection for improved performance. Mahalanobis D^2 analysis separated the accessions into six clusters and identified marked divergence among several cluster combinations, particularly Clusters II and VI. Such divergence may assist in selecting contrasting parents for future crossing programmes. DUS-based characterisation further distinguished the accessions through qualitative morphological descriptors and supported varietal identification and germplasm management. Overall, the combined use of morphological characterisation, correlation analysis, path coefficient analysis, and multivariate diversity assessment provided a coherent basis for identifying promising traits and genetically diverse parental material.

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Declaration of AI Use

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Competing Interests

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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