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Analysis of Morphological Diversity in Traditional and Improved Rice Varieties

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Abstract

Rice is a crucial cereal crop, providing sustenance for over half of the global population. With the increasing demand for food due to rapid population growth and the loss of arable land, enhancing rice productivity is essential. Rice landraces harbor unique genetic traits, including resilience to biotic and abiotic stresses, making them valuable for breeding programs. This study focuses on the morphological characteristics and genetic variability of indigenous rice landraces collected from South India, which are known for their resilience to diverse environmental conditions. Field experiments were conducted to evaluate 175 rice landraces alongside 28 improved varieties for yield-related traits during the *kharif* season at the College of Agriculture, Mandya using alpha lattice design. Significant differences ($p < 0.05$) were observed in four out of seven traits analyzed with improved varieties exhibiting greater plant height, while landraces showed higher tiller numbers. Statistical analyses, highlighted substantial genetic diversity among genotypes with high broad-sense heritability (>60%) and genetic advance for all traits assessed. Notably, traits such as panicle weight and total tillers demonstrated strong heritability, indicating that they are predominantly influenced by additive gene action. Understanding the phenotypic relationships among traits will inform targeted breeding strategies, ultimately contributing to the conservation and utilization of rice landraces for sustainable agricultural practices and food security.

Keywords : Landraces, Genetic diversity, Phenotypic traits, PCV, GCV, Heritability, GAM

Rice (*Oryza sativa* L.) is the world's most significant cereal crop, serving as a staple food for over half of the global population (Malik *et al*., 2022). Known as a 'global grain,' rice thrives under diverse environmental conditions and is cultivated in more than 100 countries (Mahmoud *et al*., 2014 and Sahu *et al*., 2022). With the rapid growth of the human population, there is an urgent need to boost food production and productivity on shrinking arable land, which is being lost to urbanization and industrialization. Experts estimate that food production must double by 2050 to meet future demands (Ray *et al*., 2013). As a result, enhancing rice productivity has become a critical focus of current research.

India harbors a rich heritage of indigenous rice landraces, which have adapted to diverse agro-ecosystems. These landraces are vital for local food security and play a key role in promoting sustainable agricultural development. They serve as a unique reservoir of traits such as disease and pest resistance, enhanced nutritional quality and tolerance to challenging environments. Known for their resilience, landraces can withstand both abiotic and biotic stresses, ensuring stable crop yields even under harsh conditions (Oladosu *et al*., 2020). Their gene pools play a vital role in conserving biodiversity, supporting ecosystem stability and long-term sustainability. As a valuable germplasm, landraces provide a rich source of adaptability genes that, when utilized, can enhance grain yields and ensure agricultural resilience (Mondal *et al*., 2016). Although landraces exhibit lower genetic diversity than their wild relatives, they possess greater diversity than modern cultivars due to their adaptation to local environments and the varied preferences of farmers. This makes them morphologically distinctive and historically significant (Pusadee *et al*., 2009 and Thomson *et al*., 2007). Landraces generally exhibit about 30 per cent greater allele richness compared to modern cultivars (Kovach & McCouch, 2008 and Zhang *et al*., 2009).

Despite their importance, landraces are at risk of disappearing as farmers increasingly favor modern hybrid varieties (Rana *et al*., 2007). While modern farming practices have boosted productivity, they have also led to a significant loss of genetic diversity in crops like rice. This reduction in diversity has left rice varieties more vulnerable to diseases and insect outbreaks, while also affecting their adaptability to different climates, agricultural practices (Upland, lowland, swampland, etc.), photoperiodic responses, and uses in food production (Bailey-Serres *et al*., 2010). Landraces offer hope, as they contain a wealth of untapped genetic diversity that can be harnessed through targeted breeding programs (Zeng *et al*., 2007). Protecting and utilizing landraces is critical for safeguarding future rice resilience, preserving biodiversity and ensuring sustainable agriculture (Latha *et al*., 2013).

Therefore, there is the need to diversify the genetic base of improved rice varieties and the first step in this process is to characterize the variation available with landrace genotypes. Evaluating phenotypic diversity often reveals traits of significant interest to plant breeders. Additionally, the effective use and conservation of the genetic diversity within the rice gene pool depend largely on a thorough understanding of the evolutionary relationships among rice species, which can guide the development of a natural classification for the genus *Oryza*. Understanding the agro-morphological diversity and distribution of variation among conserved accessions is a valuable tool for germplasm management and crop improvement strategies (De, 2015).

Material and Methods

Plant Materials

The field experiments were conducted at the experimental field located in ‘A’ Block of the College of Agriculture, Mandya, Karnataka in the year 2022. The experimental area was situated at 12^{0}34“25.4““N latitude and 76^{0}50“01.7““E longitude at an altitude of 697 meters above mean sea level (MSL).

During the *kharif* season landraces and improved varieties were transplanted using alpha lattice design, with each of it transplanted in a single row of 1 meter length and spaced 20 cm between hills. Standard agronomic practices, as recommended by the UAS-B, including regular irrigation were followed to ensure optimal crop growth. Data were collected from individual rows and subjected to statistical analysis.

Trait Measurements

Phenotypic data were collected from 175 rice landraces and 28 improved varieties, focusing on yield related traits. Days to 50 per cent flowering (DFF) were recorded as the number of days from germination until 50 per cent of the plants in each landrace and improved varieties began flowering, based on visual observation. Plant height (PH) was measured at the maturity stage, from the base of the plant at the soil surface to the tip of the main tiller panicle and averaged over five plants. The number of tillers per plant (TN) was determined by counting the total tillers per plant at the harvesting stage and averaging over five plants. Panicle length (PL) was measured from the panicle neck to the tip (excluding the awn) during the reproductive stage. Panicle weight (PW) was calculated as the total weight of five panicles, averaged for each entry (Mohanty *et al*., 2018).

Statistical Analysis

An analysis of variance (ANOVA) was performed to assess the variability among genotypes and genetic parameters for all traits using alpha lattice design in R Studio. Additionally, Welch’s two-sample t-test was applied to evaluate the differences between landraces and improved varieties. Violin plots were generated using the 'ggplot2' package in R, while Pearson correlation coefficients were calculated to examine the relationships among traits.

Genetic Variability Parameters

Phenotypic and genotypic coefficient of variation (PCV and GCV) were calculated by the formula given by Burton and DeVane (1953).

$$\mathrm{PCV}\ (\%) = \frac{\sqrt{\sigma_p^2}}{\overline{X}} \times 100$$

$$\mathrm{GCV}\ (\%) = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$$

where, $\overline{X}$ = Grand mean

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

Broad sense heritability (H) was estimated using the following formula (Allard, 1960).

$$H = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where, σ_g^2 = genotypic variance,

σ_p^2 = phenotypic variance

Expected Genetic advance (GA) was calculated by the following formula (Allard, 1960).

$$\mathrm{GA} = k \times h_b^2 \times \sqrt{\sigma_p^2}$$

where, k = selection differential (2.06) at 5 per cent selection intensity

$\sqrt{\sigma^2_p}$ = phenotypic standard deviation

The genetic advance as a percentage of the mean was estimated as:

$$\mathrm{GAM} = \frac{GA}{\overline{X}} \times 100$$

Where, GA= genetic advance; $\overline{X}$ grand mean

RESULTS AND DISCUSSION

Phenotypic Variability and Genotypic Influence on Yield-Related Traits in Rice Genotypes

The analysis of variance (ANOVA) results for seven traits *i.e.,* plant height, total number of tillers, productive tillers, non-productive tillers, panicle length, five panicle weight, and days to 50 per cent flowering are presented in Table 1. Significant differences among genotypes were observed for all traits, indicating considerable phenotypic variability. For plant height, the genotypic effect was highly significant (mean sum of squares: 953.90, $p < 0.001$). Similarly, total number of tillers showed highly significant genetic variation (16.16, $p < 0.001$). Productive tillers also exhibited a highly significant genotypic effect (11.11, $p < 0.001$), with no notable replication or block effects. Non-productive tillers showed substantial genetic variability (2.21, $p < 0.001$) and similarly lacked significant replication or block

TABLE 1

Analysis of variance for different phenotypic attributes of rice landraces and improved varieties

Source of variation	Degrees of freedom	Mean sum of square						
		Plant Height (cm)	Total number of tillers	Productive tillers (no)	Non-productive tillers (no)	Panicle length (cm)	Five Panicle weight (g)	Days to 50% flowering
Replication	1	53.15 *	1.04	3.65	0.80	6.23	0.29 *	1.89
Genotype	202	953.90 ***	16.16 ***	11.11 ***	2.21 ***	22.54 ***	17.45 ***	295.96 ***
Block/replication	12	4.21	1.11	0.97	0.77	1.62	0.06	33.59
Residuals	190	8.19	1.48	1.40	0.57	1.99	0.07	21.45

*** Significant at P=0.001, ** Significant at P=0.01, *Significant at P=0.05

effects. Panicle length revealed a highly significant genotypic effect (22.54, $p < 0.001$), while replication and block effects remained non-significant. For five panicle weight, genotypic variation was highly significant (17.45, $p < 0.001$) and a small but significant replication effect (0.29, $p < 0.05$) suggested environmental influence. Days to 50 per cent flowering displayed significant genotypic differences (295.96, $p < 0.01$), highlighting marked variability in flowering time among genotypes. Residual variation across all traits was low, indicating that the model effectively captured the observed variability. High genotypic variation for several traits indicates that genetic diversity can be exploited in breeding programmes. Highly significant variation in traits such as plant height, total tiller number and 5 panicle weight suggests strong potential for selecting high-performing genotypes. The significant genotypic effect on days to 50 per cent flowering points to opportunities for selecting genotypes with desirable flowering times, crucial for adaptation to different growing environments. Additionally, the high genotypic variation in traits like panicle length and productive tillers underscores their multigenic nature, offering possibilities for improving yield through targeted selection.

The variation between productive and non-productive tillers indicates differences in biomass allocation strategies between landraces and improved varieties, which could be exploited to enhance yields under varying conditions. Similar ANOVA based studies have been reported by Lodhi *et al.* (2023), Quadri *et al.* (2023), Sameera *et al.* (2016), Hemalatha (2018) and Lakshmeesha *et al.* (2022). Overall, the results demonstrate a wealth of genetic diversity in the rice germplasm studied. This diversity presents valuable opportunities for breeding programmes aimed at improving yield-related traits, contributing to better adaptability and sustainable agricultural practices.

Genetic Variability Parameters

In plant breeding, understanding the significance of statistical parameters like maximum, minimum, grand mean, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), broad-sense heritability, genetic advance and genetic advance as a percentage of the mean (GAM) is crucial for selecting superior genotypes and improving desired traits. Data of these parameters are given in Table 2 for days to 50 per cent flowering (DFF), plant height (PH), number of tillers per plant (TN), productive tillers,

TABLE 2

Descriptive statistics and genetic variability parameters for phenotypic attributes of rice landraces and improved varieties

	Plant Height (cm)	Total number of tillers	Productive tillers (no)	Non-productive tillers (no)	Panicle length (cm)	Five Panicle weight (g)	Days to 50% flowering
Minimum	52.40	4.67	4.00	0.00	13.70	1.23	68.52
Maximum	178.63	26.33	21.33	7.50	33.83	18.21	129.97
Grand Mean	96.86	10.85	9.18	1.68	23.70	5.40	98.86
Standard Error	1.54	0.15	0.12	0.06	0.17	0.15	0.63
Standard Deviation	22.01	2.96	2.50	1.18	3.50	2.96	12.60
Genotypic Coefficient of variation	22.45	24.96	24.01	54.06	13.52	54.62	11.85
Phenotypic Coefficient of variation	22.55	26.19	25.67	62.73	14.16	54.73	12.30
Heritability (Broad Sense)	0.99	0.91	0.87	0.74	0.91	1.00	0.93
Genetic Advance	44.60	5.32	4.24	1.61	6.31	6.06	23.24
Genetic Advance as percentage of mean	46.05	49.02	46.24	95.98	26.60	112.30	23.51

non-productive tillers, five panicle weight (PW) and panicle length (PL).

Mean Performance

The grand mean represents the average performance of all genotypes for a particular trait. In plant breeding, the grand mean serves as a reference point for comparing individual genotypes. Genotypes performing above the grand mean are considered superior, while those below may require improvement. Plant height ranged from 52.40 cm to 178.63 cm with an overall average of 96.86 cm. The total number of tillers varied between 4.67 and 26.33, an averaging of 10.85. On average, 9.18 productive tillers were observed, ranging from 4 to 21.33, while non-productive tillers averaged 1.68 with range from 0 to 7.50. The mean panicle length was 23.70 cm, with a minimum of 13.70 cm and a maximum of 33.83 cm. The average weight of 5 panicles was 5.40 g, with values ranging from 1.23 g to 18.21 g. Days to 50 per cent flowering ranged from 68.52 to 129.97 days, with an average of 98.86 days.

Genotypic and Phenotypic Coefficients of Variation

GCV quantifies genetic variation relative to the mean, indicating the genetic potential for selection, while PCV measures total variation, including genetic and environmental components. A large gap between PCV and GCV suggests strong environmental influence, complicating trait selection. The results showed that the GCV was slightly lower than the PCV for all traits analyzed, indicating minimal environmental influence on trait expression. This suggests that phenotype-based selection could be an effective approach for enhancing these traits.

High estimates of GCV (>20%) were observed for 5-panicle weight (54.62%), non-productive tillers (54.06%), total tillers (24.96%), productive tillers (24.01%) and plant height (22.45%). Moderate GCV estimates (10–20%) were recorded for panicle length (13.52%) and days to 50 per cent flowering (11.85%). Similarly, high PCV estimates (>20%) were noted for non-productive tillers (62.73%), 5-panicle weight (54.73%), total tillers (26.19%), productive tillers (25.67%) and plant height (22.55%). Moderate PCV estimates (10–20%) were recorded for panicle length (14.16%) and days to 50 per cent flowering (12.30%).

The high and moderate estimates of GCV and PCV for different traits provide valuable insights into the genetic and phenotypic variability present in the population, which is crucial for plant breeding efforts. The traits with high GCV values, such as 5-panicle weight, non-productive tillers, total tillers, productive tillers and plant height, indicate a high degree of genetic variation. This suggests that these traits are strongly influenced by genetic factors, making them highly amenable to selection and improvement through breeding programmes. Similarly, the high PCV estimates for these traits imply that there is significant overall variability (including both genetic and environmental factors) in the population. However, the relatively small differences between GCV and PCV values for traits like plant height, 5-panicle weight and productive tillers suggest that environmental influence on these traits is limited and most of the variation is genetically determined. This makes these traits ideal candidates for selection. On the other hand, moderate GCV and PCV values for traits such as panicle length and days to 50 per cent flowering indicate that while there is variability present, the genetic component may be less prominent compared to environmental effects. These traits might still be improved through selection, but the response may be slower. Overall, traits with high GCV and PCV values provide strong targets for breeding programmes, as genetic variation is a key driver of progress in selecting for desirable traits. Moderate variability traits may also be useful but would require careful management of environmental factors to achieve the desired improvements.

Heritability and Genetic Advance Over Per cent Mean

Heritability estimates act as predictive tools, reflecting the reliability of phenotypic valuses for trait selection. High heritability is especially advantageous for efficient trait selection. As per Johnson *et al*. (1955), heritability is classified as low (<30%), moderate (30-60%) and high (>60%). In this study, all the traits displayed high heritability with values ranging from 74 to 100 per cent. High broad-sense heritability estimates (>60%) were observed for 5-panicle weight (100%), plant height (99%), days to 50 per cent flowering (93%), total tillers (91%), panicle length (91%), productive tillers (87%) and non-productive tillers (74%).

Genetic advance is a crucial metric for estimating the potential improvement from selection within a population. When considered alongside heritability, it offers a more precise indicator of selection effectiveness (Johnson *et al*., 1955). In this study, all traits exhibited high genetic advance as a percentage of the mean, ranging from 23.51 to 112.30 per cent. Notably, high genetic advance (>20%) was observed for 5-panicle weight (112.30%), non-productive tillers (95.98%), total tillers (49.02%), productive tillers (46.24%), plant height (46.05%), panicle length (26.60%) and days to 50 per cent flowering (23.51%).

High heritability along with high genetic advance was observed for all traits *viz.,* plant height, total number of tillers, productive tillers, non-productive tillers, panicle length, 5 panicle weight and days for 50 per cent flowering. This suggests that these traits are predominantly governed by additive gene action, making their selection highly advantageous for improvement. Similar studies on GCV, PCV, heritability and genetic advance for the analyzed traits were done by Sanku *et al*. (2022), Adhikari *et al*. (2018), Duraiswamy *et al*. (2023), Shanmugam *et al*. (2023), Jebakani *et al*. (2023), Dixit *et al*. (2022) and Channannavar *et al*. (2020). Together, these parameters provide a comprehensive understanding of trait variability and guide breeders in developing effective selection strategies for crop improvement.

Analysis of Interrelationships among Phenotypic Traits

The phenotype of a plant is determined by the interaction of multiple traits, making the analysis of their interrelationships critical for understanding their influence on plant performance. In this study, correlations among key traits were analyzed, providing insights into their associations and potential implications for breeding strategies.

Plant height (PH) exhibited positive correlations with panicle length (PL) (0.43), days to 50 per cent flowering (DFF) (0.43) and 5-panicle weight (PW) (0.31), indicating that taller plants are likely to have longer panicles, delayed flowering and higher panicle weight. These traits are often linked to plant vigor and yield potential, suggesting that selection for increased height could indirectly enhance these characteristics. However, PH showed negative correlations with non-productive tillers (NT) (-0.32), total tillers (TT) (-0.23), and productive tillers (PT) (-0.14). This trade-off implies that taller plants may produce fewer tillers overall, which must be considered in breeding programmes aiming to balance plant architecture and yield components. Days to 50 per cent flowering (DFF) showed positive correlations with PH (0.43), PL (0.39) and PW (0.30), highlighting its association with plant vigor traits. Similarly, PW exhibited positive correlations with both PH (0.31) and PL (0.22), reinforcing the interdependence of these yield-related parameters. These associations suggest that selecting for delayed flowering could indirectly improve panicle traits and overall plant stature. Non-productive tillers (NT) were positively correlated with TT (0.61) and PT (0.29), indicating that genotypes producing more total tillers also tend to have a proportion of non-productive tillers. The strong positive correlation between TT and PT (0.94) is particularly noteworthy, as it suggests that most tillers contribute directly to productive outcomes. Breeding programmes can capitalize on this relationship by focusing on improving total tiller number while minimizing non-productive tillers to maximize yield.

The observed correlations provide valuable guidance for breeding strategies. For instance, the positive associations among PH, PL and PW suggest that these traits can be improved simultaneously through selection. However, the negative relationship between PH and tiller traits points to a potential trade-off, requiring careful management to achieve optimal

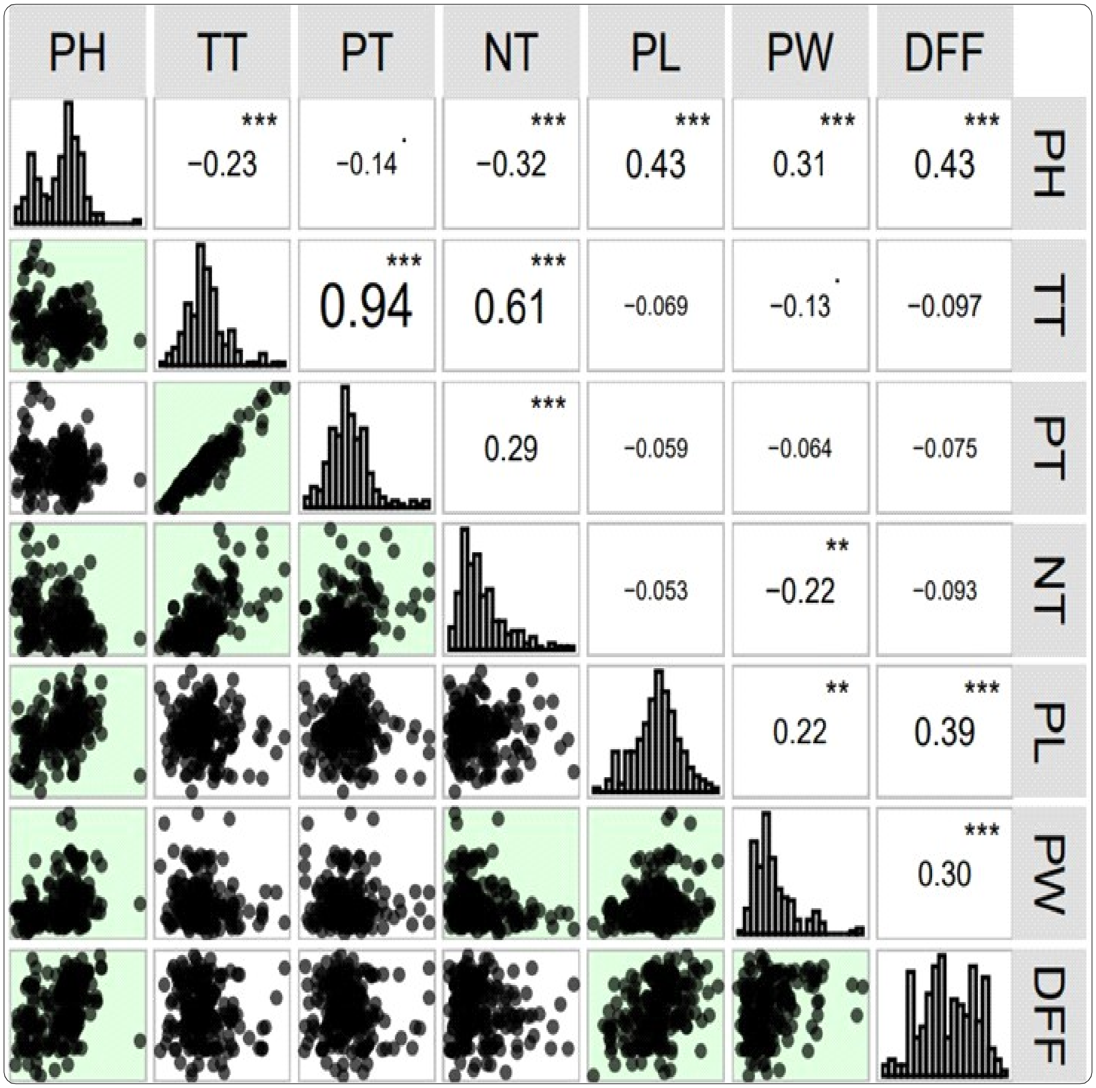

Fig. 1 : Phenotypic correlation coefficient among different traits in rice landraces and improved varieties

PH- Plant height, TT- Total number of tillers, PT- Productive tillers, NT- Non-productive tillers, PL- Panicle length, PW- Five panicle weight, DFF- Days to 50% flowering

outcomes. Moreover, the strong correlation between TT and PT highlights the importance of selecting genotypes with a higher proportion of productive tillers. Similar correlation studies were done by Adhikari *et al*. (2018), Jebakani *et al*. (2023) and Dixit *et al*. (2022).

Overall, these findings emphasize the need to understand trait interrelationships to design effective breeding strategies. By leveraging these correlations, breeders can target traits that align with specific goals, such as improving yield components or optimizing plant architecture, while managing the inherent trade-offs among traits.

Comparison between Landraces and Improved Varieties

A comparison between landraces and improved varieties is essential for understanding the genetic diversity, adaptability and productivity of different rice genotypes. Landraces, which are traditionally cultivated varieties, have evolved over time in specific local environments, often possessing unique traits like resilience to biotic and abiotic stresses. However, they may exhibit lower yields compared to improved varieties, which have been developed through modern breeding techniques for higher productivity, disease resistance and uniformity in traits. By comparing these two groups, researchers aim to evaluate their performance across various traits, such as yield, plant height, tillering ability and stress tolerance, to identify the strengths of each group. This comparison provides insights into how the genetic diversity of landraces can complement breeding efforts for improved varieties, contributing to sustainable agriculture, genetic conservation and future crop improvement. Out of the 7 traits analyzed, 4 showed significant differences ($p < 0.05$), indicating a substantial variation between rice landraces and improved varieties (Table 3).

The differences between these groups are illustrated through violin plots in Fig. 2. Improved varieties demonstrated greater plant height, panicle length and weight of five panicles compared to landraces. Conversely, landraces exhibited a higher total number of tillers, productive tillers and non-productive tillers than improved varieties. However, the days to 50 per cent flowering were nearly identical for both landraces and improved varieties. In conclusion, the analysis presented in Fig. 2 highlights the distinct characteristics of improved varieties and landraces, showcasing the strengths and weaknesses inherent in each group. While improved varieties excel in terms of plant height, landraces demonstrate greater tillering capacity, which may contribute to their resilience and adaptability in diverse environments. The differences in panicle length and weight further emphasize the varied breeding objectives that have shaped these groups. Interestingly, the similar days to 50 per cent flowering observed in both landraces and improved varieties suggest a shared adaptability in terms of flowering time, which could be beneficial for synchronizing cultivation practices. Understanding these differences not only enhances our appreciation of the genetic diversity within rice but also informs breeding strategies aimed at combining the desirable traits of both landraces and improved varieties for sustainable agricultural practices and enhanced food security.

The present study highlights the significant phenotypic diversity among rice landraces and improved varieties, emphasizing the potential of landraces as a valuable genetic resource for enhancing rice productivity. The analysis revealed considerable variation in key agronomic traits with significant differences observed between landraces and improved varieties, particularly in terms of tillering and panicle characteristics. The high heritability estimates and genetic advance for traits such as plant height, total tillers and panicle weight suggest that these traits are largely influenced by additive gene action, making them suitable candidates for selection in breeding programmes.

Furthermore, the positive correlations among various traits indicate that selection for one trait could positively influence others, facilitating the improvement of overall yield potential. The findings underscore the importance of conserving indigenous rice landraces, as they harbor unique traits that can enhance resilience against biotic and abiotic stresses. As agricultural challenges intensify due to climate change and increasing population demands, the integration of landrace genetic diversity into breeding strategies will be crucial for developing improved rice varieties that ensure food security and sustainable agricultural practices in the future. Overall, this

TABLE 3

T test results for comparison between rice landraces and improved varieties

	Plant Height	Total number of tillers	Productive tillers	Non-productive tillers	Panicle length	Five Panicle weight	Days to 50% flowering
P-value	1.0401×10^{-9}	5.0703×10^{-9}	1.3986×10^{-1}	1.8288×10^{-5}	1.4088×10^{-1}	4.76664×10^{-5}	5.2412×10^{-1}

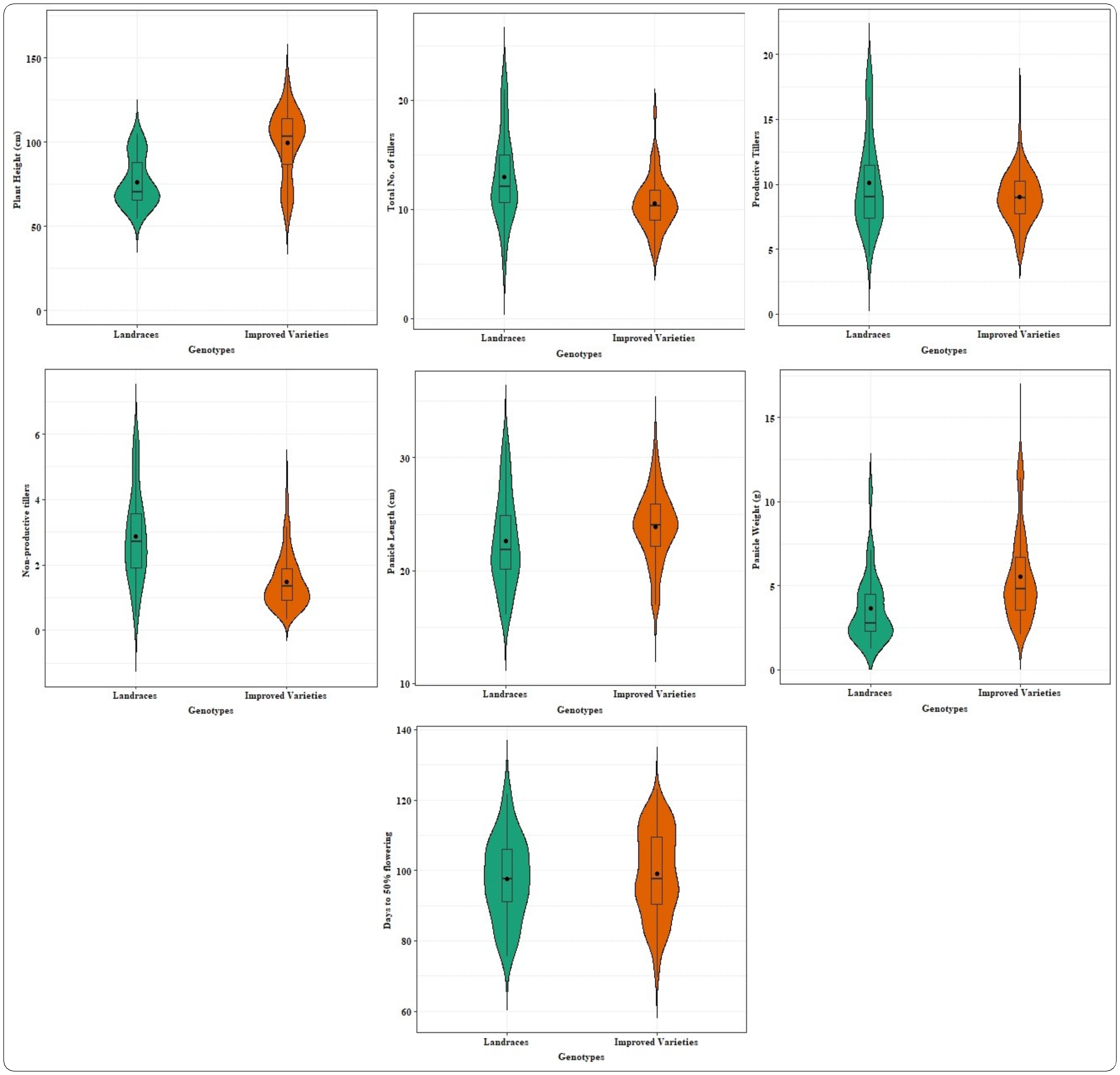

Fig. 2 : Violin plots depicting variation in different phenotypic attributes in rice landracesand improved varieties

Plate 1 : General view of the rice landraces and improved varieties from seedling stage to reproductive stage

research contributes to the broader understanding of rice genetics and offers insights that can guide future breeding efforts aimed at enhancing rice productivity while preserving biodiversity.

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