



RESEARCH ARTICLE

Identification of elite product lines through genetic and multivariate analyses for dry direct-seeded rice systems

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Abstract

Dry direct-seeded rice (DDSR) is a promising substitute for puddled transplanted rice, particularly in regions facing climate-induced water scarcity, high greenhouse gas emissions and labour shortages. In view of these emerging challenges, the current investigation was undertaken to quantify genetic variability, understand trait interrelationships, perform cluster grouping and identify superior breeding lines suited to dry direct-seeded rice ecosystems. During the kharif season of 2022, 80 genotypes comprising 71 advanced breeding lines developed at International Rice Research Institute (IRRI), South Asia Hub, Hyderabad, along with nine adapted checks, were evaluated under dry direct-seeded conditions at Agricultural Research Station, Kunaram, Professor Jayashankar Telangana Agricultural University. Restricted maximum likelihood analysis revealed significant genetic variation for all seven agro-morphological traits studied. Genetic parameters with violin plots displayed early maturity, moderate plant height, stable test grain weight and clear yield differences among genotypes, providing a strong basis for selecting lines suited to dry direct-seeded ecosystems. High heritability (84.4 %) coupled with high genetic advance (31.2 %) for grain yield confirmed that direct selection would be effective. Phenotypic correlation analysis, histograms and scatter plots showed that grain yield did not exhibit a significant positive association with any single component trait, suggesting that yield is governed by the coordinated performance of multiple traits rather than the dominance of a single character. The first two principal components accounted for 44.46 % of the total variation, revealing meaningful trait associations and multivariate differences among genotypes. Cluster analysis grouped the genotypes into 10 distinct clusters with contrasting trait combinations, providing practical guidance for parent selection and crossing strategies. Five elite breeding lines were identified and nominated to the All India Coordinated Rice Improvement Programme for multi-location national testing, of which IR144564-3-47-1-1-B and IR127364-46-2-1 subsequently advanced to AVT-I and AVT-II, respectively, demonstrating the effectiveness of integrated genetic and multivariate analyses in identifying promising materials for DDSR varietal development.

Keywords: cluster analysis; correlation analysis; dry direct-seeded rice; genetic variability; principal component analysis; violin plots

Introduction

Rice (*Oryza sativa* L.) is a principal food crop that constitutes a primary source of nutrition for a substantial proportion of the global population, sustaining more than 3.5 billion people worldwide (1, 2). It is cultivated in more than 100 countries covering nearly 165 million hectares, with Asia contributing nearly 90 % of global production (3, 4). Rice occupies approximately 51 million hectares in India, contributing around 150 million metric tonnes to national production with an average productivity of 2.9 tonnes per hectare, ranking second globally (5). Rising population pressure, per capita consumption of approximately 45 kg per year and heavy reliance of vulnerable populations on rice for daily caloric intake emphasise the urgent need to develop high-yielding, climate-resilient rice varieties through integrated genetic analysis of yield and its component traits.

Conventional puddled transplanted rice is highly water

intensive, with substantial losses through evaporation, transpiration and deep percolation, thereby exacerbating water scarcity in rice-growing regions (6). These constraints have promoted dry direct-seeded rice (DDSR) as a resource-efficient alternative, as it avoids puddling and continuous flooding, thereby reducing irrigation water use by 18–23 % and labour requirements by 22–31 % (7). This method of crop establishment shortens the crop duration relative to traditional system, facilitating timely crop rotations and improved system efficiency (7, 8). Moreover, it permits substantial reductions in emissions and production costs relative to traditional transplanted rice (9, 10). Despite these advantages, the productivity of DDSR is often limited as most high-yielding varieties have been developed and well adopted to transplanted conditions and exhibit poor adaptation under dry direct-seeded conditions (11, 12). This highlights the requirement of targeted breeding programmes to develop cultivars specifically adapted to DDSR systems.

Under DDSR situations, grain yield is governed by intricate gene interactions and significant genotype $\times$ environment effects, which often limit selection efficiency. Consequently, robust statistical analysis of diverse germplasm is essential to identify high-yielding genotypes and to develop rice varieties well adopted to DDSR ecosystems (13). Hence, an in-depth understanding of genetic variability is essential for effective selection, as it facilitates the expansion of the genetic base and allows reliable assessment of trait inheritance in germplasm or advanced breeding lines (14). In addition to genetic variability, the concurrence of high estimates of heritability and genetic advance is indicative of the preponderance of additive gene action, thereby rendering such traits highly responsive to direct phenotypic selection (15).

Correlation analysis is a crucial statistical tool for understanding the nature and magnitude of associations among yield-related traits and their influence on crop productivity (16). Principal component analysis (PCA) enables uncovering complex interrelationships, decomposition and interpretation of variation across multiple traits, offering a holistic view of genetic diversity within a population. This method is valuable for identifying the most influential traits that contribute to overall diversity and for recognising superior genotypes within breeding materials. Additionally, PCA has proven effective in dissecting intricate quantitative traits by isolating principal components that account for most of the observed variation in multi-trait data (17).

Hierarchical cluster analysis, among the diverse methods used to assess diversity, is a powerful multivariate technique for grouping genotypes into homogeneous clusters based on phenotypic traits. Such grouping is crucial, since the magnitude of heterosis and transgressive segregants in hybrid populations often correlate positively with genetic divergence between parents. By applying cluster analysis, genotypes that combine high-heritability adaptive traits with elevated yield potential can be systematically identified (15).

Development of rice varieties with high yield potential and adaptability to DDSR establishment through conventional breeding continues to be a practical, economical and sustainable strategy for improving national rice productivity. The efficacy of selecting superior genotypes, however, depends largely on the magnitude of genetic variability, heritability, expected genetic advance of the key traits and the breeder's selection efficiency, knowledge on interrelationships and genetic divergence of the traits among the lines. Accordingly, present investigation was designed to quantify the magnitude of genetic variability, estimate heritability, genetic advance and genetic divergence, elucidate interrelationships among agronomic traits and identify key yield determinants and superior genotypes in rice under DDSR targeted breeding programmes.

Materials and Methods

Experimental site and plant material

The field trial was carried out during the kharif season of 2022 at the Agricultural Research Station, Kunaram, Professor Jayashankar Telangana Agricultural University (PJTUAU), Telangana, India. The site of experiment is located at 18.6° N latitude and 79° E longitude, at an elevation of 231 m above mean sea level, with silty loam soil (Electrical conductivity (EC) = 0.86 dS m⁻¹; pH = 7.4). A total of 80 rice

genotypes were evaluated, encompassing 71 advanced breeding lines developed at the International Rice Research Institute (IRRI), South Asia Hub, Hyderabad, Telangana, specifically targeted for DDSR systems, along with nine check varieties namely, DRR Dhan 44, KNM 1638, IR 64, IR 91648-B-89-B, MTU 1010, Naveen, KNM 118, Sahabghadidhan and Vandana. These checks are recognised for their adaptation to dry direct seeded environments.

The trial was laid out with 2 replications in an alpha lattice design to control field variability more effectively than a simple randomised design. Each plot measured 5 m² with 20 cm inter row spacing. Direct seeding was carried out under dry soil conditions and all recommended agronomic management practices were followed during entire crop period to ensure uniform growth and development.

Crop establishment and management

The experimental field was prepared under dry conditions using conventional tillage to obtain a fine and uniform seedbed suitable for dry direct seeding. Seeds were sown manually in rows spaced 20 cm apart at a seed rate of 25 kg ha⁻¹ at a depth of approximately 2–3 cm. A recommended fertiliser dose of 120 : 60 : 40 kg N : P₂O₅ : K₂O ha⁻¹ was applied, with the full dose of phosphorus and potassium and one-third of nitrogen applied as basal. The remaining nitrogen was top-dressed in two equal splits at active tillering and panicle initiation stages.

Weed management was carried out through the application of Pendimethalin 30 % emulsifiable concentrate (EC) as a pre-emergence herbicide within 48 hr of sowing, followed by Bispyribac-sodium 10 % suspension concentrate (SC) as a post-emergence herbicide at approximately 25 days after sowing to effectively control emerging weed flora. One hand weeding was performed as required to maintain a weed-free environment during critical crop growth stages. Supplemental irrigations were provided whenever necessary to ensure uniform crop establishment and to avoid severe moisture stress, particularly during tillering, flowering and grain-filling stages. The crop was grown under warm and humid agro-climatic conditions, with minimum and maximum temperatures ranging from 19.94 to 28.00 °C and 33.75 to 36.12 °C, respectively. The highest monthly rainfall (753.0 mm) was recorded in July, accompanied by 22 rainy days, while no rainfall was received during November and December, providing favourable dry conditions for crop maturity and harvesting. Standard plant protection measures were adopted throughout the crop season to minimise damage from insect pests and diseases. All recommended agronomic practices for dry direct-seeded rice cultivation in the region were followed to ensure normal crop growth and development.

Trait recording

Observations were recorded on seven agro-morphological traits following standard procedures. Days to 50 % flowering (DFF) was quantified as the number of days from sowing until 50 % of plants in a plot had flowered. Plant height (PH) was recorded as the distance in centimetres from soil surface to the panicle tip at maturity. Panicle length (PL) was measured in centimetres from the panicle base to its apex. Number of productive tillers per m² (NPTPM²) was counted at maturity. Number of filled grains per panicle (NFGPP) was recorded from representative panicles. Test grain weight (TGW) was measured as the weight of 1000 grains in grams. Grain yield in kg ha⁻¹ (GYKGPHA) was noted on a plot basis and converted to kg ha⁻¹.

Statistical analysis

Components of variance were estimated using the restricted maximum likelihood (REML) procedure in GenStat for Windows, Release 15.1 (VSN International Ltd., Hemel Hempstead, UK). The following linear mixed model was fitted: $Y_{ijk} = \mu + R_i + B_j(i) + G_k + \varepsilon_{ijk}$

where Y_{ijk} represents the observed value of the k^{th} genotype in the j^{th} block within the i^{th} replication, μ is the overall mean, R_i is the fixed effect of replication, $B_j(i)$ is the fixed effect of block nested within replication, G_k is the random effect of genotype and ε_{ijk} is the residual error. Variance components were estimated using average information (AI) algorithm implemented in GenStat. Best linear unbiased predictors (BLUPs) were generated for all genotypes and used for subsequent analyses.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated from REML-derived variance components following standard biometrical procedures. Phenotypic variance was obtained as the sum of genotypic and residual variance components. Broad-sense heritability (H^2) and genetic advance as percent of mean (GAM) were estimated to assess the magnitude of genetic variability and the expected response to selection. Phenotypic correlation coefficients among traits were computed to understand pairwise relationships. Principal component analysis was performed using standardised trait values to identify the key axes of variation and to visualise genotype and trait associations through biplots. Hierarchical clustering analysis was conducted based on Euclidean distance using Ward's method to group genotypes into clusters according to overall similarity across traits. All multivariate analyses were carried out and graphical illustrations were generated in R software (Version 4.5.2). The software packages were used including ggcorplot for correlation matrix visualisation, factoextra for principal component analysis and biplot generation, reshape2 for data restructuring and dendextend and circlise for hierarchical clustering and circular dendrogram visualisation.

Results

Genetic variability among rice genotypes under dry direct-seeded rice conditions

Restricted maximum likelihood analysis revealed significant genotypic variation ($p \leq 0.05$) for all 7 traits evaluated under DDSR conditions (Table 1). Table 1 also provides a summary of the mean values, ranges and genetic parameters for all traits assessed. The DFF varied from 79 to 94 days, with an average of 87.9 days and

corresponding violin plot (Fig. 1A) shows that majority of genotypes cluster closely around the mean, with only a limited number showing minor deviations earlier or later flowering. The PH varied from 62.7 to 92.8 cm, averaging 80.8 cm. The violin plot (Fig. 1B) shows a balanced distribution, wherein most genotypes concentrate around medium height. Number of productive tillers per m^2 varied between 189.0 and 269.0, with an average of 217.5. The violin plot of this trait (Fig. 1C) exhibits a wider spread than flowering and PH. The PL varied from 19.6 to 24.5 cm, exhibiting a mean value of 21.5 cm. The violin plot (Fig. 1D) relatively displays a narrow, centered distribution, reflecting moderate and consistent genotypic variation. The NFGPP ranged from 113.0 to 154.0, averaging 132.9. The violin plot of this trait (Fig. 2A) exhibits moderate variability, with some lines extending towards higher grain numbers. TGW varied from 19.4 to 24.8 g, averaging 22.6 g and violin plot of this trait illustrates a narrow, centrally concentrate distribution, with the majority of genotypes cluster tightly around the mean and displaying low variability (Fig. 2B). Grain yield in kg ha^{-1} displayed the widest variation among all traits, varying from 3210.0 to 6241.0 kg ha^{-1} with an average of 4494.1 kg ha^{-1} . The corresponding violin plot shows the widest spread, clearly distinguishing lower from higher yielding lines, with some genotypes substantially outperforming the average (Fig. 2C).

The PCV values were higher than GCV values for all traits. Grain yield recorded the highest GCV (16.51 %) and PCV (17.97 %), followed by plant height (GCV 10.82 %, PCV 13.60 %) and productive tillers per m^2 (GCV 10.53 %, PCV 13.46 %). Days to 50 % flowering showed the narrowest difference between GCV (4.71 %) and PCV (5.01 %). Broad-sense heritability ranged from 61.3 % for productive tillers per m^2 to 89.9 % for plant height. Grain yield showed high heritability (84.4 %) coupled with the highest genetic advance as percent of mean (31.2 %).

Trait associations under dry direct-seeded rice conditions

The correlation matrix revealed generally weak to moderate associations among the evaluated traits (Fig. 3). Grain yield showed weak correlations with days to flowering (-0.10), plant height (-0.09), productive tillers per m^2 (-0.19), panicle length (0.11), filled grains per panicle (0.15) and test grain weight (0.04). A significant positive correlation was observed between plant height and panicle length ($r = 0.54^{***}$), whereas filled grains per panicle exhibited a significant negative correlation with test grain weight ($r = -0.31^{**}$). Histograms and scatter plots indicated substantial variability among genotypes with no strong linear relationship between grain yield and individual component traits.

Table 1. Genetic variability parameters of seven agro-morphological traits in 80 rice genotypes evaluated under dry direct-seeded rice conditions

Traits	Genotypic variance	Mean	Range	Heritability (%)	GCV (%)	PCV (%)	GAM (%)
DFF	17.2*	87.9	79.0-94.0	88.3	4.71	5.01	9.1
PH	60.2*	80.8	62.7-92.8	89.9	10.82	13.60	18.7
NPTPM ²	522.6*	217.5	189.0-269.0	61.3	10.53	13.46	17.0
PL	1.8*	21.5	19.6-24.5	69.8	9.58	10.10	11.1
NFGPP	210.4*	132.9	113.0-154.0	63.3	6.45	7.72	17.7
TGW	2.6*	22.6	19.4-24.8	81.8	7.06	7.81	13.2
GYKGPHA	549305.0*	4494.1	3210.0-6241.0	84.4	16.51	17.97	31.2

DFF: days to 50 % flowering; PH: plant height; NPTPM²: number of productive tillers per m^2 ; PL: panicle length; NFGPP: number of filled grains per panicle; TGW: test grain weight; GYKGPHA: grain yield (kg ha^{-1}); GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; GAM: genetic advance as percentage of the mean; significant at $p \leq 0.05$.

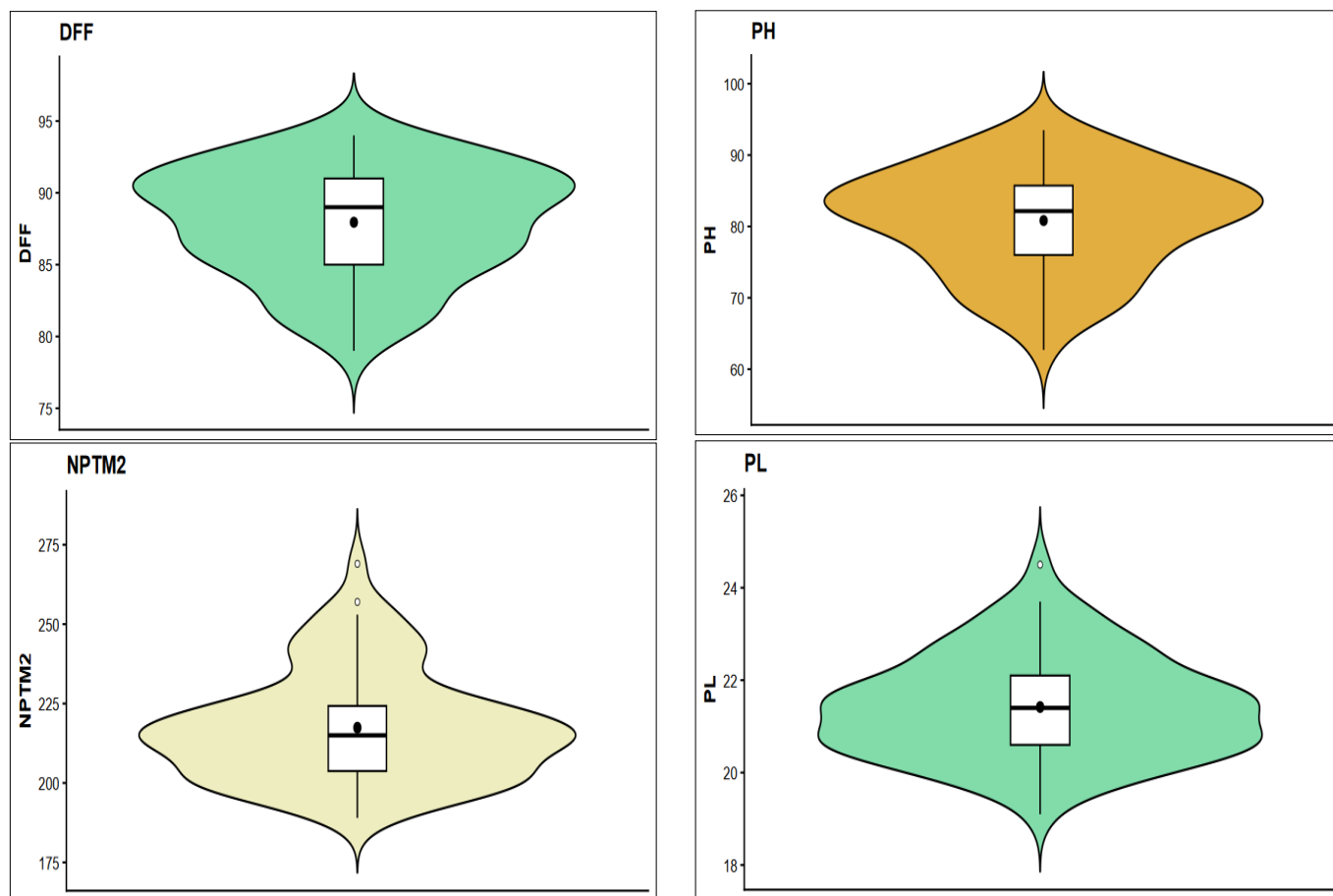


Fig. 1. Phenotypic distribution and variability. A: days to 50 % flowering; B: plant height; C: number of productive tillers per m²; D: panicle length through violin plots among 80 rice genotypes evaluated under dry direct-seeded conditions. The inner box indicates the interquartile range and the dot represents the mean.

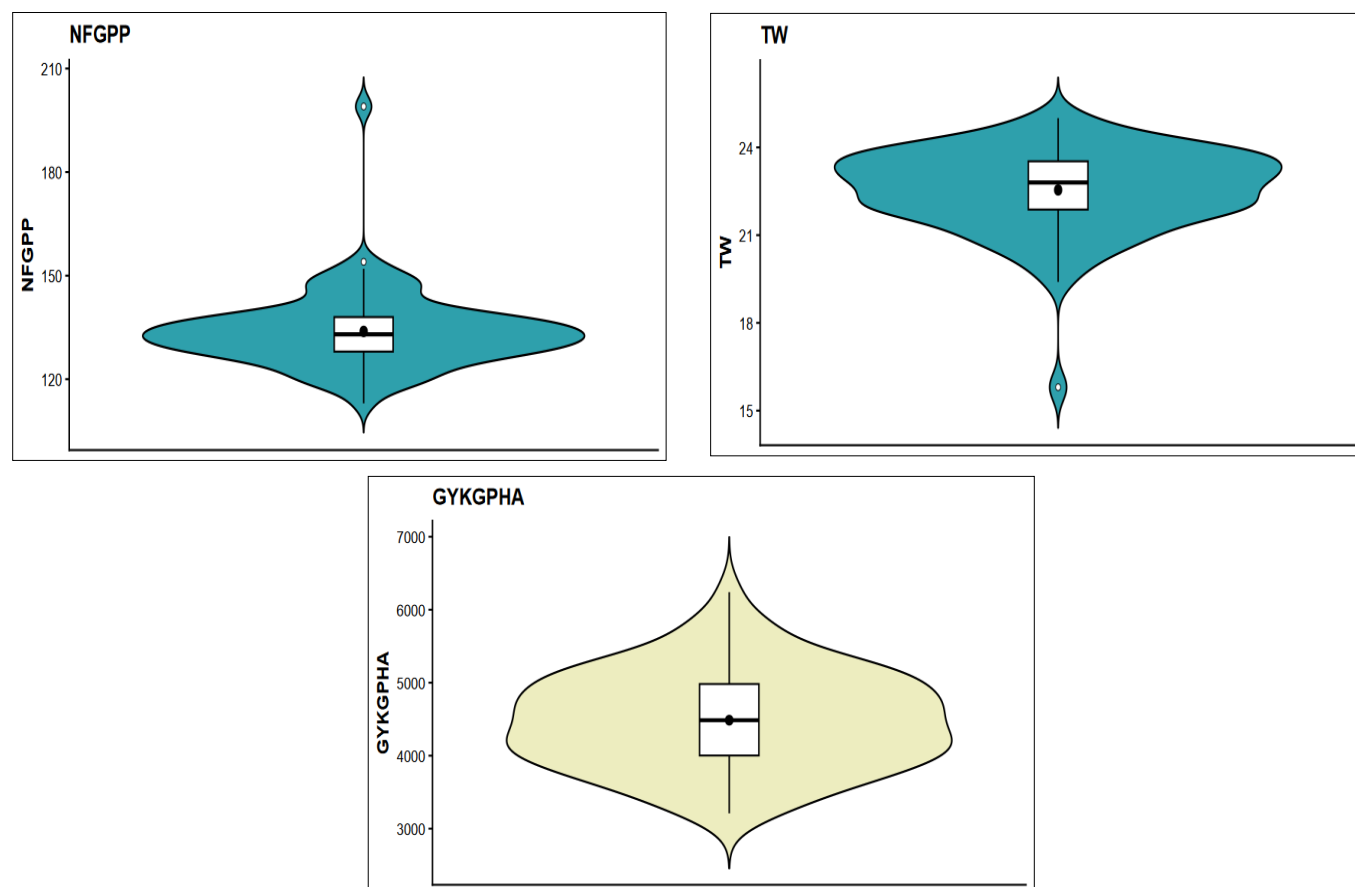


Fig. 2. Phenotypic distribution and variability. A: number of filled grains per panicle; B: test grain weight; C: grain yield in kg ha⁻¹ through violin plots among 80 rice genotypes evaluated under dry direct-seeded conditions. The inner box indicates the interquartile range and the dot represents the mean.

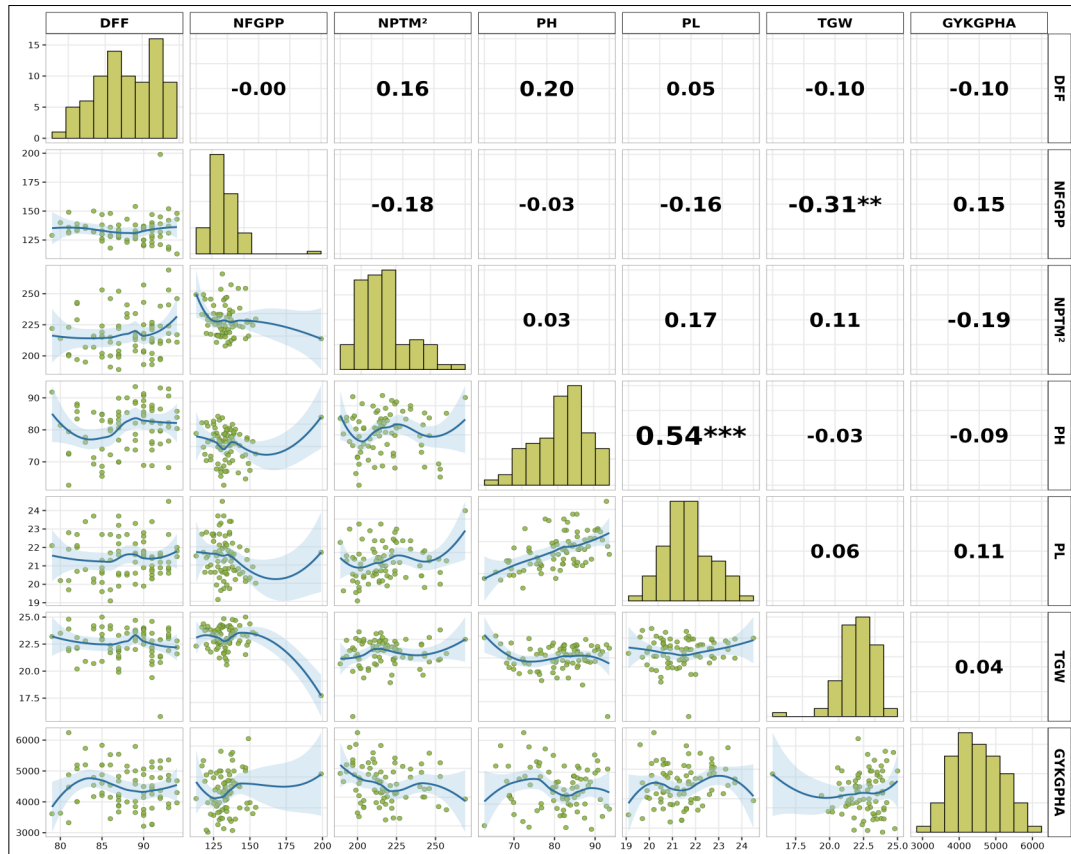


Fig. 3. The scatter plot matrix illustrating histograms of the variables in the diagonal, pairwise scatter plots with fitted trend lines in lower panels and Pearson correlation coefficients in upper panels for seven agro-morphological traits under dry direct seeded rice.

DFF: days to 50 % flowering; PH: plant height; NPTM²: number of productive tillers per m²; PL: panicle length; NFGPP: number of filled grains per panicle; TGW: test grain weight; GYKGPHA: grain yield (kg ha⁻¹).

Principal component analysis

Three principal components had eigenvalues greater than one based on the Kaiser criterion, collectively explaining 62.05 % of the total variation (Table 2) (18). The first principal component (PC1) accounted for 24.74 % of the variation, followed by PC2 (19.71 %) and PC3 (17.59 %). The first two principal components together explained 44.46 % of the total variation. The PCA biplot shows a wide distribution of genotypes across all quadrants, indicating substantial diversity within the breeding population (Fig. 4). Filled grains per panicle and grain yield contributed positively to PC1, whereas plant height, panicle length and productive tillers per m² contributed negatively.

Cluster analysis and cluster performance

Hierarchical clustering grouped the 80 genotypes including the checks into ten distinct clusters (Fig. 5). Cluster VII contained the largest number of genotypes (16), followed by Cluster II (11), Clusters

III and IV (10 each), Cluster I (9), Clusters V and VI (8 each), Cluster VIII (6), while Clusters IX and X were monogenotypic. Considerable variation was observed among cluster means for all traits (Table 3).

Cluster X recorded the highest grain yield (5099 kg ha⁻¹) and the highest NFGPP (199), followed by Cluster V (4970 kg ha⁻¹) and Cluster VII (4903 kg ha⁻¹). Cluster IX exhibited the highest productive tillers per m² (269), PH (93 cm) and PL (25 cm). Cluster VI was the earliest flowering group (82 days), while Cluster V and Cluster IX recorded the highest TGW (24.0 g). Cluster VIII recorded a notably high tiller density (246 per m²) with moderate PL (21 cm).

Identification of elite breeding lines

Among the 71 advanced breeding lines evaluated under DDSR conditions, five elite lines were identified based on grain yield, agronomic performance and phenotypic acceptability (Table 4). IR127299-36-2-2 recorded the highest grain yield (5832 kg ha⁻¹),

Table 2. Principal component loadings, eigenvalues and percentage contribution of seven agro-morphological traits in 80 rice genotypes under dry direct-seeded rice conditions

Trait	PC1	PC2	PC3	PC4	PC5
DFF	-0.27	0.24	0.47	-0.56	0.55
PH	-0.54	0.42	-0.11	0.27	0.13
NPTM ²	-0.37	-0.28	0.33	-0.40	-0.68
PL	-0.57	0.24	-0.36	0.04	-0.23
NFGPP	0.35	0.53	0.08	-0.14	-0.29
TGW	-0.18	-0.56	-0.35	-0.17	0.29
GYKGPHA	0.17	0.19	-0.63	-0.63	-0.04
Eigenvalue	1.73	1.38	1.23	0.87	0.78
Percent Variance	24.74	19.71	17.59	12.36	11.20
Cumulative Percent Variance	24.74	44.46	62.05	74.41	85.62

DFF: days to 50 % flowering; PH: plant height; NPTM²: number of productive tillers per m²; PL: panicle length; NFGPP: number of filled grains per panicle; TGW: test grain weight; GYKGPHA: grain yield (kg ha⁻¹); PC: principal component.

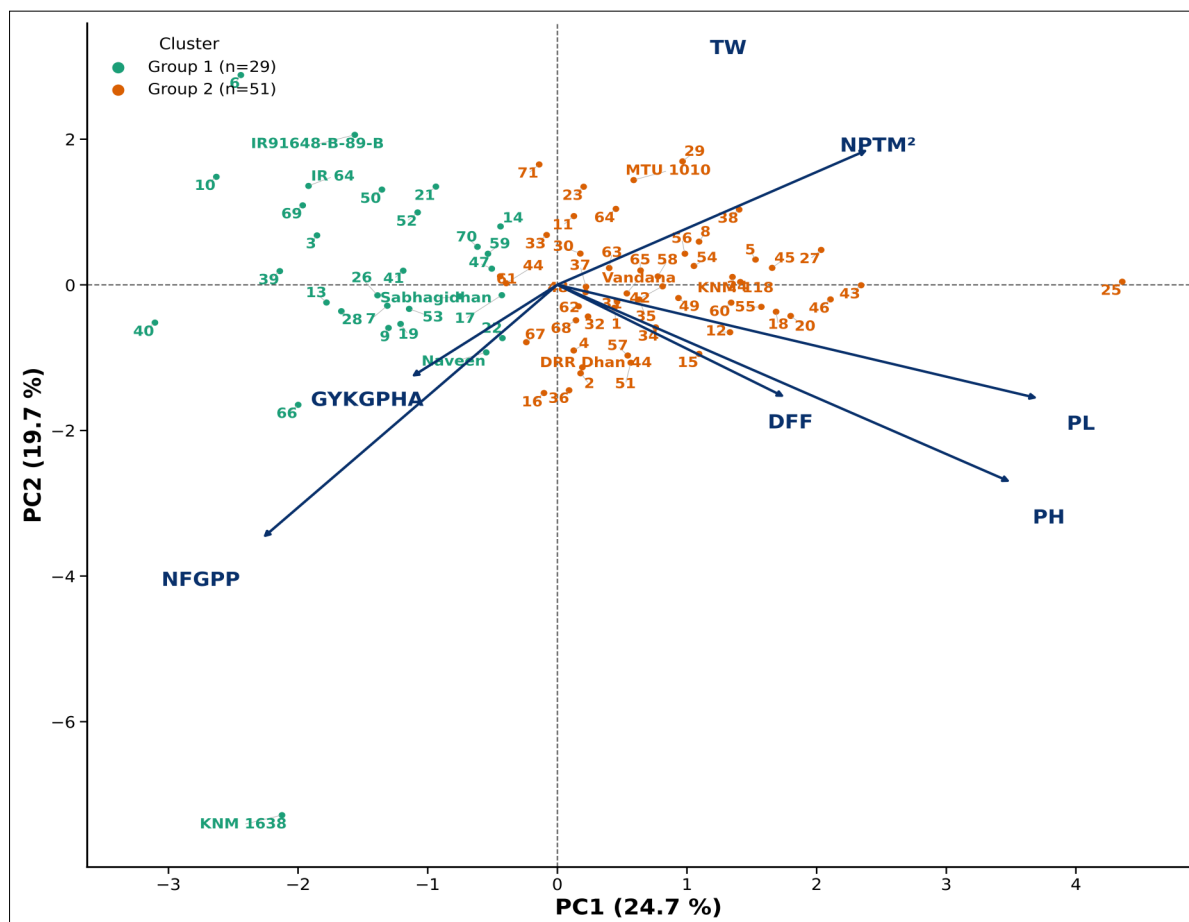


Fig. 4. Distribution of 80 rice genotypes based on seven agro-morphological traits under dry direct seeded conditions in principal component analysis biplot.

DFF: days to 50 % flowering; PH: plant height; NPTM²: number of productive tillers per m²; PL: panicle length; NFGPP: number of filled grains per panicle; TGW: test grain weight; GYKGPHA: grain yield (kg ha⁻¹).

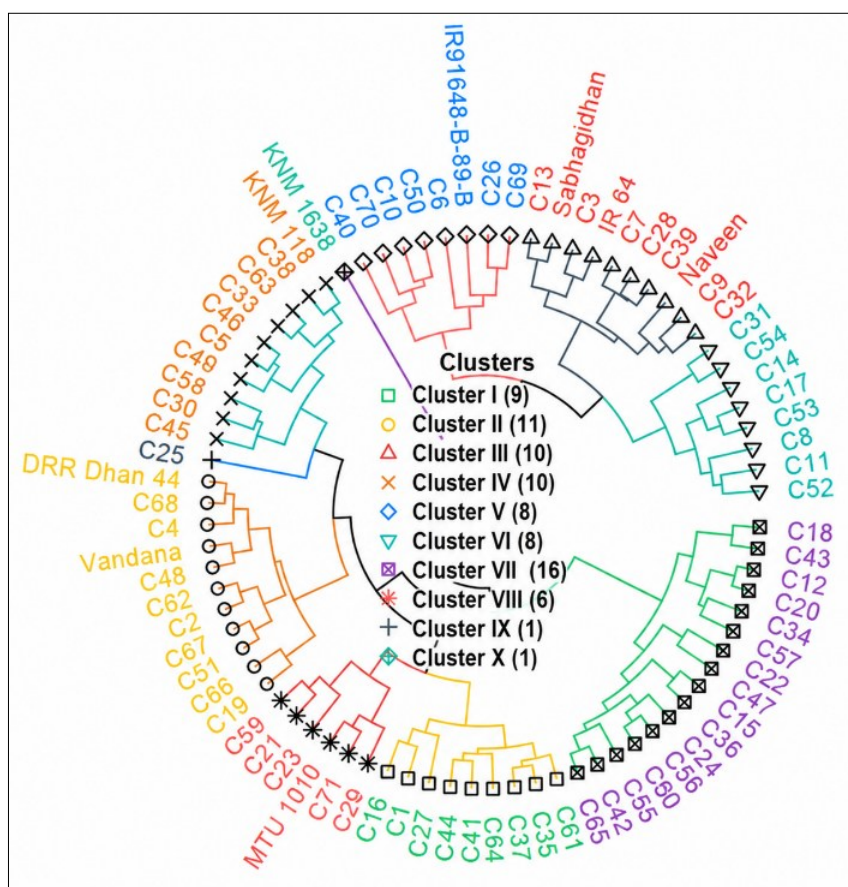


Fig. 5. Circular hierarchical clustering of 80 rice genotypes based on Euclidean distance using Ward's method under dry direct seeded rice.

Table 3. Mean values of seven agro-morphological traits across ten clusters identified through hierarchical analysis under dry direct-seeded rice conditions

Cluster	DFF	PH	NPTPM ²	PL	NFGPP	TGW	GYKGPHA
Cluster I	92	79	221	21	126	21	4131
Cluster II	92	83	207	21	141	23	4714
Cluster III	86	77	205	21	134	21	4277
Cluster IV	90	87	221	21	131	23	3765
Cluster V	85	69	216	20	141	24	4970
Cluster VI	82	85	219	21	134	23	4251
Cluster VII	87	85	215	23	130	23	4903
Cluster VIII	90	73	246	21	128	23	4702
Cluster IX	93	93	269	25	131	24	3933
Cluster X	92	93	197	22	199	16	5099

DFF: days to 50 % flowering; PH: plant height; NPTPM²: number of productive tillers per m²; PL: panicle length; NFGPP: number of filled grains per panicle; TGW: test grain weight; GYKGPHA: grain yield (kg ha⁻¹).

Table 4. Phenotypic performance of five promising breeding lines nominated to AICRIP for national testing under dry direct-seeded rice conditions

zSl. No.	IR DESIGNATION	DFF	PH	NPTPM ²	PL	NFGPP	TGW	GYKGPHA
1	IR125026-108-1-1	91	86	193	21.50	127	22.20	5126
2	IR127299-36-2-2	85	66	199	19.60	130	24.10	5832
3	IR127364-46-2-1	92	75	210	20.60	145	22.90	5329
4	IR12N234-1	86	79	246	21.70	118	24.20	5529
5	IR144564-3-47-1-1-B	89	78	208	23.30	130	23.70	5003

DFF: days to 50 % flowering; PH: plant height; NPTPM²: number of productive tillers per m²; PL: panicle length; NFGPP: number of filled grains per panicle; TGW: test grain weight; GYKGPHA: grain yield (kg ha⁻¹).

followed by IR12N234-1 (5529 kg ha⁻¹), IR127364-46-2-1 (5329 kg ha⁻¹), IR125026-108-1-1 (5126 kg ha⁻¹) and IR144564-3-47-1-1-B (5003 kg ha⁻¹). IR12N234-1 recorded the highest NPTM² (246) and TGW (24.2 g), whereas IR127364-46-2-1 exhibited the highest NFGPP (145). All five lines were nominated to the All India Coordinated Rice Improvement Programme (AICRIP) during 2024–25 for multi-location evaluation. Subsequently, IR144564-3-47-1-1-B and IR127364-46-2-1 advanced to AVT-I and AVT-II, respectively.

Discussion

The significant variation observed among the evaluated genotypes confirms the presence of substantial genetic diversity within the breeding population, providing opportunities for effective selection under DDSR conditions (19, 20). In the present investigation, majority of the lines showed earliness. In direct-seeded rice systems, especially within water-limited environments, early maturation allowed for the timely completion of the crop prior to critical soil moisture depletion. Under the dry-season conditions prevalent in South India, this flowering period was effectively aligned for relay cropping between major crops or for incorporation into intensified rotational practices, thereby substantiating the relevance of the statistical findings to field performance (21).

Across all the traits, PCV values were higher than GCV values (19), as anticipated in DDSR owing to the heterogeneity in soil moisture and microenvironments relative to transplanted systems. The relatively small differences between GCV and PCV for days to 50 % flowering and test grain weight, with supporting violin plots revealing compact distributions indicate limited environmental influence on these traits and suggest that phenotypic performance can reliably reflect genetic potential. Similar observations have been reported in rice breeding populations, where traits with narrow differences between GCV and PCV were considered stable across environments and suitable for selection (19, 22, 23).

The high heritability estimates observed for plant height, days

to 50 % flowering, test grain weight and grain yield indicate a strong genetic contribution to trait expression (19). The extended spread variability, consistent with the relatively larger disparity between GCV and PCV and minimal heritability observed for productive tillers per m² suggests a stronger environmental influence on this trait, likely reflecting the sensitivity of tillering to soil moisture variability and plant density under DDSR establishment conditions, which implies that selection for tillering ability may be more effective under managed and uniform field conditions rather than under the variable establishment typical of dry seeding (23–25).

In particular, the combination of high heritability and high genetic advance for grain yield suggests the predominance of additive genetic effects and highlights the potential effectiveness of direct selection for yield improvement. Comparable findings have been reported in rice by previous researchers, who emphasised that traits exhibiting high heritability and genetic advance provide greater opportunities for achieving genetic gain through selection (19, 20, 23). The grain yield range observed in this study, with elite lines reaching above 5800 kg ha⁻¹, compares favourably with reported national average productivity levels for direct-seeded rice in India, indicating that the advanced breeding lines evaluated here carry meaningful yield potential for deployment in DDSR target environments (8, 10, 11).

Correlation analysis revealed that grain yield was only weakly associated with individual component traits, indicating that productivity under DDSR is governed by the collective interaction of several agronomic characteristics rather than by a single dominant trait (26). This has a direct implication for breeding strategy that indirect selection for yield through any single component trait is unlikely to be effective under DDSR conditions and selection indices combining multiple traits simultaneously would be more appropriate for identifying high-yielding genotypes in this system. The significant positive association between plant height and panicle length suggests that these traits are influenced by related growth processes, while the negative association between filled

grains per panicle and test grain weight reflects the commonly observed trade-off between grain number and grain size in rice (27). The weak negative association between flowering duration and grain yield further supports the importance of early maturity for adaptation to water-limited production environments, where earlier flowering genotypes may avoid terminal drought stress and complete grain filling under more favourable conditions (21, 28).

Principal component analysis effectively summarised the multidimensional variability present within the breeding materials. The first two principal components explained 44.46 % of the total variation, indicating that a relatively small number of traits accounted for a substantial proportion of the observed diversity. Similar level of explained variation has been reported in rice diversity studies employing multivariate approaches (29). The close association of grain yield with filled grains per panicle in the biplot suggests that reproductive efficiency contributed substantially to productivity under DDSR conditions. At the same time, the separation of test grain weight from grain number traits further illustrates the contrasting contribution of these yield components, which is consistent with the correlation analysis.

The clustering pattern revealed considerable genetic divergence among the evaluated genotypes, resulting in the formation of ten distinct groups. Such divergence is highly valuable for breeding programmes because crosses between genetically distant parents are more likely to generate broader segregation and novel trait combinations in subsequent generations (30). The contrasting cluster means observed for grain yield, tillering ability, grain number and maturity indicate the availability of complementary parental sources within the breeding population. This diversity provides opportunities to combine favourable traits such as early maturity, high grain number, superior tillering ability and enhanced grain yield in future crossing programmes targeting DDSR adaptation. Cluster IX was monogenotypic and comprised only IR 129477-3425-97-4-3-3. Therefore, the high plant height (92.8 cm) and productive tillers m⁻² (269) reflect the characteristics of this individual genotype rather than a cluster pattern. Cluster X, comprising solely the locally adapted check variety KNM 1638, recorded the highest cluster mean grain yield, driven predominantly by an exceptionally high number of grains per panicle. However, as this is a monogenotypic cluster, the comparison is more appropriately made at the individual genotype level. All five elite IRRI breeding lines individually surpassed the yield of KNM 1638, confirming that targeted breeding for DDSR adaptation has produced lines with yield potential exceeding that of established regional checks, a meaningful benchmark for advancement through national testing pipelines.

One of the most important outcomes of the present study was the identification of five elite breeding lines with superior performance under DDSR conditions. These lines were subsequently nominated to the AICRIP for multi-location evaluation. Notably, IR144564-3-47-1-1-B and IR127364-46-2-1 advanced to AVT-I and AVT-II, respectively. Their advancement through the national testing system provides independent validation of the selection strategy employed in this study and demonstrates the practical utility of integrating genetic variability analysis, trait association studies and multivariate approaches for identifying promising breeding materials. Similar approaches have been successfully used to identify superior genotypes adapted to direct-seeded and aerobic rice production systems (31, 32). Although the present investigation provides valuable insights into variability and

diversity under DDSR conditions, further evaluation across multiple locations and seasons will be necessary to assess genotype × environment interactions and yield stability. Future research should focus on integrating DDSR-specific adaptive traits, including early seedling vigour, root system architecture, weed competitiveness, anaerobic germination ability and lodging resistance, with grain yield and agronomic performance. The incorporation of genomics-assisted breeding approaches may further accelerate the development of high-yielding and climate-resilient rice varieties adapted to DDSR ecosystems (8, 10, 12, 13).

Conclusion

The present study revealed substantial genetic variability and diversity among 80 rice genotypes evaluated under dry direct-seeded rice (DDSR) conditions. High heritability coupled with moderate to high genetic advance for several traits indicated good prospects for effective selection. Multivariate analyses identified distinct genetic groups and highlighted promising genotypes with superior agronomic performance and grain yield. Five elite breeding lines were nominated to the All India Coordinated Rice Improvement Programme (AICRIP) for multi-location evaluation, of which IR144564-3-47-1-1-B and IR127364-46-2-1 have since advanced to AVT-I and AVT-II respectively, while the remaining three lines continue in national testing, demonstrating their potential for wider adaptation and varietal development.

These findings provide valuable genetic resources for DDSR breeding and support the use of integrated variability and diversity analyses for identifying superior breeding materials. Future research should focus on multi-environment evaluation of promising genotypes, assessment of DDSR-specific adaptive traits such as early seedling vigour, root architecture and weed competitiveness and the integration of genomic and phenomic tools to accelerate the development of high-yielding and climate-resilient rice varieties for direct-seeded production systems.

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Authors' contributions

SS conceived and led the research, coordinated the experimental work, prepared the initial manuscript draft and facilitated communication among the team. DA supported the research programme and assisted in conducting the study. PJP and CV provided the genetic materials and performed the statistical analyses. All authors read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflicts of interest to declare.

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