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GENETIC DIVERSITY AND TRAIT INTERRELATIONSHIPS IN RICE UNDER RAINFED DIRECT-SEEDED CONDITIONS

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ABSTRACT

Direct-seeded rice (DSR) is a resource-efficient alternative to transplanted puddled rice but its adoption needs a clear understanding of the genetic variability and trait interrelationships under rainfed direct seeding conditions. To address this, in present study 126 diverse rice genotypes were evaluated under DSR during the *kharif*-2022 and *kharif*-2023 season to assess genetic variability and characterize multi-trait relationships across key agronomic traits through different statistical approaches. Mixed-model analysis revealed strong genotypic effects for maturity, plant architecture and reproductive traits, while grain yield and biomass exhibited substantial genotype × year interaction. Correlation and PCA results showed that grain yield was primarily driven by biomass accumulation, spikelet fertility and partitioning efficiency. BLUP-based clustering separated the germplasm into clear performance groups and highlighted an elite cluster with favorable multi-trait profiles. Six genotypes, including established checks (THAVALAKANNAN, MADHURAJ 55 and IGKV R1) and promising accessions/ germplasm line (KALAI::IRGC 33151-2, UPL RI 7::IRTP 9897-C1 and CHAO KHIE KHOUAY::IRGC 90968-1), exhibited consistently strong BLUP ranks for grain yield, biological yield, and harvest index. These findings demonstrate substantial genetic diversity within the panel and provide a data-driven foundation for selecting high-performing material suited to rainfed DSR.

Key words: Direct-seeded rice; Genetic variability; Trait interrelationships; Principal component analysis; Best Linear Unbiased Predictions

Introduction

Rice (*Oryza sativa* L.), which provides the major source of food to more than half of the world's population, is a key factor in global food security. However, traditional cultivation methods, especially puddled transplanted rice (PTR), are heavy consumers of resources as they require lots of water, labor, and energy. These methods are increasingly unsustainable in the face of contemporary climate change and socioeconomic challenges (Negi *et al.*, 2024) and it is, therefore, necessary to favor crop establishment techniques that are more efficient in terms of the use of resources.

DSR has emerged as one of the viable alternatives to traditional methods, wherein seeds are directly sown into the field without going through the nursery and transplanting process. This approach offers key advantages, such as saving a lot of water (12-35%), reducing the labor burden, shortening crop duration, and lowering greenhouse gas emissions since soil puddling is eliminated, as is continuous flooding (Kumar and Ladha, 2011; IRRI-DSR Consortium, 2025). Additionally, DSR provides timely crop cycles that allow intensification and lead to increased farm productivity and sustainability (Balasubramanian and Hill, 2002). Its increasing number of adopters is representative of a wider transition towards rice production systems that are not only more climate-resilient but also economically viable (Farooq *et al.*, 2011).

Despite these advantages, the success of DSR largely relies on the the availability of suitable genotypes. Direct seeding causes rice plants to face stress at the early growing stage, for instance, water stress, competition with weeds, and lack of seedling establishment. Therefore identifying cultivars with vigorous emergence, stable growth and efficient yield formation is essential. In the direct-seeding system, major agronomic traits such as shoot dry weight, days to maturity, plant height, panicle length, grain yield, biological yield, spikelet fertility, and harvest index can offer reliable information and knowledge about the potential performance of the genotypes (Kumar and Ladha, 2011; Farooq *et al.*, 2011; Chauhan *et al.,* 2017). In order to improve DSR-adapted varieties and determine the physiological basis of yield, it is equally important to study the genetic variability and interactions of these traits (Prakash *et al.,* 2024).

Although DSR has major possibilities, there is still a substantial gap in research that comprehensively evaluates genetic diversity and trait relationships across a broad range of rice genotypes under rainfed direct-seeded conditions. Addressing this gap requires robust statistical tools capable of capturing genotypic performance across environments and dissecting complex trait interactions. In this study, we evaluated 126 diverse rice genotypes under rainfed direct-seeded conditions over two years and assessed genetic variability, trait relationships and multi-trait performance using a combination of mixed-model BLUPs, multivariate analyses and hierarchical clustering. This integrated approach provides a detailed understanding of genotype behavior under DSR and supports the identification of the high-yielding, resilient rice varieties, which are eco-friendly and well-adapted to DSR systems.

Materials and Methods

Plant Material and Experimental Site

The present study was carried out at the research farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh (21°162 N, 81°362 E; altitude 289.6 m) during the *kharif*-2022 and *kharif*-2023 cropping season under rainfed direct seeded rice (DSR) conditions. A diverse set of 126 different rice genotypes (Supplementary Table S1) including germplasm lines, breeding lines, and widely used check varieties were evaluated for phenotypic traits and genotypic variability under low-input rainfed DSR conditions.

Experimental Design and Crop Management

The experiment was established in a randomized complete block design (RCBD) with two replications in each year. Each block contained all 126 genotypes, including checks. To mitigate the effects of spatial heterogeneity, the sequence of genotypes was reversed in the second replication. Seeds were sown directly in well-prepared fields at a spacing of 20 × 20 cm to ensure uniform plant density. The crop was grown under nitrogen and phosphorus-deficit conditions to evaluate performance of genotypes under low-input rainfed DSR systems (Kumar and Ladha, 2011). Standard DSR crop management practices were followed according to the IRRI evaluation guidelines (IRRI, 2013).

Phenotypic Data Collection

Data of eight agronomically important traits significant for performance assessment under rainfed DSR was taken: shoot dry weight (SDW, g plant^{-1}), days to maturity (DTM, days), plant height (PH, cm), panicle length (PL, cm), grain yield (GY, g m^{-2}), biological yield (BY, g m^{-2}), spikelet fertility (SF, %) and harvest index (HI). SDW was determined at 35-40 days after sowing to represent early vegetative biomass and early vigor. PH and PL were obtained at maturity, whereas GY, BY, SF, and HI were recorded at harvest; DTM was recorded from period of sowing to physiological maturity. For each genotype within a replication, five plants were randomly selected, and the observations were taken. The average value of these five plants was determined and thereafter used for all statistical .

Statistical Analysis

The dataset included 126 genotypes evaluated for eight traits during two years with two replication. Linear mixed models were fitted to quantify variance components across years and to obtain best linear unbiased predictions (BLUPs) for genotypes. Year was considered as a fixed effect in these models, while genotype, replication, and genotype × year interaction were considered as random effects. From the mixed mode ANOVA, F-test was used to assessed significance of fixed effects (Year). Significance of random effects (Genotype and G × Y) was assessed using likelihood ratio tests (LRT). Broad-sense heritability across years was calculated using variance components following standard multi-year RCBD formulas.

R software version 4.5.0 was used for all statistical analyses (R Core Team, 2025). The subsequent packages were employed for specific analyses: *lme4*, *sommer*, and *asreml* for variance components and mixed-model analyses; *agricolae*; *FactoMineR* and *factoextra* for multivariate analysis, including principal component analysis (PCA); *Hmisc* and *corrplot* for correlation analyses; and *ggplot2* for data visualization.

Result and Discussion

Phenotypic variation of traits across seasons

Significant phenotypic variability was observed

Table 1: Descriptive statistics of eight agronomic traits in 126 rice genotypes evaluated under rainfed direct-seeded condition during *kharif*-2022 and *kharif*-2023.

Trait	Year	Mean	Standard deviation	Min	Max	Range	Coefficient of variation (%)
Shoot dry weight (g plant^{-1})	2022	4.07	0.79	2.00	6.60	4.60	19.36
Shoot dry weight (g plant^{-1})	2023	4.18	1.01	2.40	7.20	4.80	24.06
Days to maturity	2022	119.33	10.12	95.00	160.00	65.00	8.48
Days to maturity	2023	119.76	10.31	101.00	161.00	60.00	8.61
Plant height (cm)	2022	93.13	17.60	59.47	159.17	99.70	18.90
Plant height (cm)	2023	86.69	15.45	57.00	141.67	84.67	17.82
Panicle length (cm)	2022	21.62	2.30	15.97	27.87	11.90	10.62
Panicle length (cm)	2023	22.03	2.61	13.97	29.30	15.33	11.86
Grain yield (g m^{-2})	2022	168.58	78.49	20.00	426.11	406.11	46.56
Grain yield (g m^{-2})	2023	67.70	40.97	5.00	303.33	298.33	60.52
Biological yield (g m^{-2})	2022	617.56	180.68	171.67	1332.22	1160.56	29.26
Biological yield (g m^{-2})	2023	321.55	103.83	76.67	813.33	736.67	32.29
Spikelet fertility (%)	2022	82.03	3.02	72.00	87.79	15.79	3.68
Spikelet fertility (%)	2023	81.72	3.15	70.13	86.96	16.83	3.85
Harvest index	2022	0.27	0.08	0.06	0.61	0.55	30.81
Harvest index	2023	0.20	0.08	0.04	0.65	0.61	38.98

among 126 rice genotypes evaluated under rainfed direct-seeded rice (DSR) conditions across two seasons (Table 1). SDW, an indicator of early vigor and seedling establishment showed moderate means (~4.1 g plant^{-1}) with high variability (CV 19-24%). This high variability observed in recent reports on the significance of early vigor showing its importance for crop establishment and weed competitiveness under DSR by Negi *et al.,* (2024) and Vyshnavi *et al.,* (2025). DTM was remarkably stable across years (mean ~119 days, CV <9%), indicating stable genetic control of developmental duration despite seasonal fluctuations as reported earlier by Goyal *et al.,* (2022). In contrast, architectural traits like PH (CV ~18–19%) and PL (CV ~ 10-12%) varied moderately between years, indicating vegetative responses to seasonal conditions. Similar patterns of robust diversity and environmental response in architectural traits have been observed by Rashad Khan *et al.,* (2023).

Yield-related traits showed the highest seasonal variations. GY decreased significantly from 168.6 to 67.7 g m^{-2}, with its CV increasing from 46.56% to 60.52%. While SF remained stable (mean ~82%, CV <4%), BY also decreased substantially. This suggests reproductive success was less sensitive than total biomass and grain production, as reported in earlier DSR studies by Ahmed *et al.,* (2025) and Goyal *et al.,* (2022), where genotype × environment interactions cause different responses in growth and yield components. HI declined from 0.27 to 0.20 with increased variability (CV 31–39%), implying reduced partitioning efficiency. This pattern aligns with studies on DSR systems by Kumar and Ladha (2011), reporting that biomass accumulation and harvest index are key yield determinants significantly influenced by environmental factors.

In summary, traits like DTM and SF were stable across seasons, while SDW, GY, BY, and HI responded strongly to seasonal change. This broad phenotypic spectrum provides a solid foundation for further genetic analysis and selection of genotypes for rainfed DSR.

Mixed-Model ANOVA

The mixed-model ANOVA revealed significant variations in how various traits were genetically influenced by genotypes, years, and their interaction under specific growing condition like DSR (Table 2). Year effects for most of the traits including SDW, DTM, PH, PL, and SF, showed non-significant variations, and thus there mean levels remained relatively stable across 2022 and 2023 despite seasonal variation. In contrast, year effect showed significant variations for GY, BY and HI, which is indicative of differences in biomass production and resource allocation that were specific to respective years as earlier reported by Kumar and Ladha (2011).

Genotypic effects were highly significant for several traits, except for SDW ($p > 0.05$), signifying the absence of genetic variation for early vigor in these genotypes when evaluated under these conditions. The strong genetic control reported for maturity, plant architecture, and yield components proves substantial underlying genetic diversity. This is an important finding for breeders, as it demonstrates that these traits are amenable to genetic improvement through selection even in a challenging DSR

Table 2: Mixed-model ANOVA showing the effects of year, genotype, and genotype × year interaction on eight agronomic traits under rainfed direct-seeded condition.

Trait	Year (F-test)		Genotype (LRT X^2)		Genotype × Year (LRT X^2)	
	F-value	P-value	X^2-value	P-value	X^2-value	P-value
Shoot dry weight (g plant^{-1})	1.1	0.320 ns	0	1.000 ns	61.09	5.46E-15 ***
Days to maturity	0.37	0.551 ns	98	4.19E-23 ***	128.99	6.81E-30 ***
Plant height (cm)	2.62	0.244 ns	76.28	2.46E-18 ***	1.56	0.211 ns
Panicle length (cm)	0.09	0.795 ns	12.97	0.0003 ***	0	0.976 ns
Grain yield (g m^{-2})	39.62	0.014 *	5.63	0.0178 *	49.48	2.00E-12 ***
Biological yield (g m^{-2})	54.49	0.011 *	13.63	0.00022 ***	39.9	2.68E-10 ***
Harvest index	12.19	0.061 ns	6.63	0.010 *	9.58	0.001 **
Spikelet fertility (%)	0.22	0.681 ns	4.5	0.033 *	7.81	0.005 **

F-tests were used for fixed year effects, while likelihood ratio tests (LRT) were used for random genotype and interaction effects. Level of significance: ns = $p > 0.05$; * = $p \leq 0.05$; ** = $p \leq 0.01$; *** = $p \leq 0.001$, ns = not significant.

environment, aligning with studies by Sandhu *et al.*, (2021) that show major loci often govern these characteristics.

Interaction effect of Genotype × year (G x Y) were significant for SDW, DTM, GY, BY, HI, and SF. These highly significant interactions are a distinct feature of plant breeding in stress-prone environments, where responses of genotypes are not uniform for varying stress intensities and seasonal variations, as reported by Kumar *et al.*, (2012) and Ceccarelli (1996). In contrast, several traits such as PH and PL showed negligible G×Y interactions, hence indicating their stability and the reliability in selecting for these morphological traits based on performance in fewer seasons. Overall, the results show that yield-related traits (GY, BY, HI) were strongly influenced by the environment as well as genotype x year interaction, whereas a few traits (DTM, PH, PL, SF) were stable. As a result, multi-year evaluation is crucial for identifying stable genotypes for rainfed DSR.

Genetic variability and inheritance patterns under DSR

Genetic parameter estimates indicated contrasting contributions of genetic and environmental effects to trait expression under rainfed direct-seeded rice (DSR) conditions (Table 3). Broad-sense heritability (H^2) was high DTM (0.7) and moderate for PH (0.5), indicating stable expression and good scope for selection of these traits across seasons. In contrast, SDW exhibited zero heritability, suggesting that early vigor was predominantly governed by environmental and year-specific effects under DSR conditions, as reported in earlier studies by Rashad Khan *et al.*, (2023) and Vyshnavi *et al.*, (2025).

Yield-related traits like GY (H^2 = 0.2), BY (0.3), HI (0.2), PL (0.1), and SF (0.1), showed low heritability, suggesting strong environmental influence and pronounced genotype × year interactions typical of rainfed and DSR systems as supported by Kumar and Ladha, (2011) and Sandhu *et al.*, (2021). Phenotypic coefficients of variation were consistently higher than genotypic coefficients for all traits, with GY exhibiting the highest PCV (53.1%) with moderate GCV (21.2%), indicating wide phenotypic diversity but limited efficiency of direct phenotypic selection. SF had the lowest variability, with a PCV of 3.8% and a GCV of 1.3%. This confirms the stability of the trait across different environments, as supported by Kumar *et al.*, (2025) and Saran *et al.*, (2023).

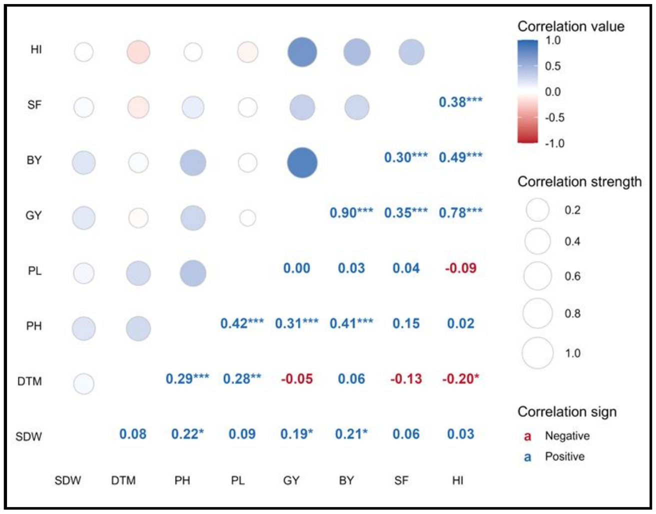

Fig. 1: Pearson correlation matrix among eight agronomic traits in 126 rice genotypes evaluated under rainfed direct-seeded cultivation. Traits include: biological yield (BY), days to maturity (DTM), grain yield (GY), plant height (PH), panicle length (PL), shoot dry weight (SDW), spikelet fertility (SF) and harvest index (HI). The color and size of each bubble represent the direction and magnitude of the Pearson correlation coefficient (r), respectively. Blue color indicates positive correlations and red color indicates negative correlations. Numeric values and asterisks denote the correlation coefficient and its significance level (*p<0.05, **p<0.01, ***p<0.001).

Table 3: Estimate of genetic parameters and variance components for eight agronomic traits in 126 rice genotypes grown under rainfed direct-seeded conditions.

Trait	Mean	σ^2g	σ^2gy	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2	GAM (%)
Shoot dry weight (g plant^{-1})	4.1	0.0	0.4	0.4	0.8	0.0	21.9	0.0	0.0
Days to maturity	119.6	73.4	21.5	9.7	104.6	7.2	8.6	0.7	10.4
Plant height (cm)	89.9	142.6	4.7	127.6	274.9	13.3	18.4	0.5	14.2
Panicle length (cm)	21.8	0.7	0.0	5.4	6.1	3.7	11.3	0.1	0.8
Grain yield (g m^{-2})	118.1	628.1	1429.7	1870.6	3928.3	21.2	53.1	0.2	7.0
Biological yield (g m^{-2})	469.6	5353.3	6202.4	10202.8	21758.5	15.6	31.4	0.3	7.9
Spikelet fertility (%)	81.9	1.2	1.6	6.8	9.5	1.3	3.8	0.1	0.3
Harvest index	0.2	0.0	0.0	0.0	0.0	13.3	34.4	0.2	4.1

Note: σ^2g: Genotypic variance, σ^2gy: Genotype × Year (Environment) Interaction Variance, σ^2e: Environmental variance, σ^2p: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, H^2: Broad-sense heritability, GAM: Genetic advance as percentage of mean.

Genetic advance as a percentage of the mean (GAM) was moderate for PH (14.2%) and DTM (10.4%), suggesting reasonable expected response to selection. In contrast, SDW, SF, and PL had negligible GAM (<1%) whereas, GAM values (< 10 %) observed for yield and reproductive traits, indicating limited genetic gain due to non-additive gene action and strong environmental modulation. Notably, genotype × year interaction variance constituted a significant proportion of total variance for GY and BY, emphasizing the importance of multi-year evaluation for identifying stable genotypes under rainfed DSR conditions as reported by Kumar *et al.,* (2020) and Huang *et al.,* (2021). Overall, phenological (DTM) and architectural traits (PH) appear more reliable for selection under rainfed DSR, whereas improvement of yield traits (GY, BY, HI) and SDW requires strategies that account for strong environmental and year-specific effects.

Trait relationships and yield-driving components

Correlation analysis on the pooled dataset and year-wise resulted in significant and interpretable associations between the attributes investigated under rainfed DSR conditions (Fig. 1; Supplementary Table S2). GY was found to have strong positive association with BY and HI establishing the fact that these two traits are the most important factors determining the yield of the crop under unfertilized-DSR conditions. Moderate positive association was found between SF and final GY suggests that fertile spikelet are still of prime importance for the conversion of biomass into grain yield, as noted by Kriti *et al.,* (2025) and Negi *et al.,* (2024).

PH showed moderate association with GY, BY, and PL indicating superiority in their accumulation for taller plants. In contrast, DTM showed negative associations with GY and HI, suggesting that longer growth duration did not lead to better yields in this low-input system. Similar studies under DSR were observed by Mahender *et al.,* (2015), Chen *et al.,* (2009) and Kumar *et al.,* (2020) have found that early to medium duration genotypes often perform better, as they can escape late-season moisture stress and maintain greater reproductive efficiency.

Year-wise correlation patterns revealed seasonal modulation of trait relationships. SDW had positive correlations with both GY and BY in 2022 but failed to show any correlations in 2023, suggesting that early vigor did not contribute to yield formation under unfavorable establishment conditions. In contrast, GY showed strong positive correlations with both BY and HI, consistent across both seasons; these correlations are stable as indicated by Xin *et al.*, (2021), Kaur and Singh (2017), and Liu (2025).

Overall, while SDW, PH, and PL exhibited seasonal variation, the inter-relationships of GY, BY, HI, and SF are stable, making them suitable trait for selection under nutrient-limited direct-seeded rice. Seasonal variation highlights the need for multi-year evaluation to identify consistently performing genotypes.

Principal Component Analysis (PCA)

Principal component analysis (PCA) of pooled and year-wise dataset justified the correlation results by showing a distinct multivariate structure among traits (Fig. 2; Supplementary Tables S3 and S4). The total variation of 61.83% was explained by first two principal components (PC1: 35.7%, PC2: 26.1%). PC1 was predominantly driven by GY, BY, HI, and SF, representing a yield efficiency axis. PC2 was mainly influenced by DTM, PH, and PL, reflecting a phenology-architecture axis. This multivariate separation aligns with previous studies by Gupta *et al.*, (2022), Muthuramu (2023) and Prakash *et al.*, (2024) showing that yield-related traits and structural traits form independent principal axes in low-input or direct-seeded rice environments. SDW loaded strongly on PC3, indicating its relative independence from yield and architectural traits and its sensitivity to seasonal conditions. The separation of early vigor on its own axis shows how seedling growth is sensitive to moisture and establishment conditions in DSR, where vigor does not always link with final yield when environmental stress is present, as observed by Sandhu *et al*., (2019).

The PCA biplot (Fig. 2) from pooled data showed close grouping of GY, HI, BY, and SF, indicating their coordinated expression across years. PC1 distinguished high-yielding, resource-efficient genotypes from low-yielding ones, while PC2 distinguished genotypes by DTM and PH. This separation of architectural traits from yield traits aligns with reports in direct-seeded systems by Ghosh *et al*., (2025) and Chandra *et al*., (2025).

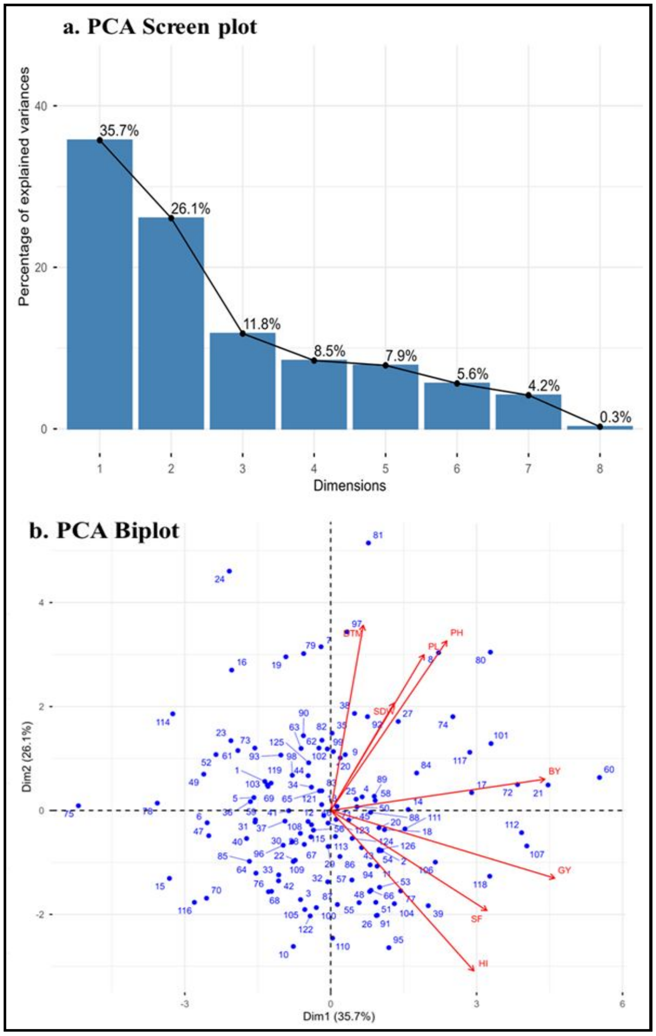

Fig. 2: Principal component analysis (PCA) of 126 rice genotypes for eight agronomic traits. (a) Scree plot showing the percentage of variance explained by each principal component. (b) Biplot of PC1 and PC2, illustrating genotype distribution and trait loadings. Genotypes are represented by numbers. Trait vectors (arrows) show the direction and strength of each trait's contribution to the principal components. BY: Biological yield, DTM: Days to maturity, GY: Grain yield, PH: Plant height, PL: Panicle length, HI: Harvest index, SF: Spikelet fertility.

Season-wise PCA revealed meaningful differences supported to pooled structure (Supplementary Table S4). In 2022, PC1 (41.85% variance) was driven by GY, BY, and SDW, linking early vigor to performance in a favorable season. In 2023, PC1 (35.14% variance) was governed by GY, HI, and BY, with a minimal contribution from SDW (1.49%). This indicates that early vigor contributed less to genotypic differences under the likely moisture or establishment challenges of 2023, while yield remained linked to biomass and partitioning efficiency. This seasonal decoupling of vigor from yield has been observed in other DSR studies by Sandhu *et al*., (2019) and Kumar and Ladha (2011) particularly where early-season stress affects crop establishment.

Overall, the pooled and year-wise PCA results demonstrate that GY under rainfed DSR is primarily governed with BY production and HI, with SF. playing a supportive role. While early vigor and phenological traits influence performance in a season-dependent manner, yield-related traits form a stable core selection criterion across years.

Genotype grouping and performance clusters based on BLUPs

Hierarchical clustering based on standardized BLUP values for eight agronomic traits grouped the 126 rice genotypes into distinct performance clusters under rainfed DSR conditions (Fig. 3; Supplementary Table S5). The clustering pattern revealed substantial genetic diversity within the panel and enabled clear differentiation of genotypes based on multi-trait performance, consistent with the use of BLUP-based clustering for germplasm characterization under variable environments (Mohammadi and Prasanna, 2003).

One cluster comprised elite, high-performing genotypes characterized by consistently positive BLUP values for GY, BY, SDW, and SF. This cluster included KALAI::IRGC 33151-2, THAVALAKANNAN, UPL RI 7::IRTP 9897-C1, CIWINI SML::IRGC 50942-1, MADHURA 55, TA PAI MAUNG::IRGC 7292-1, SWARNA, etc. These genotypes exhibited balanced performance across yield components and strong adaptation to rainfed direct-seeded conditions through efficient biomass production and assimilate partitioning as reported by Melandri *et al*., (2021) and Anandan *et al*., (2021). The presence of well-established check varieties within this cluster further validates the robustness of the BLUP-based evaluation.

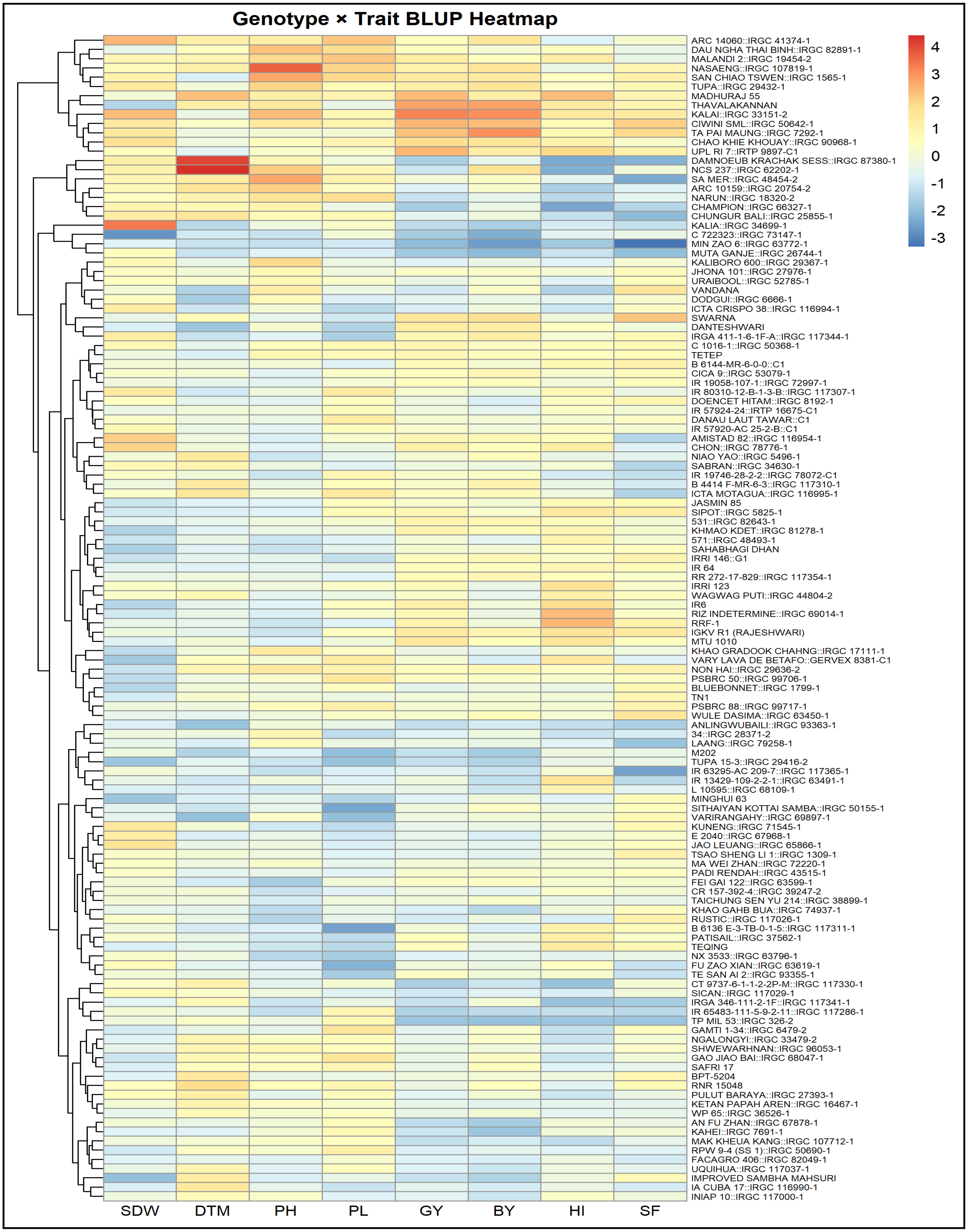

Fig. 3: Hierarchical clustering and heatmap of 126 rice genotypes based on standardized BLUP values for eight agronomic traits. The dendrogram represents genetic similarity. The heatmap colors represent z-scores for each trait (red: above mean, blue: below mean).

Other clusters represented genotypes with specific trait combinations, including tall and late-maturing types, early-maturing semi-dwarf genotypes, and entries with high biomass but lower harvest index. Genotypes identified as having high biomass but reduced partitioning efficiencies suggest that there is possibility for improvement through breeding techniques, as stated in earlier rice breeding literature by Peng *et al*., (2008) and Wei *et al*., (2018).

A distinct cluster consisting of genotypes characterized by consistently low BLUP values for most yield-related traits, indicating poor adaptation to DSR, likely due to limitations in early establishment, stress, or reproductive efficiency. Intermediate clusters showed mixed performance patterns, reflecting diverse genetic backgrounds and variable trait expression under DSR.

A subset of six genotypes including known checks (THAVALAKANNAN, MADHURAJ 55 and IGKV R1) and promising accessions/germplasm lines (KALAI::IRGC 33151-2, UPL RI 7::IRTP 9897-C1 and CHAO KHIE KHOUAY::IRGC 90968-1) ranked consistently superior for GY, BY and HI across years to signify their potential for use in rainfed direct seeded systems. overall, the above results from BLUP clustering, PCA structure, and trait correlation studies among the traits confirms that the groups of genotypes based on the values of BLUP represent consistent biological patterns rather than artifacts of any single method, but indicate real phenotypic differences that matter for breeding in direct-seeded conditions.

Conclusion

This study showed high phenotypic as well as genetic variation among rice genotypes evaluated for rainfed direct seeding, which highlights their potential for improving adaptation and productivity traits under low-input conditions. Medium to high heritability and genetic advance was observed for traits associated with early vigor, biomass and reproductive efficiency, thereby indicating their ability for efficient selection. Grain yield and biomass were found more susceptible to changes associated with different growing environments across different years due to significant genotypic x year interactions, thereby emphasizing the importance of environmental conditions associated with a specific year on performance pattern under rainfed cultivation. Integrated correlation, principal component, and BLUP-based clustering analyses consistently demonstrated that grain yield under rainfed direct seeding is primarily governed by biomass production, efficient assimilate partitioning, and spikelet fertility. A small group of genotypes showed stable and superior multi-trait performance across years, identifying them as promising candidates for cultivation and for use as donor parents in breeding programs targeting direct-seeded rice system. Overall, the integrated findings provide a comprehensive understanding of trait dynamics under rainfed DSR condition and offer a strong basis for developing resilient high-yielding cultivars suited to water-saving rice production systems.

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