PLANT SCIENCE TODAY
ISSN 2348-1900 (online)
Vol x(x): xx–xx
https://doi.org/10.14719/pst.2658

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RESEARCH ARTICLE

Assessment of variability parameters and diversity of panicle architectural traits associated with yield in rice (*Oryza sativa* L.)

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ARTICLE HISTORY
Received: 10 May 2023
Accepted: 13 August 2023
Available online
Version 1.0 : 14 October 2023

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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Jasmin S A, Prasanth P H, Ramchander S, Kumar P D, Devasena N, Naveenkumar R, Thankappan S, Kingsly N B J. Assessment of variability parameters and diversity of panicle architectural traits associated with yield in rice (*Oryza sativa* L.). Plant Science Today (Early Access). https://doi.org/10.14719/pst.2658

Abstract

The rice panicle, a pivotal reproductive structure, signifies the transition from vegetative to reproductive growth in plants. Comprising components such as the rachis, primary and secondary branches, seed quantities and branch lengths, panicle architecture profoundly influences grain production. This study delves into the diversity of panicle architecture traits and scrutinizes variability parameters across 69 distinct rice genotypes. Our findings underscore substantial variations in panicle architecture traits among genotypes. Particularly noteworthy are traits with the highest coefficient of variation (CV%), encompassing the count of secondary branches, single plant yield, productive tillers per plant, seeds per secondary branch and panicle weight. Correlation analysis reveals robust positive connections between panicle weight, the number of filled grains per panicle, 1000-grain weight and single plant yield. The number of secondary branches exhibits the most substantial phenotypic coefficient of variation (PCV%) at 47.14%, accompanied by a genotypic coefficient of variation (GCV%) of 43.57%. Traits such as days to 50% flowering, plant height and number of filled grains per panicle manifest high heritability (97.04%, 91.24% and 76.22% respectively) and notable genetic advancement (23.11%, 39.62% and 47.49%). The principal component analysis identifies the primary component (PC1) as the principal contributor to variance. Biplot analysis accentuates positive correlations between attributes like the number of filled grains per panicle, panicle length, plant height, primary branch count, panicle weight, seeds per primary branch and the number of secondary branches with single plant yield. By employing Mahalanobis D^2 statistics, the classification of genotypes into 6 distinct clusters reveals clusters III and IV as distinguished by their significant inter-cluster and intra-cluster distances. This comprehensive analysis unveils the potential for harnessing panicle architecture traits to enhance grain production and advances our comprehension of intricate relationships within diverse rice genotypes.

Keywords

Cluster analysis; correlation; heritability; panicle structure; principal component analysis

Introduction

Rice (*Oryza sativa* L.) is a semi-aquatic grass species cultivated globally. In India, the crop is referred to as "dhanya", symbolizing "the subsistence of the human race" (1). It covers 11% of the world's arable land and occupies approximately 30% of the area allocated for grain crops. Recent research suggests an anticipated 12% increase in the global population. Consequently, meeting the escalating demand for rice necessitates boosting productivity by at least 13% and increasing rice production by 500 million metric tonnes (2).

The inflorescence of rice is known as panicle. Panicle production initiates when the plant transitions from vegetative to reproductive growth (3). The shoot apical meristem of rice transforms into an inflorescence meristem, which further develops into a primary branch meristem before undergoing abortion during the reproductive growth phase. Successive formation of secondary branch meristems on the main branch occurs, which then differentiate into spikelet branch meristems and lateral spikelet meristems. Concurrently, the top of the primary branch meristem divides into a terminal spikelet meristem. These developmental processes collectively contribute to the formation of the essential structure of the rice panicle (4). The panicle comprises various components including the rachis, primary branches, secondary branches (5), as well as other factors such as the number of seeds per panicle, seeds per primary and secondary branches, length of primary and secondary branches and panicle length – all of which constitute the panicle architecture.

In rice, the panicle architecture has been the main focus of high-yield breeding (5, 6). The primary rachis produces the primary branch, which further branches into the secondary branches. This panicle branching determines the grain count per panicle (4). Grain number and grain weight, oftern referred to as 2Gs, represents 2 complex traits controlled by numerous quantitative trait loci (QTLs), playing a pivotal role in enhancing rice yield (7). The length of the panicle, the number of primary branches and secondary branches, and the number of spikelets or grains are all quantitative aspects of panicle architecture that have an impact on crop yield (8). Over the last 22 years, a multitude of genes involved in panicle development have been identified and functionally characterized. Genes like Short Panicle 1 (*Sp1*), Direct and Erect Panicle 2 (*DEP2*) and Direct and Erect Panicle 3 (*DEP 3*) affect the panicle length (8), the genes *OsSPL14*, Aberrant Spikelet and Panicle 1 (*ASP1*), Aberrant Panicle Organization 1 (*APO1*) control branch number (9). Undulate Rachis -1 (*Ur1*) which is a dominant gene governs the development of primary branches and secondary branches (10). Enhancing grain number per panicle is influenced by genes such as grain number 1 a (*Gn1a*), grain number per panicle 1 (*GNP1*) (11), grain length and awn development (*GAD1*) (12), awn 1(*An1*) (13) and plant architecture and yield 1 (*PAY1*) (14). Moreover, the gene regulator of grain number1 (*RGN1*) orchestrates both grain number and shape (4).

Various studies have identified simple sequence repeats (SSR) markers corresponding to different panicle architecture traits. For instance, a study by (15) Reported ten SSR markers associated with the Panicle Length, situated on chromosomes 2, 3, 5, 6, 8 and 9, derived from a natural population in East and Southeast Asia. Likewise, other markers like RM5833 and RM5707 located on chromosome 2 have been associated with erect panicles (16), RM7329 on chromosome 6 linked with the secondary branching (10), marker RM413 present in chromosome 5 associated with the number of spikelets per panicle (17), RM3430 on the chromosome 6 associated with primary branching (18) and marker RM140 located on the chromosome 1 are linked with the short panicle trait (19).

Small regulatory molecules known as phytohormones have an impact on almost every aspect of plant growth and development. Among these hormones, such as cytokinins, auxins and gibberellins, they collectively orchestrate the emergence and growth of rice inflorescences. These hormonal cues are particularly critical for rice yield attributes due to their intricate interplay and cross-talk (20). For instance, cytokinin, a plant hormone, controls both primary branch number and the grain number (21), as well as length of the panicle (22-24). Auxin controls the branching in rice panicles (25) and gibberellins play a major role in controlling the panicle size (26). The objective of this study is to conduct a comprehensive exploration of the variation in panicle architecture traits across traditional and adaptable rice varieties. The ultimate aim is to identify optimal candidates among these lines, which can then be strategically integrated into forthcoming rice breeding programmes. This integration is anticipated to effectively enhance the crop's yield potential for the future.

Materials and Methods

Plant Material

The genetic material for this study comprised 69 germplasm lines sourced from various regions of southern India. These lines include both landraces and varieties (Supplementary Table S1).

Field trial

The experimental study was conducted at the South farm of Karunya Institute of Technology and Sciences in Coimbatore during the *Kharif* and *Rabi* season of the year 2022. The genotypes were grown in 3 replications using a randomized block design (RBD) with a spacing of 20 × 20 centimeters, covering a total field area of 7840.8 sq ft. The crop was cultivated following the recommended crop management practices, which include appropriate irrigation, fertilizer and pesticide usage.

Phenotyping of the germplasm lines

Phenotyping for all the accessions was performed manually. The plants were marked after being randomly selected. A total of 13 quantitative morphological traits related to panicle architecture and other relevant morphological traits were measured. These includes duration for 50% flowering (days), plant height (cm), number of productive tillers, panicle length (cm), number of primary branches, number of secondary branches, number of seeds per primary branch, number of seeds per secondary branch as well as yield- related traits such as panicle weight (g), number of filled grains, spikelet fertility %, grain weight per thousand grains (g) and single plant yield (g).

Statistical analysis

The mean data collection from the 2 seasons were subjected to statistical analysis using STAR (Statistical Tool for Agricultural Research) version 2.0.1, developed by the IRRI (International Rice Research Institute) and R package (https://cran.r-project.org/) version 4.2.2. Various statistical analyses were conducted, including Analysis of variance (ANOVA), correlation, variability analysis phenotypic variance (PV), genotypic variance (GV), environmental variance (EV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), Environmental coefficient of variation (ECV), heritability (H^2), genetic advance (GA) and grand average mean (GAM), principal component analysis (PCA) and cluster analysis.

Results

All the statistical analyses performed in this research were centered on the mean performance of genotype, which was derived from the collected data. The results of the analysis of variance conducted for the 13 traits related to panicle and yield exhibited significant variations among the 69 genotypes, indicating diversity among these genotypes across all the assessed characteristics (Supplementary Table S2). Descriptive statistics (Mean, minimum, maximum, standard error of difference, coefficient of variation and critical difference) were calculated and are summarized in Table 1. Additionally, Fig. 1A provides a visualization of the different types of panicle observed during the course of this study.

Table 1. Descriptive statistics of panicle architecture and yield attributing traits among 69 rice genotypes

Character	Minimum	Maximum	Range	Mean	Standard error difference (SE(d))	Coefficient of variation (CV%)	Critical difference (CD) at 5%
Days to 50% flowering (Days)	90.00	134.00	44.00	107.22	1.38	10.68	2.57
Plant height (cm)	64.83	135.33	70.50	97.31	2.46	21.02	2.50
Number of productive tillers per plant (Nos)	3.00	17.33	14.33	6.98	0.32	37.93	5.24
Panicle length (cm)	14.67	32.33	17.66	20.78	0.42	16.81	3.80
Number of primary branches (Nos)	5.00	13.00	8.00	7.90	0.19	19.92	1.10
Number of secondary branches (Nos)	6.00	38.00	32.00	18.03	0.97	44.79	1.28
Number of seeds per Primary branch (Nos)	6.25	21.86	15.61	13.62	0.45	27.28	23.82
Number of seeds per secondary branch (Nos)	3.16	17.13	13.97	6.80	0.30	37.03	3.21
Panicle weight (g)	1.15	3.81	2.66	2.34	0.08	28.79	1.36
Number of filled grains per panicle (Nos)	70.00	183.33	113.33	121.15	3.34	22.90	3.86
Spikelet fertility percentage (%)	57.89	95.00	37.11	81.97	1.00	10.18	2.57
1000 grain weight (g)	13.26	36.20	22.94	21.65	0.65	24.79	2.50
Single plant yield (g)	5.83	30.08	24.25	18.18	0.87	39.70	5.24

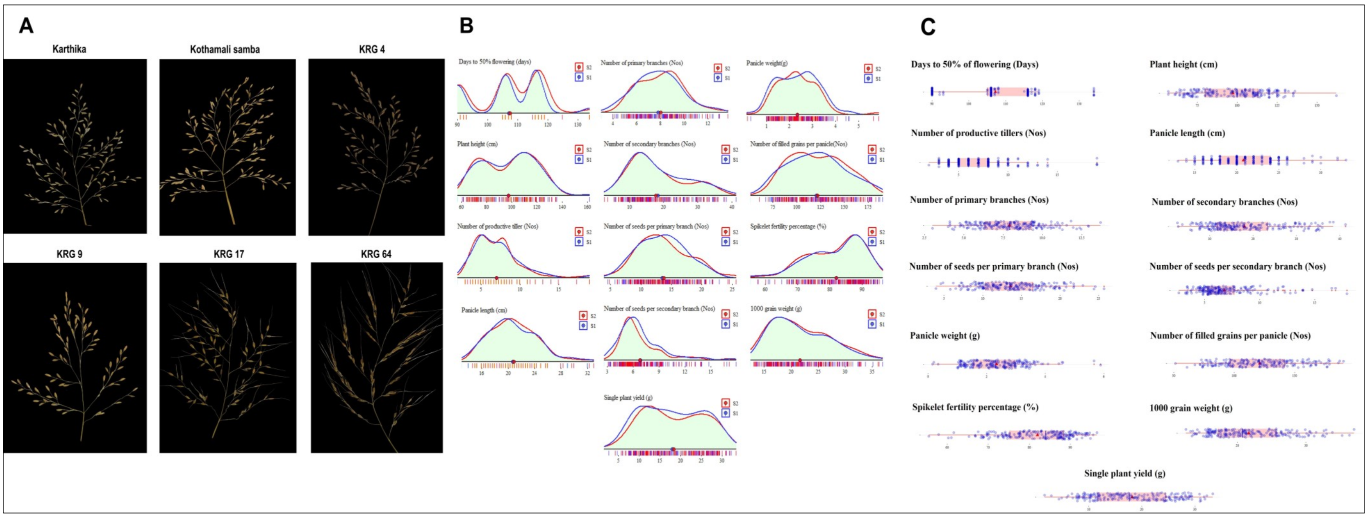

Fig. 1. A- Panicle architecture trait variations observed in Karthika- Open panicle type, Kothamali samba – Open panicle type, KRG 4- Intermediate panicle type, KRG 9 – Compact panicle type, KRG 17- Loose panicle type, KRG 64- Loose panicle type. **B-** Frequency distribution of panicle architecture and yield attributing traits among 69 rice genotypes. **C-** Box plot of the panicle architecture and yield attributing traits among 69 rice genotypes.

The trait, number of filled grains per panicle, displayed the highest mean value of 121.15, encompassing a range from 70.00 to 183.33. Following closely, "days to 50% flowering" exhibited a mean of 107.22 within a range of 90.00 to 134.00. The mean for "plant height" was the highest amongst the measured traits, with a value of 97.31, spanning from 64.83 to 135.33. Additionly, the trait "spikelet fertility" demonstrated a mean value of 81.97, ranging from 57.89 % to 95.00 %. The extent of variations amongst the genotypes across 3 replications was presented through frequency distribution charts depicting panicle architecture and yield-attributing traits across 69 rice genotypes (Fig. 1B). Within the studied genotypes, the coefficient of variation (CV%) ranges from 10.18% to 44.79%. Notably, the highest CV% was exhibited by the number of secondary branches (44.79), followed by single plant yield (39.70%), number of productive tillers per plant (37.93%), Number of seeds per secondary branch (37.03%) and panicle weight (28.79%), while the lowest CV% was observed in spikelet fertility % (10.18%) (Table 1).

The mean performance, shown in Supplementary Table S3, highlighted notable variations among different rice genotypes. The landrace 'Makom' exhibited the highest plant height (135 cm), whereas the variety 'Babtla' showed the lowest plant height (64.83 cm). The variety 'CO51' exhibited more productive tillers (17.33 Nos) while 'KRG 45' showed less productive tillers (3.00 Nos). Moving to panicle architecture trait, panicle length was high in landrace 'Kalasarnel' (32.33 cm) whereas 'KRG 24' has a shorter length (14.67 cm). The landrace 'Keerai samba' displayed a larger number of primary branches (13.00 Nos) while 'KRG 64' had a smaller count (5.00 Nos). Similarly, the trait "number of secondary branches" indicated that 'KRG 2' had more branches (38.00 Nos) and ' Superponni 43' had fewer branches (6.00 Nos). Landrace 'Sithiraikar' showcased high number of seeds per primary branch (21.86 Nos), while 'Renjini' variety exhibited a lower count (6.25 Nos). Likewise the landrace ' Mysore malli' had more seeds per secondary branch and 'IR50' had a smaller number of seeds per secondary branch. Panicle weight was greater in 'KRG 9' (3.81 g) and lower in 'Chinnar' (1.15 g). Filled grains were more in 'Kalasar nel' (183.33 Nos) and less in 'KRG 64' (70.00 Nos). The spikelet fertility was greater in 'Kalasar nel' (95 %) while 'Prathyasa' had lower (57.89%). The 1000 grain weight for all the varieties ranges from 13.26 to 36.20 for 'JCL nel' and 'KRG 30' respectively. Furthermore, single plant yield was greater in 'Karumkuruvai' (30.08 g) and lower in 'KRG 24' (5.83 g). The Box plots illustrates the variation present across the genotypes for the panicle architecture and yield attributing traits (Fig. 1C).

Trait association analysis

The calculated correlation coefficient for all the analyzed traits are depicted in (Fig. 2A). The results exhibited notable relationships between various traits. Notably, panicle weight (0.42***), number of filled grains per panicle (0.23ns) and 1000-grain weight (0.50***) exhibited strong positive correlations with single plant yield. Among these yield-attributing traits, panicle weight displayed significant positive correlations with plant height (0.40***) and panicle length (0.46***). Likewise, the number of filled grains per panicle displayed significantly positive correlations with several other architectural traits like plant height (0.42***), panicle length (0.57***), number of primary branches (0.35**), number of secondary branches (0.29*), seeds per primary branch (0.26*) and panicle weight (0.54***). Yield attributing trait, 1000-grain was positively correlated with panicle length (0.04ns). Similarly, spikelet fertility exhibited positive correlation with plant height (0.26*), panicle length (0.25*), seeds per secondary branch (0.29*) and filled grains per panicle (0.63***). Moreover, the panicle architecture trait's such as the number of primary branches (0.39***) and seeds per primary branch (0.46***) displayed positive correlations with the number of secondary branches.

Conversely, significant negative correlations were observed between the number of filled grains and the number of productive tillers (-0.25*), plant height and the number of productive tillers (-0.25*) and the number of secondary branches and seeds per secondary branch (-0.52***).

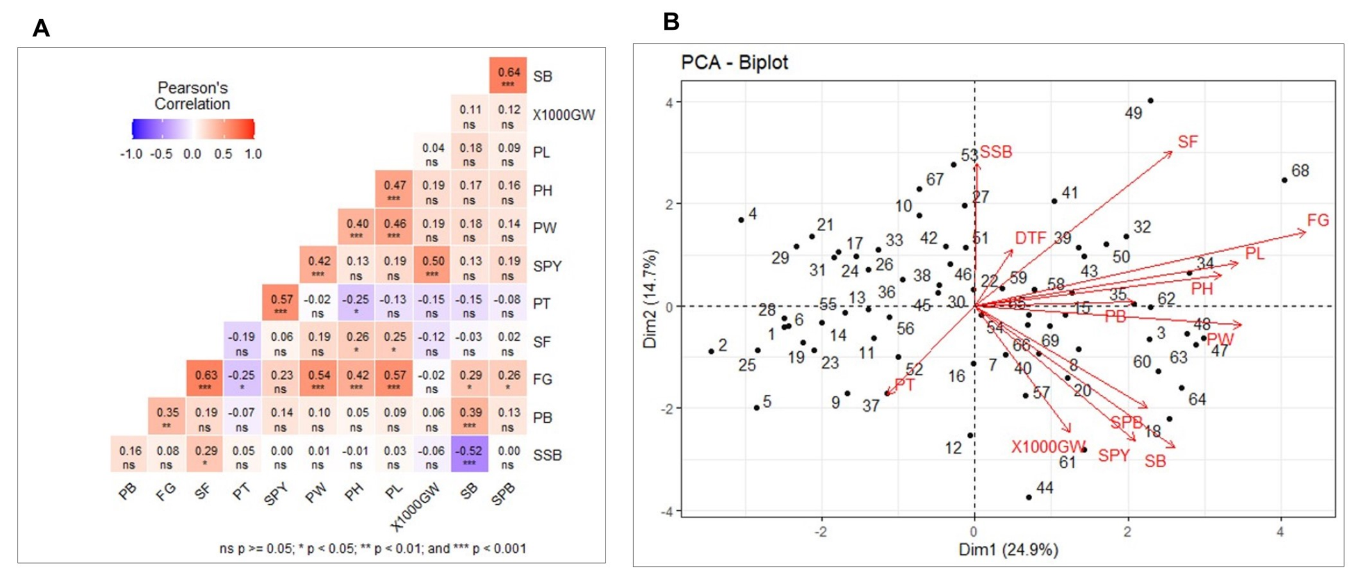

Fig. 2. A- Correlplot of panicle architecture and yield attributing traits in 69 rice genotypes. **B-**PCA biplot between PC1 and PC2.

Variability analysis

The variability analysis results (PV, GV, EV, PCV, GCV, ECV, H^2, GA and GAM) were calculated for the 13 quantitative traits (Table 2). The findings unveiled that the phenotypic variance (PV) is greater than genotypic variance (GV) for all the examined parameters. Similarly, PCV is greater than GCV, suggesting a minor impact of environmental factors on the studied traits. Notably, traits such as plant height, number of productive tillers, number of primary branches, number of secondary branches, number of seeds per primary branch, number of seeds per secondary branch, panicle weight, number of filled grains, 1000 grain weight and single plant yield exhibited elevated PCV and GCV. Despite the PCV and GCV values for traits like number of productive tillers and panicle weight, these traits demonstrated substantial environment influence, indicated by ECV values of 25.54% and 33.87% respectively, rendering them less reliable. Furthermore, the traits days to 50% flowering, panicle length and spikelet fertility showed moderate PCV and GCV. The highest PCV% and GCV% were found in the number of secondary branches (47.14% and 43.57%) and the lowest (Moderate) in spikelet fertility (10.37% and 10.09%).

All the traits showed a high broad-sense heritability. The highest heritability was observed in 1000 grain weight (97.59%) while the lowest was in panicle weight (28.04%). The trait days to 50% flowering show higher heritability (97.04) and genetic advance (23.11), followed by plant height exhibiting higher heritability (91.24) and genetic advance (39.62), and the trait number of filled grains also exhibited high heritability (76.22%) and genetic advance (47.49%). These finding suggests that the observed heritability is likely attributed to additive gene effects indicating that selection based on these traits could yield effective results. The GAM% ranges from 20.20%, (lowest in the case of spikelet fertility %) to 82.94% (highest in the number of secondary branches).

Table 2. Variability parameters of panicle architecture traits and yield attributing traits among 69 rice genotypes

Character	PV	GV	EV	PCV%	GCV%	ECV%	H^2	GA	GA % of Mean
Days to 50% flowering (Days)	133.68	129.72	3.95	10.78	10.62	1.85	97.04	23.11	21.56
Plant height (cm)	444.29	405.35	38.94	21.66	20.69	6.41	91.24	39.62	40.71
Number of productive tillers per plant (Nos)	9.13	5.95	3.18	43.28	34.94	25.54	65.17	4.06	58.11
Panicle length (cm)	13.90	11.35	2.54	17.94	16.21	7.67	81.71	6.27	30.19
Number of primary branches (Nos)	4.07	1.68	2.39	25.54	16.40	19.58	41.24	1.71	21.70
Number of secondary branches (Nos)	72.26	61.72	10.54	47.14	43.57	18.00	85.42	14.96	82.94
Number of seeds per Primary branch (Nos)	17.49	11.95	5.54	30.71	25.39	17.29	68.33	5.89	43.23
Number of seeds per secondary branch (Nos)	6.65	6.18	0.47	37.94	36.58	10.06	92.26	4.94	72.65
Panicle weight (g)	0.87	0.24	0.63	39.92	21.14	33.87	28.04	0.54	23.06
Number of filled grains per panicle (Nos)	915.06	697.42	217.64	24.97	21.80	12.18	76.22	47.49	39.20
Spikelet fertility %	72.30	68.34	3.96	10.37	10.09	2.43	94.53	16.56	20.20
1000 grain weight (g)	29.26	28.56	0.70	24.99	24.69	3.88	97.59	10.87	50.24
Single plant yield (g)	55.92	50.19	5.73	41.13	38.96	13.16	89.76	13.83	76.04

Number of replications = 3

Principal component analysis (PCA)

The phenotypic variation in 13 architecture traits was examined by principal component analysis (PCA). The 3 principal components (PC) exhibiting eigenvalues 3.23, 1.91 and 1.72 respectively, exhibited more variation among the 69 genotypes (Supplementary Table S4). The PC1 displays 24.92% of the total variation, the highest variation was observed in the number of filled grains per panicle (0.47), followed by panicle length (0.38), panicle weight (0.38) and plant height (0.35). These characteristics contribute significantly to the variance and account for the majority of the variability. The PC2 expound 14.74% of the variation and is driven by traits like spikelet fertility % (0.43), number of seeds per secondary branch (0.40) and panicle weight (0.38), which exhibits higher degree of variations within the datasets. The PC3 described 13.24% of the variation and is characterized by traits such as single plant yield (0.52), number of productive tillers per plant (0.49) and number of seeds per secondary branch (0.34) (Table 3). Therefore, it was obvious that PC1 exhibits the greatest degree of variance compared to other PCs (Fig. 2B).

According to the results obtained from the PCA analysis, several genotypes displayed superior performance in various traits. For instance, KRG 16, KRG 30 and Kullakar stood out in terms of the single plant yield trait. KRG 20 and KRG 14 exhibited better performance for the trait of 50% days to flowering. Illupaipoo Samba and Kullakar showed notable performance in the number of productive tillers trait. Traits like filled grains per panicle, panicle length and plant height were better exhibited by KRG 50 and TPS 3.The trait number of primary branches was excelled by LLR, Keerai samba, Kullakar, JCL nel and Kottaram samba genotypes, whereas KRG 45 and Poongar performed well in the number of seeds per primary branch trait. JCL nel showcased superior performance in the number of secondary branch trait. For the trait seeds per secondary branch, the genotypes KRG 20, Vallan samba and

Table 3. Eigenvectors for the first three principal components of panicle architecture and yield attributing traits among 69 rice genotypes

Parameters	PC 1	PC 2	PC 3
Days to 50% flowering (Days)	0.05	0.16	-0.12
Plant height (cm)	0.35	0.09	-0.01
Number of productive tillers per plant (Nos)	-0.13	-0.25	0.49
Panicle length (cm)	0.38	0.12	0.08
Number of primary branches (Nos)	0.23	0.01	-0.11
Number of secondary branches (Nos)	0.29	-0.40	-0.43
Number of seeds per Primary branch (Nos)	0.25	-0.28	-0.25
Number of seeds per secondary branch (Nos)	0.00	0.40	0.34
Panicle weight (g)	0.38	0.38	0.24
Number of filled grains per panicle (Nos)	0.47	0.21	-0.01
Spikelet fertility %	0.28	0.43	0.06
1000 grain weight (g)	0.14	-0.35	0.19
Single plant yield (g)	0.23	-0.38	0.52

KRG 65 displayed better performance. When it comes to panicle weight, Karumkuruvai and KRG 3 exhibited better performance, and for the 1000 grain weight trait, genotypes like Kullakar, RLR, KRG 16 and KRG 30 were standout performers. Additionally, in terms of spikelet fertility, genotypes such as KRG 22, CO53, KRG 22, Thooyamalli, KRG 63 and Punchakayama outperformed other varieties. Overall, the study highlights that different rice genotypes excel in different traits, showcasing the genetic diversity and potential for enhancing multiple aspects of rice yield and quality.

Cluster Analysis

The characteristics that contributed significantly to overall variance were chosen for clustering, as determined by the biplot of principal component analysis. 6 clusters were formed from the 69 genotypes using the Mahalanobis D^2 statistics (Supplementary Table S5). Among the 6 clusters, Cluster I have 8 genotypes, Cluster II encompasses 27 genotypes, Cluster III groups 20 genotypes, Cluster IV consists of 9 genotypes, Cluster includes 3 genotypes and Cluster VI is solitary with 2 genotypes. This indicates that Cluster II is the largest, followed by Cluster III, Cluster IV, Cluster I, Cluster V and Cluster VI. Most of the genotypes were grouped within Cluster II and Cluster III which may be due to their tight genetic associations (Fig. 3).

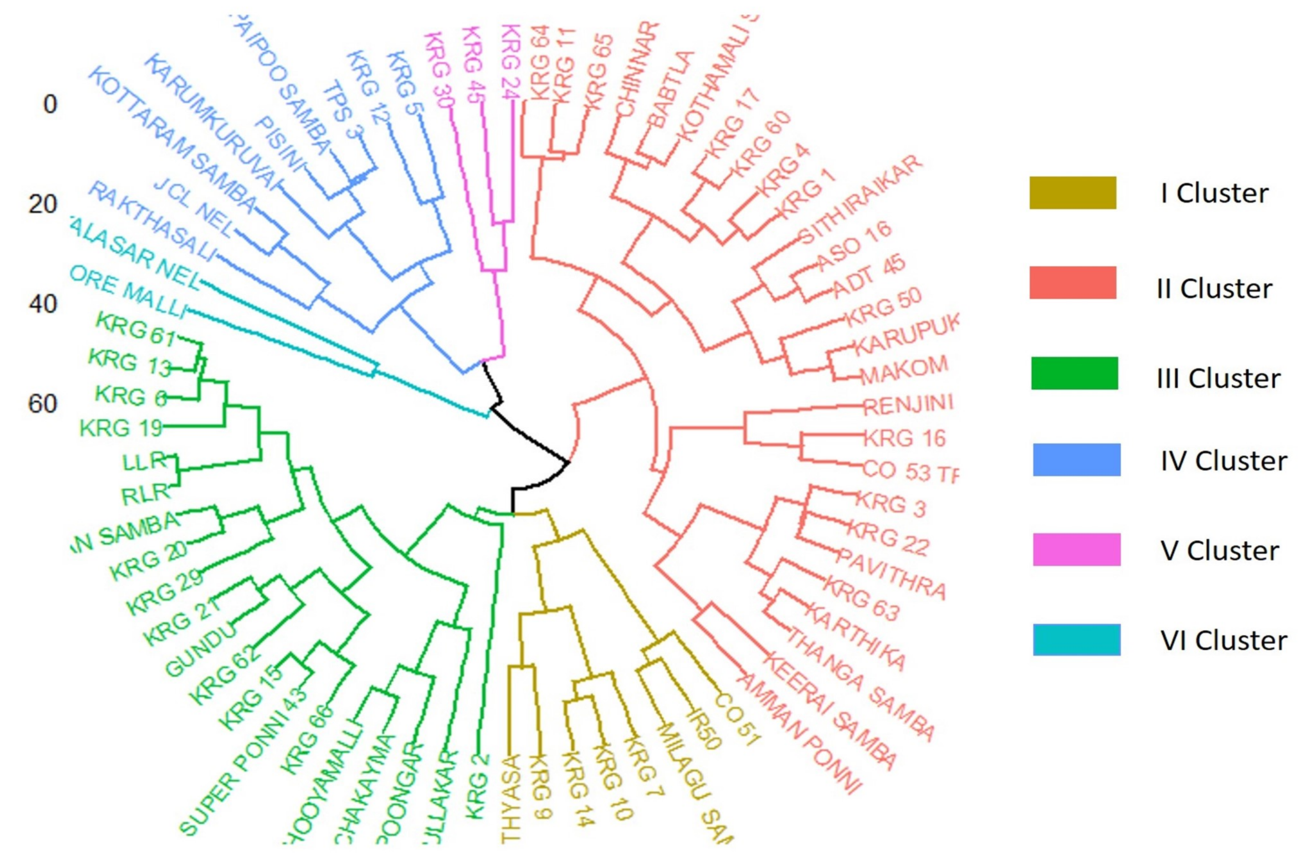

Fig. 3. Dendrogram based on Mahalanobis D^2 statistics among 69 rice genotypes.

The cluster means for different traits were mentioned in (Supplementary Table S6**)**. The highest cluster means for various traits were: Cluster VI contains the highest cluster means for 7 traits *viz*., plant height (119.17), panicle length (28.33), number of primary branches (9.00), number of seeds per secondary branch (15.15), panicle weight (3.33), number of filled grains (180.67) and spikelet fertility % (94.34), followed by cluster V which includes 2 high performing traits, number of secondary branches (28.67) and number of seeds per primary branch (17.50). Likewise cluster IV also consists of 2 traits 1000 grain weight (25.12) and single plant yield (23.76) and finally, cluster I has highest mean value to the number of productive tillers (10.83). Thus it shows that the genotypes present in cluster VI "Mysore malli" and "Kalasarnel" had the majority of best-performing traits, followed by genotypes present in cluster V "KRG45", "KRG24", and " KRG30", cluster IV with genotypes "KRG12", "KRG5", "Pisini", "Illupaipoo samba", "TPS3", "Karumkuruvai", "JCLNEL", "Rakthasali" and "Kottaram samba", and cluster I with eight genotypes "CO51", "IR50", "KRG9", "KRG7", "KRG10", "KRG14", "Prathyasa" and "Milagu samba" performing better for single trait number of productive tillers.

The mean values of both inter and intra-cluster distance were evaluated for 6 clusters (Supplementary Table S7). Cluster III (45.89) displays maximum intra-cluster distance, followed by Cluster I (41.47), cluster II (38.54), cluster VI (36.75), cluster V (33.38) and Cluster IV (32.41) showed the lowest intra-cluster distance which means the genotypes were closely related. Likewise, the inter-cluster distance between cluster III and cluster VI was higher, similarly, between cluster III and cluster V was more and the lowest inter-cluster distance is observed between clusters I and III. Genotype diversity increases with increasing inter-cluster and intra-cluster distances and conversely.

Discussion

Rice has a rich evolutionary divergence. There are thousands of different rice types cultivated around the globe, with 6000 of those variations currently being raised in India (27). These different types of rice showcase substantial variations in panicle architecture which is the base of grain yield. The extent and diversity of genetic variability present in the existing genetic stock significantly influence the effectiveness of any crop enhancement programme (28). The present study analyzed 69 rice accessions which include both the landraces and varieties. From the outcome of the analysis of variance, extensive variation was seen in all the traits for 69 genotypes, revealing that the genotypes of rice are highly variable. The frequency distribution depicted the variations of the 3 replications. Consequently, there is substantial potential for selecting various quantitative traits to enhance rice yield-contributing attributing, especially panicle-related traits. Similar findings have been reported by other studies as well (7, 29, 30).

The traits like number of filled grains per panicle, 50% days to flowering, and spikelet fertility % exhibited the highest mean values, with plant height also displaying a notable mean value. Similar results for plant height were also reported by (2, 31, 32). Plant height is an important growth parameter for any crop, as it influences or modifies yield-contributing traits, ultimately impacting grain production. The box plot exhibits the variation across genotypes in terms of panicle architecture and yield-attributing trait.

The traits namely 50% flowering (days), plant height (cm), number of productive tillers (Nos), panicle length (cm), number of primary branches (Nos), number of secondary branches (Nos), number of seeds per primary branch (Nos), number of seeds per secondary branch (Nos), panicle weight (g), number of filled grains (Nos), spikelet fertility %, grain weight per 1000 grains (g) and single plant yield (g) among the genotypes Makom, C051, Kalasarnel, Keerai samba, KRG2, Sithiraikar, Mysoremalli, KRG9, JCL nel, Karumkuruvai had significant difference. Notably, Kalasarnel outperformed the other genotypes in the 3 characteristics of panicle length, filled grains per panicle and spikelet fertility %. Therefore, these genotypes can be used for the selection process in crop improvement. A high coefficient of variation (CV%) was exhibited by the number of secondary branches, a result consistent with previous findings (8, 33). The number of secondary branches is a crucial yield-contributing trait (34, 35).

The correlation analysis revealed strong positive correlations between traits like panicle weight, number of filled grains per panicle and 1000-grain weight and single plant yield. Additionally, the number of primary branches and seeds per primary branch showed positive correlation with the number of secondary branches. These results are consistent with the findings of the previous studies (30, 35).

Several authors have reported, the selection of the desired characteristics depends significantly on the variation present among the evaluated characteristics. When both genotypic and phenotypic variability of a trait are high, the selection process for that trait becomes more robust. A greater genetic diversity within a population enhances the breeder's ability to achieve desired traits (36-38). In this study, traits like plant height, number of productive tillers, number of primary branches, number of secondary branches, number of seeds per primary branch, number of seeds per secondary branch, panicle weight, number of filled grains, 1000 grain weight and single plant yield exhibited higher phenotypic and genotypic coefficients of variation (PCV and GCV). Notably, the trait "number of secondary branches," which significantly contributes to grain yield, displayed the highest PCV% and GCV% at 47.14% and 43.57% respectively. These findings indicate that these traits hold promise for crop improvement. Similar conclusions have been reported in previous studies by (28, 29, 38).

Furthermore, it is worth noting that characteristics with high genetic advancement and substantial heritability are particularly advantageous for crop development because they are less affected by environmental factors

(29, 39). From the results, traits such as days to 50% flowering, plant height and number of filled grains per panicle exhibited both high broad sense of heritability and high genetic advance. This suggests that these traits are well-suited for selection and subsequent crop improvement efforts (40, 41).

Indeed, PCA effectively distills the essential factors and elucidates their contributions to total diversity, making it a useful instrument for accelerating the breeding programme (41, 42). In this case, the major variability is caused by the traits such as number of filled grains, panicle length, panicle weight and plant height in the PC1. Similar findings were also reported by (43, 44). The biplot diagram derived from this study explains the distribution and kind of variance for genotypes and quantitative characteristics. It shows character interactions as well as which genotypes are better for particular characteristics. The length of each vector indicates how much that characteristic contributed to the total difference; the greater the contribution, the longer the vector length.

Therefore, from the results of the biplot in the 13 characteristics, seven characters such as number of filled grains per panicle, panicle length, plant height, number of primary branches, panicle weight, seeds per primary branch and number of secondary branches are positively correlated with single plant yield. Whereas, days to 50% flowering, seeds per secondary branch, number of productive tillers and 1000 grain weight are negatively correlated with single plant yield and there is no correlation found between spikelet fertility and single plant yield.

The cluster analysis was carried out for the traits that showed highly significant variations in the PCA biplot. Therefore, the trait 50% days to flowering is excluded. The 69 genotypes were clustered into 6 clusters. Cluster II is the largest, having 27 genotypes. The highest cluster mean values were found between different clusters for the traits. For the cluster distance, Cluster III shows maximum intra-cluster distance and the inter-cluster distance between Cluster III and Cluster VI was higher. It was proposed to use distant cluster genotypes in hybridization programmes to acquire a broad spectrum of diversity among the segregates (45). In this case, the genotypes in cluster III which showed high intra-cluster distance and the genotypes between cluster III and VI which showed high inter-cluster distance can be used for hybridization programmes.

Conclusion

This study highlights the potential for increasing grain yield by focusing on genotypes that possess a higher number of secondary rachis or branches. The significance of this finding is further underscored by the suggestion that exploring the genetic composition of genotypes within clusters III and IV could yield valuable insights enhancing crop cultivation practices and ultimately improving and overall crop yield.

Acknowledgements

We would like to convey our sincere gratitude to the Karunya Institute of Technology and Sciences' Genetics and Plant Breeding Lab for providing all the necessary facilities.

Authors contributions

AJ conducted the research experiments and wrote the manuscript. HP helped in conducting the experiments. RS designed the study and supervised it. DK helped in the statistical analysis and interpretation. DN helped in genotype collection. RS, ST, NK and JK corrected and revised the manuscript.

Compliance with ethical standards

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

Ethical issues: None.

Supplementary tables

Table S1. List of 69 rice genotypes used in this study

Table S2. Analysis of variance (ANOVA) for panicle architecture and yield attributing traits among 69 rice genotypes

Table S3. Mean performance of panicle architecture and yield attributing traits for 69 genotypes

Table S4. Eigenvalues and % of variation of principal component axes among 69 rice genotypes

Table S5. Distribution of 69 rice genotypes among 6 different clusters based on Mahalanobis D^2 statistics

Table S6. Cluster mean values of panicle architecture and yield attributing traits among 69 rice genotypes

Table S7. Average inter and intra-cluster values among six clusters based on Mahalanobis D^2 statistics

References

1. Panesar PS, Kaur S. Rice: types and composition. Encyclopedia of Food and Health, Academic Press. 2016;Oxford:646-52. https://doi.org/10.1016/B978-0-12-384947-2.00596-1
2. Al-daej MI, Rezk AA, El-Malky MM, Shalaby TA, Ismail M. Comparative genetic diversity and marker-trait association using two DNA marker systems in rice (*Oryza sativa* L.). Agronomy. 2023;13 (2):329.https://doi.org/10.3390/agronomy13020329
3. Bai X, Huang Y, Mao D, Wen M, Zhang L, Xing Y. Regulatory role of FZP in the determination of panicle branching and spikelet formation in rice. Scientific Reports. 2016;6(1):1-11. https://doi.org/10.1038/srep19022
4. Li G, Zhang H, Li J, Zhang Z, Li Z. Genetic control of panicle architecture in rice. The Crop Journal. 2021;9(3):590-97.https://doi.org/10.1016/j.cj.2021.02.004
5. Agata A, Ando K, Ota S, Kojima M, Takebayashi Y, Takehara S et al. Diverse panicle architecture results from various combinations of Prl5/GA20ox4 and Pbl6/APO1 alleles. Communications Biology. 2020;3(1):302. https://doi.org/10.1038/s42003-020-1036-8

6. Han X, Tang M, Deng Y. Preliminary study on pulping of rice straw in Tris-(2-hydroxyethyl) ammonium acetate ionic liquid under microwave irradiation. Bioresources. 2014;9(4). https://doi.org/10.15376/biores.9.4.6851-6860
7. Singh RK, Kota S, Flowers TJ. Salt tolerance in rice: seedling and reproductive stage QTL mapping come of age. Theoretical and Applied Genetics. 2021;134:3495-533. https://doi.org/10.1007/s00122-021-03890-3
8. Bai S, Hong J, Li L, Su S, Li Z, Wang W et al. Dissection of the genetic basis of rice panicle architecture using a genome-wide association study. Rice. 2021;14:1-12. https://doi.org/10.1186/s12284-021-00520-w
9. Lu Y, Chuan M, Wang H, Chen R, Tao T, Zhou Y et al. Genetic and molecular factors in determining grain number per panicle of rice. Frontiers in Plant Science. 2022;13. https://doi.org/10.3389/fpls.2022.964246
10. Imai K, Murai M, Hao Y, Chiba Y, Chiba A, Ishikawa R. Mapping of rice Ur1 (Undulated rachis-1) gene with effect on increasing spikelet number per panicle and sink size and development of selection markers for the breeding by the use of Ur1. Hereditas. 2009;146(6):260-68. https://doi.org/10.1111/j.1601-5223.2009.02108.x
11. Zhai L, Wang F, Yan A, Liang C, Wang S, Wang Y et al. Pleiotropic effect of GNP1 underlying grain number per panicle on sink, source and flow in rice. Frontiers in Plant Science. 2020;11:933. https://doi.org/10.3389/fpls.2020.00933
12. Jin J, Hua L, Zhu Z, Tan L, Zhao X, Zhang W et al. GAD1 encodes a secreted peptide that regulates grain number, grain length and awn development in rice domestication. Plant Cell. 2016;28 (10):2453-63. https://doi.org/10.1105/tpc.16.00379
13. Luo J, Liu H, Zhou T, Gu B, Huang X, Shangguan Y et al. An-1 encodes a basic helix-loop-helix protein that regulates awn development, grain size and grain number in rice. Plant Cell. 2013;25(9):3360-76. https://doi.org/10.1105/tpc.113.113589
14. Wei X, Huang X. Origin, taxonomy and phylogenetics of rice. In: Rice. Elsevier. 2019; p. 1-29. https://doi.org/10.1016/B978-0-12-811508-4.00001-0
15. Liu E, Liu Y, Wu G, Zeng S, Tran Thi TG, Liang L et al. Identification of a candidate gene for panicle length in rice (*Oryza sativa* L.) via association and linkage analysis. Frontiers in Plant Science. 2016;7:596. https://doi.org/10.3389/fpls.2016.00596
16. Kong FN, Wang JY, Zou JC, Shi LX, De Jin M, Xu ZJ et al. Molecular tagging and mapping of the erect panicle gene in rice. Molecular Breeding. 2007;19:297-304. https://doi.org/10.1007/s11032-006-9062-x
17. uo J, Liu H, Zhou T, Gu B, Huang X, Shangguan Y et al. An-1 encodes a basic helix-loop-helix protein that regulates awn development, grain size and grain number in rice. Plant Cell. 2013;25 (9):3360-76. https://doi.org/10.1105/tpc.113.113589
18. Tsukahara K, Sawada H, Kohno Y, Matsuura T, Mori IC, Terao T et al. Ozone-induced rice grain yield loss is triggered via a change in panicle morphology that is controlled by aberrant panicle organization 1 gene. PLoS One. 2015;10(4):e0123308. https://doi.org/10.1371/journal.pone.0123308
19. Luan X, Liu S, Ke S, Dai H, Xie XM, Hsieh TF et al. Epigenetic modification of ESP, encoding a putative long noncoding RNA, affects panicle architecture in rice. Rice. 2019;12(1):1-8. https://doi.org/10.1186/s12284-019-0282-1
20. Chun SW, Lee JW, Ahn JY. Development and characterization of novel microsatellite markers in *Tilia amurensis* Rup using next-generation sequencing. Molecular Biology Reports. 2022;1-5. https://doi.org/10.1007/s11033-021-07035-z.
21. Jiao Y, Wang Y, Xue D, Wang J, Yan M, Liu G et al. Regulation of OsSPL14 by OsmiR156 defines ideal plant architecture in rice. Nature Genetics. 2010;42(6):541-44. https://doi.org/10.1038/ng.591
22. Li M, Tang D, Wang K, Wu X, Lu L, Yu H et al. Mutations in the F-box gene larger panicle improve the panicle architecture and enhance the grain yield in rice. Plant Biotechnology Journal. 2011;9(9):1002-13. https://doi.org/10.1111/j.1467-7652.2011.00610.x
23. Chen X, Chen M, Lin G, Yang Y, Yu X, Wu Y et al. Structural development and physicochemical properties of starch in caryopsis of super rice with different types of panicle. BMC Plant Biology. 2019;19(1):1-15. https://doi.org/10.1186/s12870-019-2101-7
24. Yoon J, Jeong HJ, Baek G, Yang J, Peng X, Tun W et al. A VIN3-like protein OsVIL1 is involved in grain yield and biomass in rice. Plants. 2021;11(1):83. https://doi.org/10.3390/plants11010083
25. Deveshwar P, Prusty A, Sharma S, Tyagi AK. Phytohormone-mediated molecular mechanisms involving multiple genes and QTL govern grain number in rice. Frontiers in Genetics. 2020;11:586462. https://doi.org/10.3389/fgene.2020.586462
26. Zhou J, Li Z, Xiao G, Zhai M, Pan X, Huang R et al. CYP71D8L is a key regulator involved in growth and stress responses by mediating gibberellin homeostasis in rice. Journal of Experimental Botany. 2020;71(3):1160-70. https://doi.org/10.1093/jxb/erz491
27. Rathna Priya TS, Eliazer Nelson ARL, Ravichandran K, Antony U. Nutritional and functional properties of coloured rice varieties of South India: A review. Journal of Ethnic Foods. 2019;6(1):1-11. https://doi.org/10.1186/s42779-019-0017-3
28. Karthikeyan P, Anbuselvam Y, Elangaimannan R, Venkatesan M. Variability and heritability studies in rice (*Oryza sativa* L.) under coastal salinity. Electronic Journal of Plant Breeding. 2010;1 (2):196-98. https://www.ejplantbreeding.org/index.php/EJPB/article/view/1904/967
29. Panda D, Sahu N, Behera PK, Lenka K. Genetic variability of panicle architecture in indigenous rice landraces of Koraput region of Eastern Ghats of India for crop improvement. Physiology and Molecular Biology of Plants. 2020;26(10):1961-71. https://doi.org/10.1007/s12298-020-00871-6
30. Gautam A, Shrestha A. Evaluation of panicle architecture traits in rice genotypes using PTRAP. Nepal Agriculture Research Journal. 2023;15(1):115-24. https://doi.org/10.3126/narj.v15i1.51533
31. Shrestha J, Subedi S, Kushwaha UKS, Maharjan B. Evaluation of growth and yield traits in rice genotypes using multivariate analysis. Heliyon. 2021;7(9):e07940. https://doi.org/10.1016/j.heliyon.2021.e07940
32. Parimala K, Raju CHS, Prasad ASH, Kumar SS, Reddy SN. Studies on genetic parameters, correlation and path analysis in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 2020;9(1):414-17. http://www.phytojournal.com/
33. Bai L, Huan S, Gu J, McClements DJ. Fabrication of oil-in-water nano emulsions by dual-channel microfluidization using natural emulsifiers: Saponins, phospholipids, proteins and polysaccharides. Food Hydrocolloids. 2016;61:703-11. https://doi.org/10.1016/j.foodhyd.2016.06.035
34. Xu Z, Chen W, Zhang L, Yang S. Design principles and parameters of rice ideal panicle type. Chinese Science Bulletin. 2005;50:2253-56. https://doi.org/10.1007/BF03182678
35. Mei HW, Xu JL, Li ZK, Yu XQ, Guo LB, Wang YP et al. QTLs influencing panicle size detected in two reciprocal introgressive line (IL) populations in rice (*Oryza sativa* L.). Theoretical and Applied Genetics. 2006;112:648-56. https://doi.org/10.1007/s00122-005-0167-0
36. Mazid MS, Rafii MY, Hanafi MM, Rahim HA, Latif MA. Genetic variation, heritability, divergence and biomass accumulation of rice genotypes resistant to bacterial blight revealed by quantitative traits and ISSR markers. Physiologia Plantarum. 2013;149 (3):432-47. https://doi.org/10.1111/ppl.12054

37. Ndjiondjop MN, Semagn K, Sow M, Manneh B, Gouda AC, Kpeki SB et al. Assessment of genetic variation and population structure of diverse rice genotypes adapted to lowland and upland ecologies in Africa using SNPs. Frontiers in Plant Science. 2018;9:446. https://doi.org/10.3389/fpls.2018.00446
38. Herawati R. Genetic analysis of grain yield of f 4 populations for developing new type of upland rice. SABRAO Journal of Breeding and Genetics. 2019;51(1). https://sabraojournal.org/genetic-analysis-of-grain-yield-of-f4-populations-for-developing-new-type-of-upland-rice/
39. Mishra SS, Behera PK, Panda D. Genotypic variability for drought tolerance-related morpho-physiological traits among indigenous rice landraces of Jeypore tract of Odisha, India. Journal of Crop Improvement. 2019;33(2):254-78. https://doi.org/10.1080/15427528.2019.1579138
40. Akinwale MG, Gregorio G, Nwilene F, Akinyele BO, Ogunbayo SA, Odiyi AC. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). African Journal of Plant Science. 2011;5(3):207-12. https://doi.org/10.3923/ijpbg.2011.224.234
41. Gunasekaran A, Seshadri G, Ramasamy S, Muthurajan R, Karuppasamy KS. Identification of newer stable genetic sources for high grain number per panicle and understanding the gene action for important panicle traits in rice. Plants. 2023;12(2):250. https://doi.org/10.3390/plants12020250
42. Das S, Das SS, Chakraborty I, Roy N, Nath MK, Sarma D. Principal component analysis in plant breeding. Biomolecule Reports. 2017;3:1-3. https://www.mdpi.com/journal/biomolecules
43. Al-daej MI, Rezk AA, El-Malky MM, Shalaby TA, Ismail M. Comparative genetic diversity assessment and marker-trait association using two DNA marker systems in rice (*Oryza sativa* L.). Agronomy. 2023;13(2):329. https://doi.org/10.3390/agronomy13020329
44. Saito H, Orn C, Thun V, Ouk M, Tomita A, Sasaki K et al. Diversity of traits related to panicle architecture and grain size in Cambodian rice germplasm and newly developed mini-core collection. Japan Agricultural Research Quarterly: JARQ. 2023;57(1):21-35. https://doi.org/10.6090/jarq.57.21
45. Chakma SP, Huq H, Mahmud F, Husna A. Genetic diversity analysis in rice (*Oryza sativa* L.). Bangladesh Journal of Plant Breeding and Genetics. 2012;25(1):31-39. https://doi.org/10.3329/bjpbg.v25i1.17010