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RESEARCH ARTICLE

Genetic diversity, agronomic performance and nutritional quality evaluation of rice landraces of different duration groups

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Abstract

This study was conducted during the *Kharif* season of 2023 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute to evaluate the genetic diversity, agronomic performance and nutritional quality of 44 rice genotypes, including landraces and improved varieties. The experiment was laid out in a randomized block design (RBD) and observations were recorded on various traits, including yield components and nutrient content. Results revealed substantial genetic variability in yield-related traits, such as productive tillers and filled grains, supporting targeted breeding efforts. High heritability and genetic advance in three characters which suggests the potential for selection-based improvements in certain traits through pedigree breeding, while others may benefit from heterosis breeding strategies. Correlation analysis indicated a significant positive association between single plant yield and internode length, number of productive tillers and number of filled grains per panicle. Principal component analysis provided insights into trait importance and relationships. ADT 45 excelled in short duration cropping with high yield and grain quality traits. The landraces Nelsolia and Kerala Sundari showed robust performance in yield-related traits under medium- and long-duration cropping systems, respectively. Nutrient analysis of top rice varieties across durations showed higher iron (Fe) and zinc (Zn) in brown rice. ADT 45 exhibited elevated Fe and Zn, while Kalarpallai has higher protein content among the short-duration varieties. Nelsolia and Anandhanur Sannam had high nutrient content among the medium-duration varieties. Among the long-duration varieties, Rajora and Tholokattai stood out for their superior levels of iron (Fe), zinc (Zn) and protein. Overall, this study provides valuable insights into rice genetic diversity, agronomic performance and nutritional quality, informing breeding strategies for improved rice varieties.

Keywords: brown rice; correlation analysis; genetic advance; heritability; heterosis breeding; internode length; pedigree breeding; principal component analysis; productive tillers; randomized block design; single plant yield; yield components

Introduction

Rice (*Oryza sativa* L.) is a fundamental staple crop cultivated extensively across diverse agroecological regions, providing substantial annual yields that sustain more than half of the global population (1). With the global population projected to reach 9.77 billion by 2050, ensuring food security through the enhancement of staple crops like rice is of critical importance. The *Oryza* genus comprises two cultivated species: *Oryza sativa*, widely grown in Asia and globally and *Oryza glaberrima*, domesticated in West Africa and valued for its tolerance to abiotic and biotic stresses (2). Traditional rice landraces, developed and maintained by farmers over generations, represent an invaluable reservoir of genetic diversity. These landraces possess unique traits such as drought tolerance, pest and disease resistance and high nutritional quality (3). However, their cultivation has declined due to the widespread adoption of high-yielding modern varieties. Despite this, efforts to conserve and utilize landraces remain crucial, especially in the context of climate change and sustainable agriculture (4).

Past research has highlighted the genetic richness of rice landraces and their potential in breeding programs, particularly for stress resilience, grain quality and adaptation to marginal environments (5, 6). However, most studies have focused either on agronomic traits or on nutritional profiling in isolation. There is a growing need for integrated evaluations that combine both agronomic performance and nutritional quality to inform more holistic breeding strategies. With the growing consumer interest in diverse and value-added rice varieties, an emerging market for landrace-based products has developed. This trend is driven by their distinctive flavours, superior nutritional profiles (such as higher iron, zinc and protein content) and strong cultural heritage appeal (7). Given this background, a comprehensive assessment of rice landraces, encompassing both agronomic and nutritional dimensions across different maturity groups, is essential. Such integrated evaluations can provide valuable insights into the dual potential of these landraces-not only as sources of resilience and adaptability but also as contributors to nutritional enhancement. This study evaluates selected rice landraces and improved varieties to identify genotypes that combine high yield with superior grain quality, aiming to bridge the gap between productivity and nutritional value in rice breeding.

Materials and Methods

Plant materials and growth conditions

The experiment included 41 traditional rice landraces and three check varieties-ADT (R) 45, improved white ponni and CR 1009 SUB-1-representing short-, medium- and long-duration groups, respectively, totalling 44 genotypes. These genotypes were evaluated for variability in agronomic and quality traits. During the *Kharif* season of 2023, seedlings were first raised in a nursery and transplanted into the main field at 27 days old. The trial was laid out in a randomized block design (RBD) with three replications. Each genotype was grown in three rows of 3 m length with a spacing of 30 × 20 cm. Biometrical observations were recorded on five randomly selected plants of each genotype per replication for yield and related components. For evaluating quality traits, composite samples were drawn from five random plants in each replication.

Planting material used

The 44 genotypes were classified based on maturity duration into three groups: short (90-120 days), medium (120-140 days) and long duration (150-185 days). The short-duration group included 13 landraces with ADT (R) 45 as the check; the medium-duration group included 19 landraces with Improved White Ponni as the check; and the long-duration group comprised 9 landraces with CR 1009 SUB-1 as the check. A detailed list of varieties is provided in Table 1.

Productive traits observation

The following productive traits were recorded from five randomly selected plants per replication: days to flowering, plant height, culm diameter, culm wall thickness, fourth internode length, panicle length, number of productive tillers per plant, number of filled grains per panicle, biomass yield per plant, number of spikelets per panicle, grain weight and single plant yield.

Genotype selection for nutrient analysis

Based on a selection index developed using PB Tools software (version 1.4, 2014), the top-performing genotypes across short-, medium- and long-duration groups were identified for quality trait analysis. These selected genotypes, along with the check varieties, were evaluated for iron (Fe), zinc (Zn) and protein content.

Nutrient estimation

Iron and Zinc

The concentrations of Fe and Zn in both polished and unpolished rice samples were estimated using Energy Dispersive X-ray Fluorescence Spectrometry (ED-XRF), a non-destructive method suitable for precise micronutrient determination.

Table 1. List of rice landraces used in the experiment

Sl.No.	Traditional paddy varieties	Days to maturity
	Short duration varieties	
1	Arupatham kuruvai	90-95
2	Kullakar	
3	ADT 45	105-110
4	Mysore Malli	
5	Rakthasali	
6	Kalarpallai	
7	Karuthakkar	110-115
8	Burma karuppu	
9	Karunguruvai	
10	Anaikomban	
11	Bhavami	110-120
12	Bamathi	
13	Manakathai	
14	Valan samba	
	Medium duration varieties	
15	Kurluthoda	120-130
16	Anandhanur sannam	
17	Shivan samba	
18	Kajji jaya	
19	Burma kavuni	
20	Seeraga sanna	
21	Chinnar	
22	Ramjeera	130-140
23	IWP	
24	Kothamali samba	
25	Nelsolia	
26	Kichili samba	
27	Singar	130-140
28	Sivappu kavuni	
29	Thanga samba	
30	Kalaratta	
31	Athur kichilli samba	
32	Kuchi patalda	
33	Saramalli	
34	Athokadaya	
	Long duration varieties	
35	Rasakadam	150-155
36	Tholokattai	
37	Kerala sundari	
38	Ramahalli	
39	Thooyamalli	155-160
40	Kalanamak	
41	Rajora	160-165
42	Ilupai poo samba	165-170
43	CR 1009 Sub 1	
44	Ottadaiyan	180-185

Protein content

The grain protein content was estimated using Near Infrared Reflectance (NIR) spectroscopy, a non-destructive technique based on the absorption of near-infrared light by molecular bonds such as N-H, C-H and O-H groups. Powdered samples of polished rice were scanned and protein content was predicted using calibrated NIR models, following the method described in the previous study (8).

Data analysis

Data from 12 quantitative traits recorded for 44 rice genotypes were subjected to statistical analysis using R Studio software (version 2025.05.1+513). Analyses included estimates of variability parameters (mean, standard deviation, heritability, genetic advance), Pearson correlation coefficients and Principal Component Analysis (PCA). Genetic diversity was evaluated through hierarchical cluster analysis and a dendrogram was constructed using the same software. Cluster mean performance was calculated using STAR software (version 2.0.1). A selection index was developed to identify promising accessions based on combined trait performance.

Results and Discussion

Results overview

The performance of 44 rice genotypes, including landraces and improved varieties, was evaluated across different growth stages with a focus on morphological traits and yield-related parameters. Significant variability was observed across traits, reflecting the diverse genetic background of the genotypes studied. This variability offers a valuable resource for breeding programs aimed at improving yield, adaptability and resilience to environmental stressors, especially under changing climate scenarios.

Genetic variability

High values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for the number of productive tillers per panicle, internode thickness, single plant yield and number of filled grains per panicle, as depicted in Table 2. Comparable findings were reported in the previous research (9, 10). Moderate PCV and GCV values were noted for biomass yield, 100-grain weight, internode length, number of spikelets per panicle, days to 50 % flowering and internode diameter, aligning with trends observed in previous landrace studies (11). Low estimates of both PCV and GCV were recorded for panicle length and plant height, consistent with the observations of Vanisree et al. (12), who also reported limited variability for these traits. The observed patterns of genetic variability, as shown in Table 2, indicate a strong genetic influence on traits such as productive tillers, internode thickness, yield per plant and grain filling, suggesting that these traits hold promise for improvement through direct selection. Moderate variability in traits like biomass yield and 100-grain weight indicate potential for gradual genetic gain through selective breeding. In contrast, low variability in panicle length and plant height suggests limited scope for selection within the current population and highlights the need for incorporating novel alleles or diverse parental lines to enhance variation in these traits (13).

Heritability and genetic advance

A significant degree of heritability, coupled with substantial genetic advance, was noted for productive tillers per plant, individual plant yield and number of filled grains per panicle, as presented in Table 2. Similar findings were also reported in the former research (10, 14-16). In contrast, traits such as biomass yield, 100-grain weight and internode length showed high heritability but only moderate genetic advance, implying a combination of additive and non-additive gene action. This result was differed from those reported in the previous study (17, 18). Therefore, it can be inferred that the three traits exhibiting both high heritability and high genetic advance were governed by additive gene action and can respond well to selection, making the pedigree method of breeding suitable for their improvement. For the remaining characters, which are under the influence of both additive and non-additive gene action (as evidenced by high heritability with moderate genetic advance in Table 2), heterosis breeding is recommended initially, followed by pedigree breeding after one or two cycles of recurrent selection.

Correlation analysis

Phenotypic correlation analysis (Fig. 1) revealed that single plant yield was significantly and positively associated with three traits: internode length, number of productive tillers per plant and number of filled grains per panicle. In contrast, it showed a significant negative correlation with days to 50 % flowering and internode diameter. Similar correlation patterns were reported in earlier studies (14, 19, 20), which highlighted positive associations between yield and traits such as productive tillers and filled grains, along with negative correlations involving flowering time and stem thickness.

The negative correlation between days to 50 % flowering and single plant yield (Fig. 1) suggests that early-maturing varieties tend to yield more compared to late-maturing ones. Therefore, intentional selection for traits like internode length, number of productive tillers per plant and filled grains per panicle could lead to simultaneous improvement in yield, as these characteristics are positively correlated with single plant yield. The physical traits such as internode diameter showed a negative correlation with yield, underscoring the importance of adopting a balanced trait selection strategy in rice breeding programs (21).

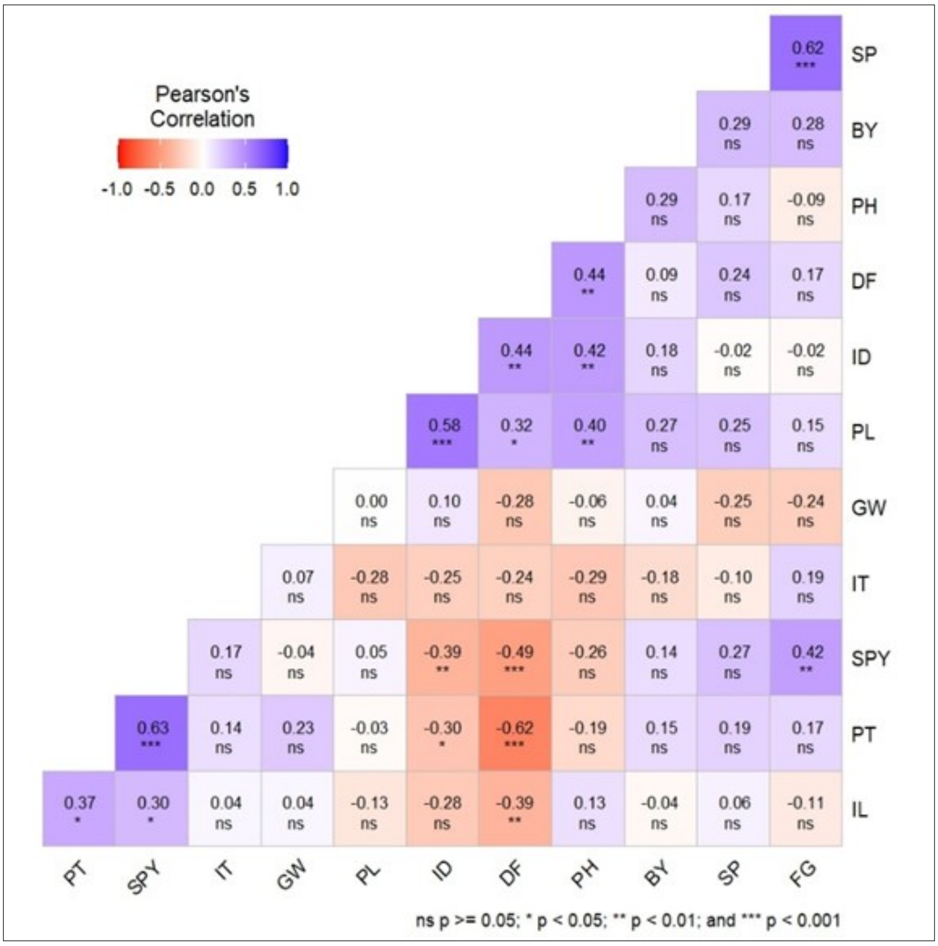
Genetic diversity

Genetic diversity analysis using STAR software grouped the 44 rice genotypes into four distinct clusters, as presented in Table 3 and illustrated in Fig. 2. Each cluster exhibited varying levels of genetic diversity. Clusters 1 and 2 were the largest clusters, each consisting of 19 genotypes, indicating a high degree of diversity within these groups. In contrast, Clusters 3 and 4 were smaller with 3 genotypes each, suggesting a more limited genetic variation among these cultivars.

Table 2. Estimates of variability parameters for yield components in rice landraces

Sl.No.	Characters	Range	Variance		Coefficient of variation		Heritability in a broad sense (%)	Genetic advance as per cent of mean
			Phenotype	Genotype	Phenotypic (%)	Genotypic (%)		
1	DF	52-153	521.91	514.47	22.11	21.95	98.57	44.91
2	PH	93.1-196.3	691.37	678.63	17.34	17.17	98.16	35.06
3	PL	15.9-36.7	17.75	17.33	17.35	17.14	97.61	34.89
4	IL	4.6-20.3	12.06	11.92	28.13	27.97	98.88	57.31
5	ID	2.4-9.1	1.38	1.36	21.96	21.78	98.38	44.51
6	IT	0.05-1.00	0.0376	0.0373	52.38	52.17	99.2	107.06
7	PT	9-109.7	396.31	395.57	63.21	63.15	99.81	129.97
8	SP	6-19	9.75	9.6	27.43	27.21	98.37	55.59
9	FG	27-234	2503.58	2494.97	50.3	50.21	99.66	102.71
10	GW	1.06-3.44	0.3029	0.3005	28.33	28.22	99.21	57.9
11	BY	121.63-398.73	5516.28	5480.1	30.78	30.68	99.34	63
12	SPY	5.12-74.1	291.65	290.88	50.82	50.75	99.74	104.42

***DF**: days to 50 % flowering; PH: plant height; PL: panicle length; IL: internode length; ID: internode diameter; IT: internode thickness; PT: number of productive tillers per plant; SP: number of spikelets per panicle; FG: number of filled grains per panicle; GW: 100-grain weight; BY: biomass yield; SPY: single plant yield.



	PT	SPY	IT	GW	PL	ID	DF	PH	BY	SP	FG
SP											0.62 ***
BY										0.29 ns	0.28 ns
PH									0.29 ns	0.17 ns	-0.09 ns
DF								0.44 **	0.09 ns	0.24 ns	0.17 ns
ID							0.44 **	0.42 **	0.18 ns	-0.02 ns	-0.02 ns
PL						0.58 ***	0.32 *	0.40 **	0.27 ns	0.25 ns	0.15 ns
GW					0.00 ns	0.10 ns	-0.28 ns	-0.06 ns	0.04 ns	-0.25 ns	-0.24 ns
IT				0.07 ns	-0.28 ns	-0.25 ns	-0.24 ns	-0.29 ns	-0.18 ns	-0.10 ns	0.19 ns
SPY			0.17 ns	-0.04 ns	0.05 ns	-0.39 **	-0.49 ***	-0.26 ns	0.14 ns	0.27 ns	0.42 **
PT		0.63 ***	0.14 ns	0.23 ns	-0.03 ns	-0.30 *	-0.62 ***	-0.19 ns	0.15 ns	0.19 ns	0.17 ns
IL	0.37 *	0.30 *	0.04 ns	0.04 ns	-0.13 ns	-0.28 ns	-0.39 **	0.13 ns	-0.04 ns	0.06 ns	-0.11 ns

Fig. 1. Phenotypic correlation coefficients for observed component traits.

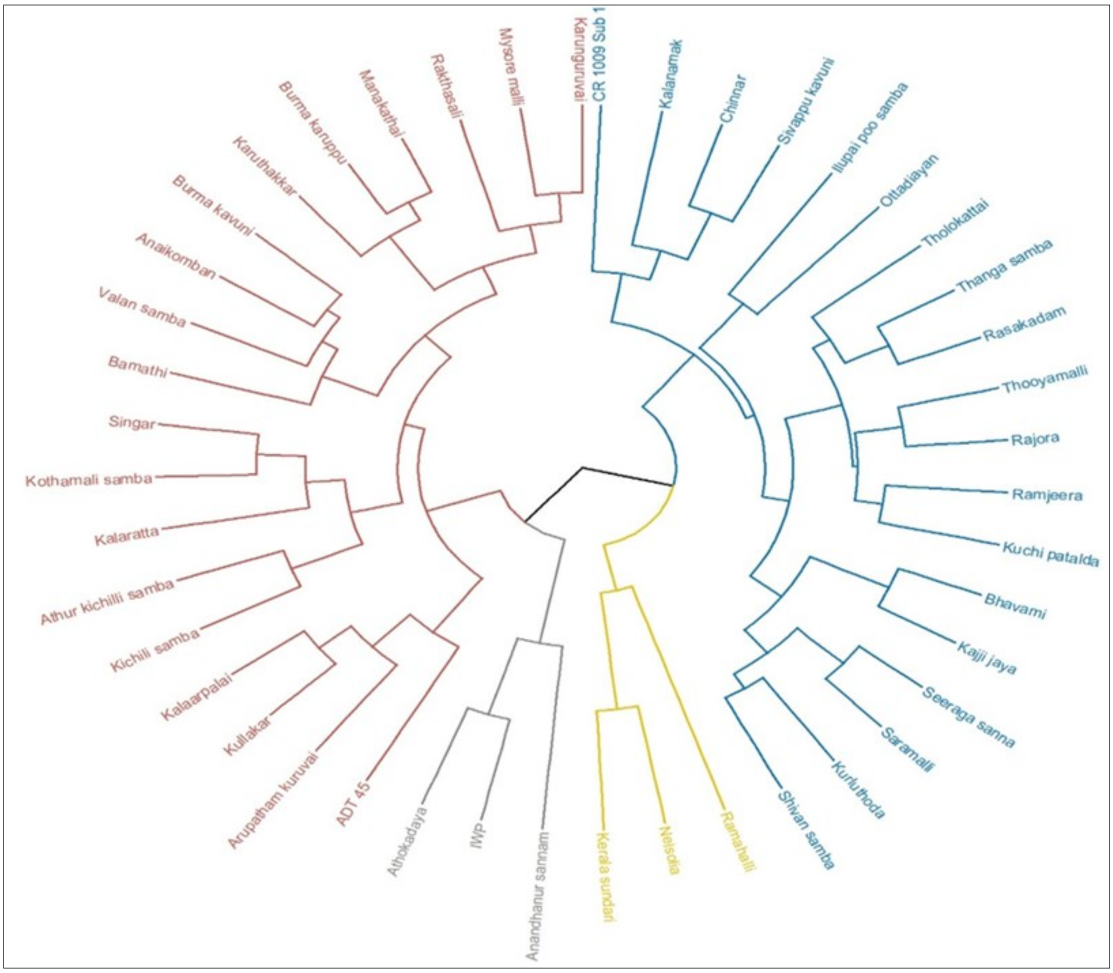


Fig. 2. Phylogenetic tree showing cultivar relationships.

Table 3. Mean performances of clusters estimated by hierarchical clustering

SI. No.	Characters	Clusters			
		I	II	III	IV
1	DF	**87.21**	116.7	105.11	**118.44**
2	PH	146.33	156.01	**128.87**	**180.31**
3	PL	22.56	24.57	**22.52**	**35.18**
4	IL	**14.36**	10.82	**10.41**	11.51
5	ID	4.83	5.87	**4.01**	**6.79**
6	IT	0.37	0.36	**0.53**	**0.25**
7	PT	41.02	**18.98**	**42.55**	39.33
8	SP	**10.49**	10.91	**16.56**	14.89
9	FG	**68.68**	107.84	**201.33**	139.45
10	GW	2.2	1.71	**1.58**	**2.12**
11	BY	232.79	**228.34**	**318.56**	299.32
12	SPY	37.23	**24.04**	**57.14**	47.62

Underlined Boldfaced indicates minimum cluster mean values.

Only boldfaced indicates maximum cluster mean values.

The genotypes in Cluster 3 recorded the highest mean performances for traits such as internode thickness, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle and single plant yield. Hence, it is considered the superior cluster among the clusters. Notably, this cluster included high-performing landraces such as Nelsolia, Kerala Sundari and Ramahalli. Similar clustering patterns were reported in the previous research (22, 23), where genotypes grouped into superior clusters also showed high values for yield-contributing traits such as productive tillers and grain number per panicle.

Principal component analysis

In the present investigation, the computation of principal component analysis was done to determine the degree of similarity among the genotypes and the relative importance of the principal components and characters involved in them. Twelve principal components (PCs) were extracted, cumulatively accounting for 100 % of the total variation. The first PC (PC 1) explained 26.8 % of the total variation and accounted for the maximum proportion of the total variability in a set of all variables followed by PC 2 (20 %) and the remaining ones accounted for progressively lesser amounts of variation. In the present study, the first PC (PC 1) had the following traits viz., days to 50 % flowering, internode diameter, plant height, panicle length and biomass yield as variables with the largest coefficient. These traits, particularly internode diameter and panicle length, appear to contribute positively to single plant yield.

PC 2 was primarily associated with grain weight and internode thickness, traits that influence plant stability and susceptibility to lodging. These findings emphasize the importance of selecting genotypes with improved structural traits to enhance yield stability. Similar previous study (24) found that PCA effectively differentiated rice genotypes based on trait combinations and identified key contributors to genetic divergence, such as plant height, grain number and panicle length. The scatter diagram based on principal component analysis (Fig. 3) is also similar to the clusters in genetic divergence. In the biplot the genotypes that are placed nearer to each other are almost homogeneous phenotypically and the genotypes that are plotted further to each other are heterogeneous and the arrow with the parameter indicates the diversity caused by each parameter in each cluster (24).

Selection index

The basic concept of using the Smith-Hazel index is to define the genetic worth of an individual based on a linear function of the genetic values of multiple traits, each weighted according to pre-assigned relative economic values (25). The advantage of this index lies in its ability to combine information on heritability, correlations among traits and economic importance if available (26). Selection indices were used to identify top-performing rice genotypes across various maturity durations, as reported (27). The selection indices calculated for short-duration, medium-duration and long-duration rice varieties provide valuable insights into the potential for improving yield-contributing traits. In short-duration varieties, ADT 45 emerged as the top-performing genotype, demonstrating superior traits such as higher single-plant yield, 100-grain weight, filled grains per panicle and productive tillers per plant, confirming its suitability for short-duration cropping systems (Table 4). In the medium-duration group, Nelsolia stood out due

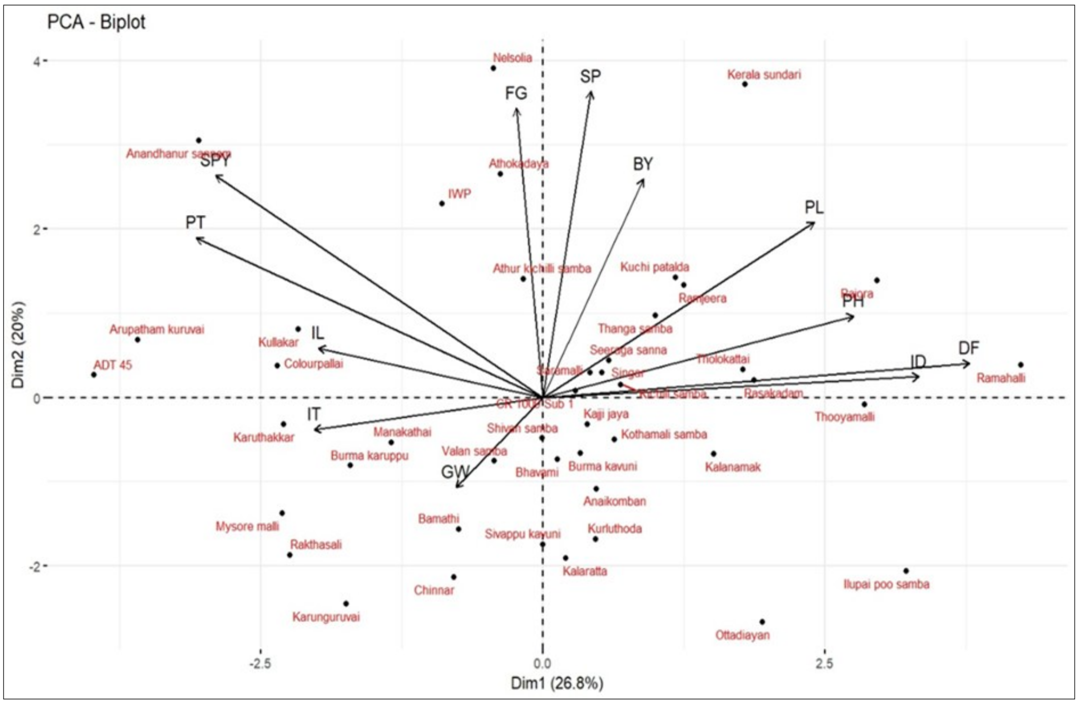


Fig. 3. Genotypes distributed by trait variation across two principal components.

Table 4. Smith Index table of top five genotypes in short-duration varieties

Genotype	DF	PT	SP	FG	GW	SPY	Smith index
ADT 45	68	57.47	10.67	113	1.4	72.84	2.52
Kalarpallai	78	60.5	11	113	2.72	52.47	1.7
Kullakaar	66	73.5	13.67	103	2.63	45.67	1.27
Arupatham Kuruvai	52.33	107	13	83	2.28	45.32	1.15
Manakathai	90.33	49	8.33	60.67	2.39	39.34	0.1
MSI	70.93	69.49	11.33	94.53	2.29	51.13	NA
MAI	78.45	47.15	9.26	70.62	2.32	40.74	NA
SDi	-7.52	22.35	2.07	23.91	-0.04	10.38	NA
EGG	-9.68	24.79	2.12	32.24	-0.12	13.73	NA

to its superior performance in single plant yield, number of spikelets per panicle and early flowering, suggesting strong adaptability and potential under medium-duration cultivation regimes (Table 5). For long-duration varieties, Kerala Sundari showed the most favourable profile, maintaining high values across multiple yield-contributing traits, highlighting its strong potential for long-duration cultivation systems (Table 6).

The identification of these top-performing genotypes underscores the importance of targeted breeding efforts to harness the genetic diversity within rice germplasm. These findings provide a solid foundation for future breeding programs aimed at developing rice varieties with improved performance and adaptability to diverse agroecological conditions.

Nutrient estimation of top-performing varieties

Nutritional evaluation of top-performing genotypes across short- medium- and long-duration cropping systems revealed considerable variation in their performance. Across all duration groups, both landraces and improved varieties consistently showed higher micronutrient levels in brown rice compared to polished rice (Fig. 4; Table 7). This aligns with the previous findings (28), which emphasized that the milling process significantly reduces the nutritional value of rice, highlighting the advantages of brown rice over its polished counterpart.

Table 5. Smith Index table of top five genotypes in medium duration varieties

Genotype	DF	PT	SP	FG	GW	SPY	Smith index
Nelsolia	106.33	70	15.67	201.67	1.87	67.18	3.45
Athokadaya	118.67	46.33	15	180.33	1.88	64.09	2.99
Anandhanur sannam	93	42	18.67	232.33	1.54	60.23	1.98
IWP	103.67	39.33	16	191.33	1.33	47.11	1.39
Saramalli	114	24	9	116	1.37	56.04	0.94
MSI	107.13	44.33	14.87	184.33	1.6	58.93	NA
MAI	105.35	27.43	12.47	119.25	1.72	35.88	NA
SDi	1.78	16.9	2.4	65.08	-0.12	23.05	NA
EGG	1.33	17.99	2.64	68.31	-0.14	18.84	NA

Table 6. Smith Index table of top five genotypes in long-duration varieties

Genotype	DF	PT	SP	FG	GW	SPY	Smith index
Kerala Sundari	123.67	31	15	154.67	1.67	66.36	3.2
CR 1009 SUB-1	148.33	18.67	14	181	2.45	29.24	1.59
Rajora	142	18.67	15	130.33	1.98	18.55	0.67
Tholokattai	120.67	20.33	13.67	115	2.2	16.45	-0.08
Kalanamak	133.67	13.67	14	100	1.6	14.47	-0.42
MSI	133.67	20.47	14.33	136.2	1.98	29.01	NA
MAI	133.97	17.7	12.2	100.27	1.86	19.05	NA
SDi	-0.3	2.77	2.13	35.93	0.12	9.97	NA
EGG	-1.74	6.45	2.76	61.45	0.16	23.01	NA

Among short-duration varieties, ADT 45 and Arupatham Kuruvai stood out for their superior nutritional attributes, while Kalarpallai was noted for its better protein profile when compared to all other genotypes, including the check variety. In medium-duration varieties, Anandhanur Sannam merged as the most promising genotype, performing well in both brown and polished forms. Nelsolia also showed potential, especially in its polished form. Among long-duration types, Rajora emerged as the best-performing genotype across both forms, while Tholokattai exhibited better protein quality than the rest.

Table 7. Fe, Zn and protein content in rice genotype

S.No.	Genotypes	Fe	Zn	Fe	Zn	Protein
		Brown		Polished		Polished
	Short duration					
1	Kalarpallai	11.3	28.1	4.1	22.8	10.64
2	Kullakar	11.2	26.6	3	20.5	8.82
3	Arupatham kuruvai	11.5	29.8	3.8	26.4	9.29
4	ADT 45	22.2	23.7	5.1	21.4	9.3
	Medium duration					
1	Nelsoiya	10.9	20.2	5.6	17.9	7
2	Athokadaya	11.3	19.6	3.3	18.2	8
3	Anandhanur sannam	11.8	25	4.4	20.9	8.58
4	IWP	13	12.2	3.1	10.3	8.7
	Long duration					
1	Kerala sundari	8.1	18.1	4.8	16.8	7.45
2	Rajora	12.8	29.2	7.3	27	7.68
3	Tholokattai	12.9	23	7.1	22.8	10.18
4	CR 1009	11.2	24.6	4.1	20.8	8.04

*Fe & Zn - mg/kg, protein - percentage.

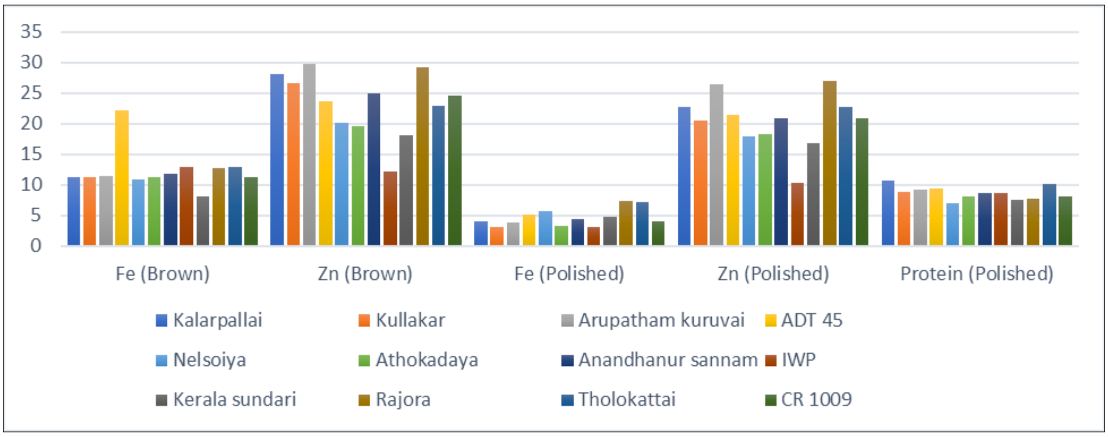


Fig. 4. Nutrient profiling of rice genotypes: Fe, Zn and protein content comparison.

These findings emphasize the importance of identifying and promoting genotypes with balanced nutritional qualities. Selecting such varieties plays a crucial role in combating micronutrient deficiencies and enhancing food security. The results further underline the need for integrating nutritional traits into mainstream breeding programs to improve overall crop quality and support better human health outcomes globally.

Conclusion

This study provides comprehensive insights into the genetic diversity, agronomic performance and nutritional composition of 44 rice genotypes across different maturity durations. The findings underscore the significance of targeted breeding efforts to enhance yield and quality traits, addressing both food security and nutritional deficiencies. Among the genotypes evaluated, ADT 45 (short-duration), Nelsolia (medium-duration) and Kerala Sundari (long-duration) emerged as top performers, exhibiting superior observations across key agronomic and nutritional traits. These cultivars offer promising candidates for cultivation across various cropping systems, supporting sustainable agricultural practices. Additionally, the diverse nutritional profiles observed emphasize the importance of selecting rice varieties with balanced nutrient content to promote human health and combat malnutrition. Future research should focus on exploiting the identified genetic variability to develop high-yielding, nutrient-rich and climate-resilient rice varieties that align with the goals of sustainable agriculture and improved human health.

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Authors' contributions

RD and RP have conceptualized the draft. RD reviewed the literature, drafted manuscript. RP finalized the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

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

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Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used the Grammarly tool in order to improve language and readability of the content. After using this tool/service, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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