Received: 05 Jul 2023 | Revised: 09 Aug 2023 | Accepted: 26 Aug 2023

Electronic Journal of Plant Breeding

Research Article

Exploring the phenotypic diversity of rice: A multivariate analysis of local landraces and elite cultivars of Tamil Nadu and Exotic Lines

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Abstract

This study aimed to assess the genetic variability, heritability, genetic gain and trait relationships of sixteen biometrical characteristics in a collection of eighty-nine rice cultivars, landraces and exotic lines. The focus was on understanding the degree of genetic divergence and identifying traits with high selection potential. The analysis revealed that economic yield improving traits like single plant yield, filled grains per panicle and total number of productive tillers showed high GCV, PCV, heritability and genetic gain implying the predominance of additive gene action and these traits can be given importance in selection and genetic advancement for yield improvement. Days to 50% flowering, plant height, total number of productive tillers, filled grains per panicle and thousand grain weight showed notable significant associations with single plant yield, with direct effects, asserting that these traits were most efficient and promising for selection. Cluster analysis revealed two clusters with cluster 1 mostly occupied by elite cultivars and cluster 2 occupied mostly by landraces and exotic lines. This information can be valuable for further studies and breeding programs, allowing researchers to focus on specific clusters for targeted genetic improvement or conservation efforts.

Keywords: Multivariate analysis, phenotypic diversity, rice, local landraces, elite cultivars

INTRODUCTION

Rice (Oryza sativa L.) is a major food crop that feeds more than half of the world's population, especially in Asia, Africa and Latin America. According to an estimate for 2022, Tamil Nadu has an area of 46.1 million hectares under rice cultivation, with a production of 130.8 million metric tonnes and a productivity of 2.8 tonnes per hectare (INDIASTAT, 2022). The high productivity of rice in Tamil Nadu is essential for ensuring a stable and sufficient food supply for its population, as well as for national and international food markets. The state's rice cultivation not only meets the domestic demand but also contributes to the overall global rice supply, thereby playing a crucial role in alleviating food shortages and supporting global food security efforts. However, the future of rice production in Tamil Nadu faces significant challenges due to the simultaneous exponential growth of the population and the impacts of climate change. Currently, most of the cultivated rice varieties in the region are focused on maximizing yield potential. While this approach has resulted in high productivity, it has also rendered these elite cultivars susceptible to both biotic and abiotic stresses. Moreover, these cultivars lack several essential nutritional characteristics. Rice exhibits remarkable genetic diversity, with numerous landraces that have

https://doi.org/10.37992/2023.1403.099

been cultivated and conserved by farmers for centuries. These landraces are locally adapted to specific agro-ecological conditions and socio-cultural preferences, and they possess valuable traits such as stress resistance, nutritional value, and quality characteristics. India is one of the leading rice producers in the world, with Tamil Nadu being an important rice-growing state in the country, boasting a rich history and tradition of rice cultivation (Thiyagarajan and Kalaiyarasi, 2010). The region hosts a diverse array of rice landraces, reflecting the cultural and linguistic heritage of the state. Ancient Tamil literature mentions the existence of approximately 400 rice landraces, categorized based on morphological attributes, maturity, seasonality, and culinary purposes. For example, Navara is a medicinal rice variety that has been used to treat diseases like chronic gastritis and peptic ulcer (Savitha and Usha, 2016). Bhat moori is another rice variety that cures anaemia and enhances blood circulation in women after child birth (Amudha *et al*., 2023). While some of these landraces persistently thrive in remote areas through continuous cultivation by local farmers, others have unfortunately fallen into disuse or have been substituted by modern varieties. The conservation and utilization of rice landraces in Tamil Nadu are therefore of paramount importance to preserve genetic diversity and ensure food security within the state (Senthil *et al.,* 2010).

Phenotypic diversity encompasses the observable variations in traits such as yield, quality, morphology, physiology, and stress tolerance among distinct rice genotypes (Courtois *et al*., 2003). This diversity mirrors the underlying genetic variation and environmental adaptability of rice populations (Zhang *et al.,* 2011). A comprehensive understanding of the phenotypic diversity exhibited by rice cultivars is instrumental in identifying valuable genes and alleles for breeding purposes, unravelling the evolutionary history and domestication patterns of rice, and ultimately aiding in the development of new rice varieties possessing desirable traits (Garris *et al*., 2005).

Therefore, this paper aims to explore and analyse the diversity of rice landraces and elite genotypes cultivated in Tamil Nadu, in addition to exotic improved lines and landraces. By utilizing 16 quantitative traits, extensive studies were conducted on genetic variability, correlation, path analysis, and diversity analysis on a dataset comprising 89 rice genotypes. The primary objective is to gain valuable insights into the phenotypic diversity exhibited by rice and enhance our understanding of the genetic composition of different rice varieties. The knowledge generated from this research holds immense significance in improving rice breeding programs and facilitating the development of novel rice varieties endowed with desirable traits, thereby contributing to enhanced agricultural productivity and food security.

MATERIALS AND METHODS

A total of 89 rice genotypes were evaluated under irrigated conditions at the Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore, India (10.5930° N and 76.5500° E) during *Rabi*, 2022. The genotypes included elite cultivars of Tamil Nadu, historical landraces of South India and exotic lines from IRRI, Philippines (**Table 1**). The seed material was obtained from the Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore.

The experiment was conducted in Randomized Block Design (RBD) with three replications. The spacing between rows and plants was maintained at 20 cm x 15 cm, respectively. This design allowed for the systematic arrangement of experimental units and the control of variability within the blocks. The genotypes were randomly assigned to the experimental units within each block to minimize the effects of any extraneous factors on the results. The recommended agronomic practices were followed for crop management. Five plants were randomly selected in each replication and 16 agronomic traits were recorded: plant height (cm), total number of tillers, total number of productive tillers, panicle length (cm), flag leaf length (cm), flag leaf width (cm), days to 50% flowering (plot basis), filled grains per panicle, chaffy grains per panicle, total grains per panicle, spikelet fertility (%), thousand grain weight (g), single plant yield (g), grain length (mm), grain width (mm) and length breadth ratio.

The R software, developed by the R Core Team in 2021, served as the primary tool for data analysis (R Core Team, 2021). To perform Analysis of Variance (ANOVA) for Randomized Block Design (RBD), custom R scripts were used. For the calculation of genotypic and phenotypic correlation, as well as genotypic and phenotypic path analysis, we employed the “variability” package in R, as described by Popat *et al.* (2020). To visualize the correlation matrix, a correlation diagram was generated using the “corrplot” package in R, which was developed by Wei and Simko, (2017). To determine the optimal number of clusters based on the Euclidean distance matrix, the “fviz_nbclust” function (Kassambara, 2016) was utilized in R, employing the silhouette method. For clustering analysis, the ward. D2 method was employed, which is a hierarchical clustering method available in R. To visualize the clustering results and create the corresponding tree diagrams, the “ggtree” package developed by Yu *et al.* in 2017 was utilized. Additionally, the “ggplot2” package developed by Wickham, (2011) was used for further visualization purposes.

RESULTS AND DISCUSSION

The ANOVA results (**Table 2**) indicated significant variation among the genotypes for all the traits studied at 5% probability level. These findings aligned with previous research on quantitative traits in rice (Hoque *et al.,* 2015;

Table 1. List of the 89 rice genotypes used in the study

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	ADT 36	31	Channangi	61	Sarapillisamba
2	ADT 37	32	Chetty samba	62	Seeraga samba
3	ADT 38	33	Chinnaadukkunell	63	Sembala
4	ADT 39	34	Chittam samba	64	Senkar
5	ADT 40	35	Godavari samba	65	Senthooram
6	ADT 42	36	Illupai poo samba	66	Sornakuruvai
7	ADT 43	37	Kallukar	67	Thengai poo samba
8	ADT 46	38	Karthigai samba (bold)	68	Thillainayagam
9	ADT 50	39	Karthigai samba (slender)	69	Thondi
10	ADT 51	40	Karuthakar	70	Thooyamalli
11	ADT 52	41	Kavuni	71	Uppumolagai
12	ADT 53	42	Kuzhiyadicham	72	Vadivel
13	ADT 54	43	Malayalathan samba	73	Varigarudan samba
14	ADT 56	44	Manavari	74	Vasanaiseeraga samba
15	ADT 57	45	Milagu samba	75	Vellaikudaivazhai
16	CO 51	46	Muthuvellai	76	ARB 64
17	CO 52	47	Mysore malli	77	RH2-SM-2-23
18	CO 53	48	Navara	78	RPHP 159
19	CO 54	49	Pal kichadi	79	RPHP 27
20	CO 55	50	Pamani samba	80	RPHP 80
21	CR 1009 SUB 1	51	Panamara samba	81	IG 26(IC 0590943- 121899)
22	TRY 2	52	Pokkali	82	IG 28(EC 728920- 117914)
23	TRY 3	53	Poongar	83	IG 41(EC 728800- 117776)
24	TRY 4	54	Poongar s/n	84	IG 43(EC 728788- 117759)
25	V10	55	Rangoon samba	85	IG 44(EC 728762- 117729)
26	Arcotkichadi	56	Rasagadam	86	IG 58(EC 728725- 117689)
27	Arubathamkuruvai	57	Red sirumani	87	IG 60(EC 728730- 117695)
28	Arupatham Samba	58	Sadai samba	88	IG 65(EC 729024- 120958)
29	Atthurkichali Samba	59	Sambarai	89	IG 72(EC 728650- 117587)
30	Basumathi	60	Sambarai s/n		

Sultana et al., 2020 and Kakar *et al.,* 2021). The mean sum of square values reflected the magnitude of variation for each trait. Also, the genotypes represented a wider range for all the quantitative traits studied. Notably some of the yield contributing traits, such that, the total grains per panicle exhibited a range of 51.00 to 226.00, while filled grains per panicle ranged from 29.67 to 210.00. Spikelet fertility spanned 58.18% to 95.98%, reflecting genetic influences on reproductive success. Thousand grain weight varied from 9.52 to 29.00 g, indicating diverse grain sizes. Single plant yield demonstrated considerable range, from 11.62 to 36.00 g.

The mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percentage of mean (GAM) for 16 agronomic traits are presented in **Table 3**. The PCV and GCV are measures of genetic variability that reflect the extent of variation due to genetic and environmental factors (Kumar *et al.,* 2018; Gowthami *et al.,* 2022 and Lakshmi et al., 2022). The PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) as per Sivasubramanian and Madhava Menon (1973). Traits with low PCV values included spikelet fertility (8.06%), grain length (9.38%) and panicle length (9.82%). Traits with moderate PCV values included days to 50% flowering (11.82%), flag leaf length (14.83%), thousand grain weight (15.01%), total number of tillers (17.93%) and length breadth ratio (19.71%). Traits with high PCV values included plant height (20.74%), single plant yield (22.60%), flag leaf width (22.14%), total number of productive tillers (27.11%), total grains per panicle (26.64%), filled grains per panicle (31.32%) and chaffy grains per panicle (32.15%). The traits with low GCV

Table 2. Analysis of variance for 16 biometrical characters

Traits	Mean sum of squares		
	Replication	Treatment	Error
Plant height	105.97	2223.42*	53.93
Total number of tillers	0.27	35.93*	1.22
Total number of productive tillers	0.34	55.14*	0.88
Panicle length	0.55	13.33*	1.63
Flag leaf length	3.32	73.06*	2.72
Flag leaf width	0.12	0.40*	0.01
Days to 50% flowering	24.82	314.51*	22.69
Filled grains per panicle	75.8	2798.37*	30.24
Chaffy grains per panicle	0.57	91.77*	1.11
Total grains per panicle	65.76	2799.04*	32.36
Spikelet fertility	2.22	135.02*	1.05
Thousand grain weight	0.92	30.18*	1.34
Single plant yield	0.37	78.48*	4.10
Grain length	0.03	0.72*	0.09
Grain width	0.01	0.35*	0.02
Length breadth ratio	0.12	0.76*	0.04

* Significance at 5% level

Table 3. Genetic parameters for 16 characters observed in 89 rice genotypes

Traits	Mean	Range		PCV (%)	GCV (%)	h^2 (%)	GAM (%)
		Min	Max				
Plant height (cm)	134.45	79.96	187.00	20.74	20.00	92.98	39.73
Total number of tillers	19.95	13.00	28.00	17.93	17.05	90.49	33.42
Total number of productive tillers	16.06	7.67	25.67	27.11	26.47	95.37	53.26
Panicle length (cm)	23.91	18.72	31.80	9.82	8.27	70.87	14.34
Flag leaf length (cm)	34.49	22.00	43.50	14.83	14.04	89.60	27.38
Flag leaf width (cm)	1.67	1.16	2.47	22.14	21.54	94.65	43.17
Days to 50% flowering	92.70	64.67	115.00	11.82	10.64	80.90	19.71
Filled grains per panicle	98.60	29.67	210.00	31.32	30.80	96.74	62.41
Chaffy grains per panicle	17.41	5.00	39.00	32.15	31.57	96.43	63.87
Total grains per panicle	116.02	51.00	226.00	26.64	26.17	96.54	52.97
Spikelet fertility (%)	83.93	58.18	95.98	8.06	7.96	97.68	16.21
Thousand grain weight (g)	22.05	9.52	29.00	15.01	14.06	87.71	27.13
Single plant yield (g)	23.78	11.62	36.00	22.60	20.94	85.83	39.97
Grain length (mm)	5.82	4.34	7.20	9.38	7.88	70.67	13.65
Grain width (mm)	2.25	1.53	2.80	15.60	14.91	91.28	29.34
Length breadth ratio	2.64	1.62	3.90	19.71	18.84	91.37	37.10

Min, minimum; Max, maximum; PCV, Phenotypic coefficient of variation; GCV, Genotypic coefficient of variation; h^2, heritability in broad sense and GAM, genetic advance as per cent of mean.

values were grain length (7.88%), spikelet fertility (7.96%), panicle length (8.27%) and days to 50% flowering (10.64%). The traits with moderate GCV values were flag leaf length (14.04%), thousand grain weight (14.06%), grain width (14.91%), total number of tillers (17.05%), and length breadth ratio (18.84%). The traits with high GCV values were plant height (20.00%), single plant yield (20.94%), flag leaf width (21.54%), total grains per panicle (26.17%), total number of productive tillers (26.47%), filled grains per panicle (30.80%) and chaffy grains per panicle (31.57%). This study showed high PCV and GCV for most of the traits, indicating high genetic variability among the genotypes studied. Similar results have been reported in previous studies on rice (Mekonnen *et al.,* 2018; Demeke *et al.,* 2020 and Islam *et al.,* 2021). Among the traits studied, high PCV combined with high GCV was observed for chaffy grains per panicle (32.15% and 31.57%, respectively), followed by filled grains per panicle (31.32% and 30.80%, respectively) and total grains per panicle (26.64% and 26.17%, respectively). These traits are important for yield improvement and can be selected for further breeding. The traits, spikelet fertility (8.06% and 7.96%, respectively), followed by grain length (9.38% and 7.88%, respectively) and panicle length (9.82% and 8.27%, respectively) recorded low PCV as well as GCV. These traits had low genetic variability and might have been influenced by environmental factors.

Heritability (h^2) is the ratio of genetic variance to phenotypic variance, which indicates the degree of transmissibility of a trait from parents to offspring (Chauhan *et al.,* 2021). Johnson *et al*. (1955) classified heritability as low (<30%), moderate (30-60%) and high (>60%). The results of the present study showed that all the traits fall into the category of high heritability (>60%), indicating that they are largely controlled by genetic factors and less affected by environmental factors (**Table 3**). Within this high heritability category, the maximum heritability was observed for spikelet fertility (97.68%) followed by filled grains per panicle (96.74%) and total grains per panicle (96.54%). The minimum heritability was observed for grain length (70.67%) followed by panicle length (70.87%) and days to 50% flowering (80.90%). These traits were found to be highly heritable and suggested to be easily improved by selection (Kujur *et al*., 2020).

The GAM is the expected gain in the trait value when selection is practiced based on phenotypic performance (Ali *et al*., 2021). Hanson et al. (1956) classified GAM as low (<10%), moderate (10-20%) and high (>20%). The results showed that most of the traits had a high GAM (>20%), indicating that they can be improved significantly by selection. The traits with high GAM values were thousand grain weight (27.13%), flag leaf length (27.38%), grain width (29.34%), total number of tillers (33.42%), length breadth ratio (37.10%), plant height (39.73%), single plant yield (39.97%), flag leaf width (43.17%), total grains per panicle (52.97%), total number of productive tillers (53.26%), filled grains per panicle (62.41%), and chaffy grains per panicle (63.87%). The traits with high GAM have high potential for yield improvement and hence priority should be given in selection (Lingaiah *et al.,* 2015; Saha *et al*., 2019). The traits with moderate GAM values were grain length (13.65%), panicle length (14.34%), spikelet fertility (16.21%) and days to 50% flowering (19.71%). These traits have low potential for yield improvement and may not respond well to selection.

Direct selection for a complex trait like yield may not result in the expected genetic gain, as it may be affected by other contributing traits (Li *et al.,* 2019). Therefore, correlation analysis can be used to identify the traits that are significantly associated with yield and can serve as indirect selection criteria (Lamichhane *et al.,* 2021). The correlation coefficients between various traits and single plant yield is presented in **Table 4, while Fig. 1** visually represents this correlation using a corrplot. The traits that had positive and significant correlations with single plant yield were total number of tillers (0.33**), total number of productive tillers (0.40**), spikelet fertility (0.37**), days to 50% flowering (0.36**), filled grains per panicle (0.36**), total grains per panicle (0.31**), panicle length (0.24*) and thousand grain weight (0.24*). These traits indicated that higher tillering ability, higher spikelet fertility, longer panicle length and heavier grains will contribute to higher yield. Similar results were obtained by previous studies for yield associated studies (Li *et al*., 2019 and Lamichhane *et al.,* 2021). The traits that had significant negative correlations with single plant yield were plant height (-0.37**) and chaffy grains per panicle (-0.29**). These traits suggested that dwarf genotypes with a lower percentage of unfilled grains or genotypes that give high spikelet fertility are desirable to attain higher yields. These results are consistent with previous studies that reported similar associations between yield and agronomic traits in different rice ecotypes (Li *et al*., 2019; Siti *et al.,* 2020 and Sravani *et al*., 2021). Therefore, selection with emphasis on plant types with less plant height and chaffy grains per panicle, high number of productive tillers, higher spikelet fertility, higher thousand grain weight and panicle length could result in yield improvement (Sravani *et al.,* 2021).

In order to explore the relationship between yield and its associated characteristics, path analysis was employed. This approach allows for the examination of both direct and indirect effects, providing a more comprehensive understanding of the factors contributing to yield. Unlike correlation analysis, which may not fully capture the significance of yield-contributing traits, path analysis enables a more nuanced assessment of their influence. The results of genotypic path analysis are presented in **Table 5**. The results indicated that among the yield-contributing traits, filled grains per panicle had the highest direct effect on single plant yield with a value of 13.49. This was followed by the total number of tillers with a positive direct effect of 3.68 and total number of tillers with a value of 2.74. Spikelet fertility also showed a positive direct effect on single plant yield with a value of 2.43. On the other hand, plant height and chaffy grains per panicle showed negative direct effects on single plant yield with values of -0.49 and -0.23, respectively. These results

Table 4. Genotypic correlation coefficients among 16 biometric traits in 89 rice genotypes

	PH	TNT	TPT	PL	FLL	FLW	DFF	FGP	CG	TGP	SF	TGW	GL	GW	L.B	SPY
PH	1	-0.33**	-0.49**	0.17^{NS}	0.39**	0.59**	-0.12^{NS}	-0.30**	0.51**	-0.20^{NS}	-0.39**	0.14^{NS}	-0.29**	0.16^{NS}	-0.27**	-0.37**
TNT	-0.33**	1	0.96**	0.15^{NS}	-0.17^{NS}	-0.19^{NS}	0.45**	0.12^{NS}	-0.16^{NS}	0.09^{NS}	0.15^{NS}	-0.00^{NS}	0.16^{NS}	-0.10^{NS}	0.14^{NS}	0.33**
TPT	-0.49**	0.96**	1	0.15^{NS}	-0.17^{NS}	-0.34**	0.42**	0.31**	-0.31**	0.26*	0.35**	0.01^{NS}	0.24*	-0.12^{NS}	0.20^{NS}	0.40**
PL	0.17^{NS}	0.15^{NS}	0.15^{NS}	1	0.03^{NS}	0.11^{NS}	0.24*	-0.03^{NS}	0.13^{NS}	-0.00^{NS}	-0.06^{NS}	0.01^{NS}	-0.07^{NS}	0.03^{NS}	-0.07^{NS}	0.24*
FLL	0.39**	-0.17^{NS}	-0.17^{NS}	0.03^{NS}	1	0.21*	-0.01^{NS}	-0.04^{NS}	0.15^{NS}	-0.01^{NS}	-0.06^{NS}	0.34**	0.04^{NS}	0.25*	-0.21*	-0.14^{NS}
FLW	0.59**	-0.19^{NS}	-0.34**	0.11^{NS}	0.21*	1	-0.01^{NS}	-0.23*	0.42**	-0.16^{NS}	-0.40**	0.03^{NS}	-0.29**	0.15^{NS}	-0.28**	-0.17^{NS}
DFF	-0.12^{NS}	0.45**	0.42**	0.24*	-0.01^{NS}	-0.01^{NS}	1	0.22*	0.06^{NS}	0.23*	0.06^{NS}	-0.04^{NS}	0.15^{NS}	0.38**	-0.26*	0.36**
FGP	-0.30**	0.12^{NS}	0.31**	-0.03^{NS}	-0.04^{NS}	-0.23*	0.22*	1	-0.09^{NS}	0.98**	0.72**	-0.09^{NS}	0.10^{NS}	-0.17^{NS}	0.18^{NS}	0.36**
CG	0.51**	-0.16^{NS}	-0.31**	0.13^{NS}	0.15^{NS}	0.42**	0.06^{NS}	-0.09^{NS}	1	0.09^{NS}	-0.66**	-0.20^{NS}	-0.25*	0.01^{NS}	-0.11^{NS}	-0.29**
TGP	-0.20^{NS}	0.09^{NS}	0.26*	-0.00^{NS}	-0.01^{NS}	-0.16^{NS}	0.23*	0.98**	0.09^{NS}	1	0.60**	-0.12^{NS}	0.05^{NS}	-0.17^{NS}	0.16^{NS}	0.31**
SF	-0.39**	0.15^{NS}	0.35**	-0.06^{NS}	-0.06^{NS}	-0.40**	0.06^{NS}	0.98**	-0.66**	0.60**	1	0.11^{NS}	0.21^{NS}	-0.14^{NS}	0.21^{NS}	0.37**
TGW	0.14^{NS}	-0.00^{NS}	0.01^{NS}	0.01^{NS}	0.34**	0.03^{NS}	-0.04^{NS}	-0.09^{NS}	-0.20^{NS}	-0.12^{NS}	0.11^{NS}	1	0.19^{NS}	0.21^{NS}	-0.08^{NS}	0.24*
GL	-0.29**	0.16^{NS}	0.24*	-0.07^{NS}	0.04^{NS}	-0.29**	0.15^{NS}	0.10^{NS}	-0.25*	0.05^{NS}	0.21^{NS}	0.19^{NS}	1	-0.07^{NS}	0.46**	0.28**
GW	0.16^{NS}	-0.10^{NS}	-0.12^{NS}	0.03^{NS}	0.25*	0.15^{NS}	0.38**	-0.17^{NS}	0.01^{NS}	-0.17^{NS}	0.14^{NS}	0.21^{NS}	-0.07^{NS}	1	-0.91**	0.05^{NS}
L.B	-0.27**	0.14^{NS}	0.20^{NS}	-0.07^{NS}	-0.21*	-0.28**	-0.26*	0.18^{NS}	-0.11^{NS}	0.16^{NS}	0.21^{NS}	-0.08^{NS}	0.46**	-0.91**	1	0.10^{NS}
SPY	-0.37**	0.33**	0.40**	0.24*	-0.14^{NS}	-0.17^{NS}	0.36**	0.36**	-0.29**	0.31**	0.37**	0.24*	0.28**	0.05^{NS}	0.10^{NS}	1

Significance levels: p < .01 '**', p < .05 '*'. PH, plant height; TNT, total number of tillers; TPT, total number of productive tillers; PL, panicle length; FLL, flag leaf length; FLW, flag leaf width; DFF, days to 50% flowering; FGP, filled grains per panicle; CG, chaffy grains per panicle; TGP, total grains per panicle; SF, spikelet fertility; TGW, thousand grain weight; SPY, single plant yield; GL, grain length; GW, grain width and L.B, length breadth ratio.

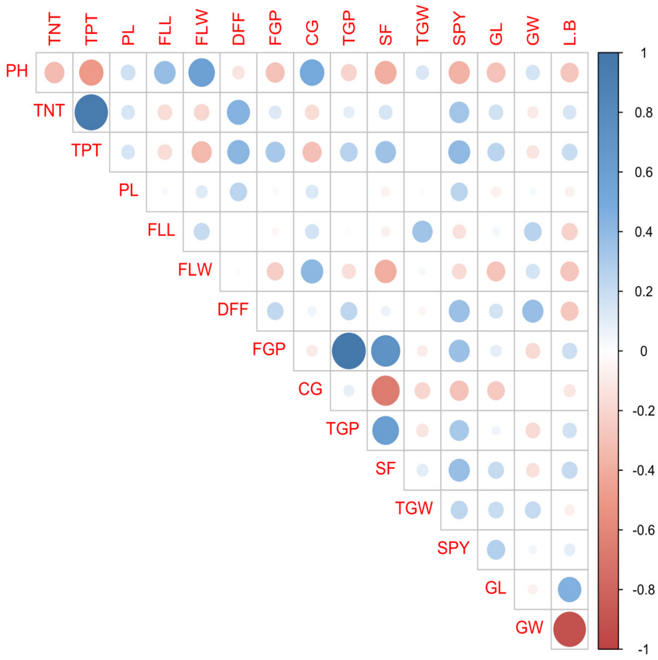

Fig. 1. Correlation plot of genotypic correlation coefficients among 16 biometric traits in 89 rice genotypes

PH, plant height; TNT, total number of tillers; TPT, total number of productive tillers; PL, panicle length; FLL, flag leaf length; FLW, flag leaf width; DFF, days to 50% flowering; FGP, filled grains per panicle; CG, chaffy grains per panicle; TGP, total grains per panicle; SF, spikelet fertility; TGW, thousand grain weight; SPY, single plant yield; GL, grain length; GW, grain width and L.B, length breadth ratio.

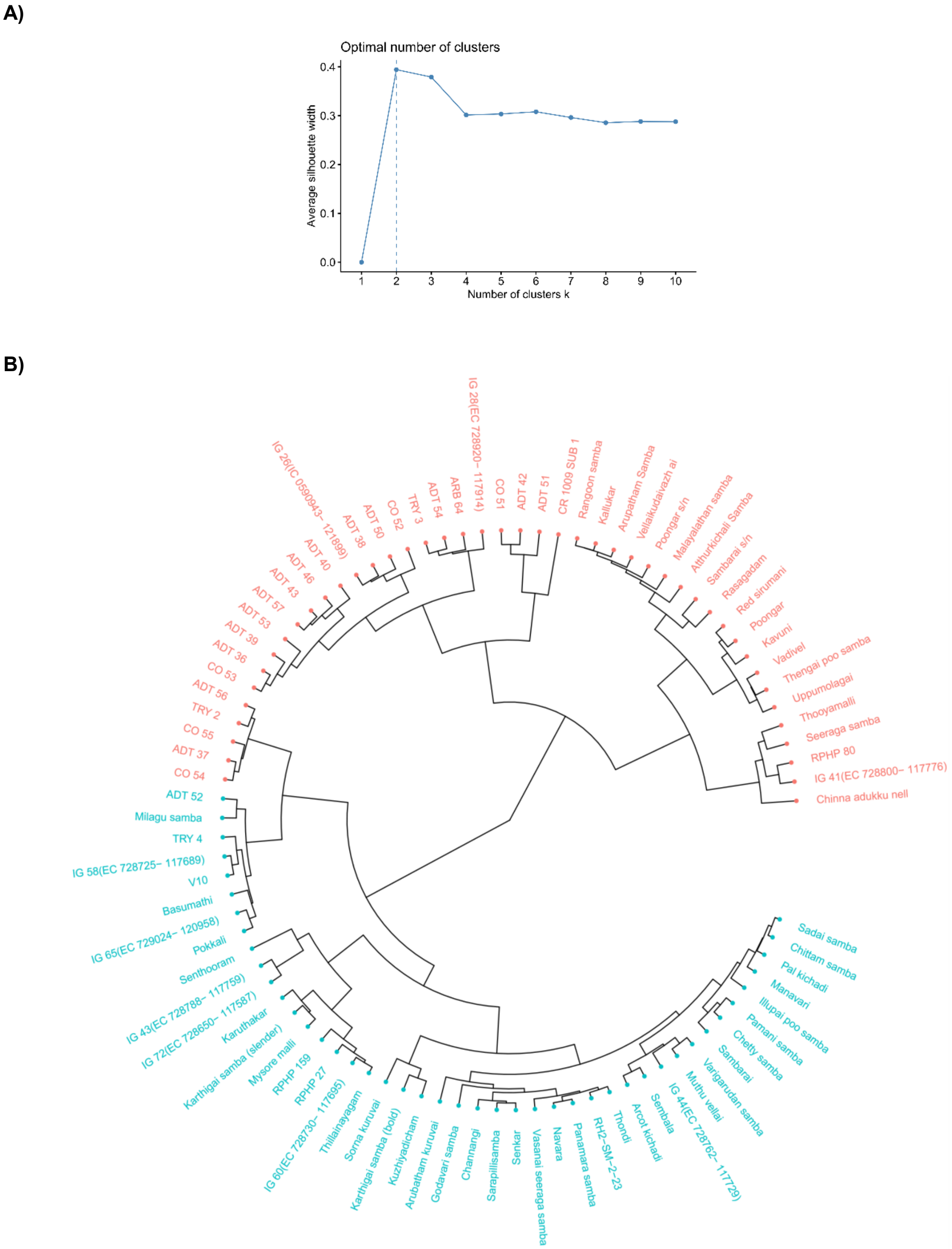

Fig. 2. A) Silhouette plot for optimal number of clusters, B) Cluster dendrogram plot of 89 genotypes

suggested that yield can be improved through deliberate selection for traits such as filled grains per panicle, total number of productive tillers, total number of tillers and spikelet fertility. Positive selection for more productive tillers and higher spikelet fertility can result in increased single plant yield. On the other hand, selection for reduced plant height and fewer chaffy grains per panicle can result in genetic gain for single plant yield.

The genetic diversity analysis conducted using the silhouette method, specifically employing the function 'fviz_nbclust', has provided insights into the clustering patterns of 89 genotypes. The results indicated the presence of two optimal clusters, which displayed significant distinctions (**Fig. 2**). Cluster 1 grouped together a total of 45 genotypes, mainly comprising elite cultivars, with a few inclusions of landraces and exotic lines.

Table 5. Direct and indirect effects partitioned by genotypic path analysis in rice genotypes

	PH	TNT	TPT	PL	FLL	FLW	DFF	FGP	CG	TGP	SF	TGW	GL	GW	L.B	Correlations SPY
PH	**-0.49**	-1.20	1.85	0.10	0.03	0.10	0.05	-3.99	0.67	2.46	0.22	0.00	0.58	0.88	-1.62	-0.37**
TNT	0.16	**3.68**	-3.58	0.09	-0.01	-0.03	-0.17	1.66	-0.21	-1.12	-0.08	0.00	-0.33	-0.53	0.83	0.33**
TPT	0.24	1.02	**2.74**	0.09	-0.01	-0.06	-0.16	0.20	-0.40	-3.08	-0.20	0.00	-0.48	-0.67	1.17	0.40**
PL	-0.08	0.54	-0.54	**0.59**	0.00	0.02	-0.09	-0.35	0.17	0.03	0.03	0.00	0.14	0.17	-0.39	0.24*
FLL	-0.19	-0.62	0.62	0.02	**0.07**	0.03	0.00	-0.52	0.20	0.13	0.04	-0.01	-0.09	1.41	-1.24	-0.14^{NS}
FLW	-0.29	-0.70	1.27	0.07	0.01	**0.16**	0.00	-3.14	0.55	1.89	0.22	0.00	0.57	0.85	-1.64	-0.17^{NS}
DFF	0.06	1.64	-1.58	0.15	0.00	0.00	**-0.39**	2.98	0.08	-2.78	-0.04	0.00	-0.30	2.08	-1.54	0.36**
FGP	0.14	0.45	-1.17	-0.02	0.00	-0.04	-0.09	**13.49**	-0.12	-11.82	-0.41	0.00	-0.19	-0.95	1.08	0.36**
CG	-0.25	-0.59	1.14	0.08	0.70	0.07	-0.02	-1.24	**-0.23**	-0.01	0.38	0.00	0.31	0.03	-0.66	-0.29**
TGP	0.10	0.34	-0.96	0.00	0.00	-0.03	-0.09	0.27	0.12	**0.69**	-0.04	0.00	-0.10	-0.95	0.96	0.31**
SF	0.19	0.54	-1.32	-0.03	0.00	-0.06	-0.02	4.75	-0.88	-5.24	**2.43**	0.00	-0.41	-0.78	1.22	0.37**
TGW	-0.07	-0.01	-0.02	0.01	0.02	0.01	0.02	-1.16	-0.26	0.46	-0.06	**0.98**	-0.38	1.15	-0.45	0.24*
GL	0.14	0.60	-0.91	-0.04	0.00	-0.05	-0.06	1.32	-0.34	-0.62	-0.12	0.00	**-1.99**	-0.38	2.71	0.28**
GW	-0.08	-0.35	0.46	0.02	0.02	0.02	-0.14	-2.32	0.01	2.06	0.08	0.00	0.14	**5.53**	-5.38	0.05^{NS}
L.B	0.13	0.52	-0.74	-0.04	-0.01	-0.05	0.10	2.48	-0.15	-1.96	-0.12	0.00	-0.92	-5.04	**5.90**	0.10^{NS}

PH, plant height; TNT, total number of tillers; TPT, total number of productive tillers; PL, panicle length; FLL, flag leaf length; FLW, flag leaf width; DFF, days to 50% flowering; FGP, filled grains per panicle; CG, chaffy grains per panicle; TGP, total grains per panicle; SF, spikelet fertility; TGW, thousand grain weight; SPY, single plant yield; GL, grain length; GW, grain width and LB, length breadth ratio.

Conversely, cluster 2 consisted of 44 genotypes, primarily made up of landraces and exotic lines, with a presence of some cultivars. The distinguishing factor between cluster 1 and 2 lay in their composition. The analysis highlighted a clear demarcation between landraces and elite cultivars. Successful differentiation by the clustering analysis underscored distinct genetic profiles and potential trait variations. This insight holds significance for future studies and breeding initiatives, enabling researchers to concentrate on specific clusters for targeted genetic enhancements or preservation endeavours.

In conclusion, this study demonstrated the significant genetic variability and heritability of important traits in rice genotypes, providing insights for selection and breeding strategies to enhance grain yield. The findings emphasized the potential for improving yield through the selection of specific traits and employing association studies to explore additional traits associated with yield. The genetic diversity analysis contributed to the understanding of distinct genetic profiles and could guide future breeding efforts for the improvement of rice varieties.

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