



Unravelling genetic diversity of South Indian rice landraces based on yield and its components

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Abstract

Traditional varieties are considered as key natural resources necessary to maintain future food security in the current climate change era. Conserving these traditional varieties are the need of the hour as they harbour many valuable genes which could be exploited for crop breeding. Genetic diversity for morphological traits in a population can be assessed using a variety of techniques, including univariate and multivariate analysis. A diverse panel of 60 traditional landraces of rice was evaluated for 14 the pattern of genetic diversity and relationship based on morphological traits by multivariate analysis like Mahalanobis' D² and principal component analyses and correlation analysis was utilized to examine the association among morphological traits. The 60 genotypes were grouped in to eight clusters based on cluster analysis. Principal component analysis revealed that the cumulative variance of 74.41 % of total variation among 14 characters was explained by the first five axes. Study of association among traits indicated that direct selection based on the traits such as number of grains per panicle, flag leaf length, kernel length, length to breadth ratio and hundred seed weight would be the traits of top priority for yield improvement in rice.

Keywords: Traditional landraces, Rice, Variability, Multivariate analysis

INTRODUCTION

Rice is a major agricultural crop in India, grown in diverse ecologies with a wide range of phenology and yield. While the demand for rice is continuously increasing with the rapid growth in the human population, the land area available for rice production is decreasing as a result of rapid urbanisation, impeding climate change and changing lifestyles. By 2025, the requirement of rice will be 758 million tonnes to meet the world's consumption, which currently is approximately at 600 million tonnes (Nakano *et al.*, 2019). To satisfy future consumer demands, there is an urgent need for new rice cultivars with high yield, resilience to both biotic and abiotic stresses and good grain quality.

Traditional varieties are known for their adaptability to the diverse environment, due to which they cope up with changing climate and also are reservoirs of pest and diseases resistant genes in rice. Therefore, utilization of traditional rice varieties would be the ideal and sustainable way to develop climate smart rice varieties with resistance to major biotic and abiotic stresses. According to N.I.Vavilov, South Asia is major centre of origin and variation for rice. This region is endowed with enormous variability in terms of qualitative and quantitative traits as well as sources of resistance to various biotic and abiotic stresses. Worldwide about 8000 botanically distinct kinds of rice exist, out of which more

than 4000 traditional varieties are found in India (Yadugiri, 2010). Therefore, these landraces may be exploited potentially and used as a donors for many number of traits. From the perspectives of selection, conservation, and effective utilisation, genetic diversity assessment is crucial in rice breeding (Mohammadi-Nejad *et al.*, 2008). Accurate assessment of land races for the proportion and patterns of genetic diversity and variability are extremely helpful for the identification of diverse parents to produce segregating offspring with the greatest genetic variability and the introgression of desirable genes from diverse germplasm into the existing genetic base (Chakravorty *et al.*, 2013).

The inherent variance among crop genotypes has been extensively summarised and described using multivariate statistical tools. Multivariate statistical tools include principal component analysis (PCA), Cluster analysis and discriminate analysis (Oyelola, 2004). PCA can be used to find similarities between variables and categorise the genotypes (Kaufman and Rouseeuw, 2009). Based on generalised distance, Mahalanobis D^2 statistics are useful for measuring the extent of genetic divergence at the genotypic level (Mahalanobis, 1936). Magnitude of genetic measures, such as broad sense heritability, genetic gain, phenotypic and genotypic variances, phenotypic and genotypic coefficients of variations (PCV and GCV), and ANOVA determines the appropriate

selection methods to be followed for the improvement of specific traits. The aforementioned tools are helpful to understand the diversity of characters in landraces and utilization in subsequent breeding programmes. Hence, this study was carried out with the objectives to assess the degree of germplasm diversity, grouping of genotypes based on variations, and genetic relationships between the traits.

MATERIALS AND METHODS

A set of 60 landraces (Table 1) were grown in Tamil Nadu Rice Research Institute (TRRI), Aduthurai, Thanjavur during *Rabi*, 2021. TRRI is situated at latitude of 10.99°N and longitude of 79.48°E. Sixty landraces were transplanted 21 days after sowing as two seedlings per hill with three replications in randomized block design with spacing of 20 x 20cm. The recommended package of practices for rice was followed for the proper establishment and growth of the crop. Observations were recorded on five random plants in each genotype in each replication for morphological characters *viz.*, days to fifty percent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), flag leaf length (FL), flag leaf width (FW), panicle length (PL), number of grains per panicle (NOG), spikelet fertility (SF), kernel length (KL), kernel breadth (KB), length to breadth ratio (LBR), hundred seed weight (HSW) and single plant yield (SPY).

Table 1. List of genotypes used in this study

S.No. Genotypes	S.No. Genotypes	S.No. Genotypes
1 <i>Aanai komban</i>	21 <i>Kaan</i>	41 <i>Kichadi samba</i>
2 <i>Aarupatham kuruvai</i>	22 <i>Kaatu Ponni</i>	42 <i>Koduvaiyan</i>
3 <i>Aathur kichadi samba</i>	23 <i>Kaatu samba</i>	43 <i>Kothamalli samba</i>
4 <i>Adukkkan</i>	24 <i>Kaivara samba</i>	44 <i>Kottanel</i>
5 <i>Athur kichadi</i>	25 <i>Kalanamak</i>	45 <i>Kottara samba</i>
6 <i>Chandai kar</i>	26 <i>Kaliyan Samba</i>	46 <i>Kudavaraghai</i>
7 <i>Chenellu</i>	27 <i>Kallundai</i>	47 <i>Kullakkar</i>
8 <i>Chinkini kar</i>	28 <i>Kandhasali</i>	48 <i>Kuruvai kalanjiyam</i>
9 <i>Chinna PUNCHAI</i>	29 <i>Karimbalan</i>	49 <i>Kuthala samba</i>
10 <i>Chinnar</i>	30 <i>Karnel</i>	50 <i>Mandamaranellu</i>
11 <i>Chithirai Kar</i>	31 <i>Karudan samba</i>	51 <i>Manjal ponni</i>
12 <i>Chitti mutyalu</i>	32 <i>Karunguruvai</i>	52 <i>Manvilayan</i>
13 <i>Edakkal</i>	33 <i>Karuppu kavuni</i>	53 <i>Mappilai samba</i>
14 <i>Gandakasala</i>	34 <i>Karuppu Nel</i>	54 <i>Maranellu</i>
15 <i>GEB-24</i>	35 <i>Karuthakar</i>	55 <i>Mattaikar</i>
16 <i>Gedumani</i>	36 <i>Katta samba</i>	56 <i>Melaki</i>
17 <i>Illupai poo Samba</i>	37 <i>Kattai kar</i>	57 <i>Milagu samba</i>
18 <i>Iravai Pandi</i>	38 <i>Kattu vanibam</i>	58 <i>Mohini Samba</i>
19 <i>Jai Sri Ram</i>	39 <i>Kattu yanam</i>	59 <i>Mullampunchan</i>
20 <i>Kuliadichan</i>	40 <i>Kichali samba</i>	60 <i>Mutrina Samba</i>

Analysis of variance for fourteen morphological traits were analyzed using R software using “agricolae” package (Mendiburu and Yaseen 2020). Correlation between the traits were estimated using “corrplot” package (Wei *et al.*, 2017). Principal component analysis was analyzed using “FactoMineR” (Husson *et al.*, 2016), “factoextra” packages (Kassambara and Mundt *et al.*, 2017). Genetic divergence by Mahalanobis’ D² statistics was estimated using “biotools” package (Da Silva *et al.*, 2017).

RESULTS AND DISCUSSION

Estimates of variance components

Variations in phenological and morphological traits associated with yield were studied to assess the genetic divergence of native landraces. The estimates of ANOVA showed wide variation ($p < 0.01$) among the traits studied (Table 2). Existence of greater diversity in the breeding materials enables higher chances of creating desired recombinants for crop improvement.

Mean performance of genotypes for trait days to fifty percent flowering ranged from 62 (*Aarupatham kuruvai*) to 130 (*Kottara samba*) days. The genotype *Chandaikar* was dwarf with the mean value of 65.63 cm, while the tallest genotype was *Kaliyan samba* (187.73). Number of tillers and productive tillers per plant were recorded high in *Aathurkichadi* (31 and 26) whereas low in *Aarupatham kuruvai* (11 and 8). Flag leaf length varied from 19.27 cm (*Aarupatham kuruvai*) to 63.27 cm (*Kaatuyanam*) while Flag leaf width ranged from 0.93 cm (*Karunguruvai*) to 1.70 cm (*Karuppu kavuni*). Mean panicle length was longest in *Chinikini kar* with 31.60 cm. In *Kaatu samba* grain number was highest with 259 grains per panicle whereas low grain number of 60 per panicle was registered in *Mattaikar*. Spikelet fertility percentage ranged from 75.10 % (*Karudan samba*) to 97.44 % (*Illupai poo samba*). Variation for the grain morphological characteristics namely kernel length, breadth, length to breadth ratio and hundred seed weight were significant ($p < 0.01$) among the landraces. The kernel length (mm), kernel breadth (mm), length to breadth ratio and hundred seed weight (g) ranged from 4.00 (*Kothamalli samba*) - 9.70 (*Chinnar*), 1.60 (*Jai Sri Ram*) - 3.40 (*Chinnar*), 1.67 (*Kothamalli samba*) - 3.95 (*Chinnapunchai*) and 0.96 (*Chittimutiyalu*) - 3.61 (*Kaatuvanibam*) respectively, among the studied accessions. *Milagu samba* was

identified as best yielder with mean single plant yield of 63.60 g and *Chittimutiyalu* was poor yielder (11.80 g).

The estimates of coefficient of variation, heritability and genetic advance as per cent of mean for the studied traits are furnished in Table 3. Phenotypic coefficient of variation (PCV) for all the traits studied were higher than the genotypic coefficient of variation (GCV). Highest PCV and GCV was recorded for single plant yield with a value of 40.16 % and 33.21 % respectively, while lowest PCV (6.82 %) and GCV (4.50 %) was observed for spikelet fertility. Estimates of PCV and GCV for all the traits were found to be moderate (10-20 %) to high (> 20 %) except for spikelet fertility which was categorised as low (< 10 %) (Saha *et al.*, 2019). The traits namely flag leaf length, number of grains, hundred seed weight and single plant yield were found to have high PCV and GCV estimates (>20 %) (Saha *et al.*, 2019) which imply that these traits had higher variability and selection of these would be fruitful for the improvement of accessions as variation of these traits mainly governed by additive genes (Baraskar *et al.*, 2014).

Relative difference (RD), a ratio of the GCV in relation to the relevant PCV (Khan *et al.*, 2020) ranged from 0.49 (Hundred seed weight) to 34.02 (Spikelet fertility percentage). Difference between PCV and GCV estimates was more for the traits namely, number of tillers (27.99), number of productive tillers (22.26), flag leaf length (12.95), flag leaf width (17.02), panicle length (20.11), number of grains per panicle (12.87), spikelet fertility (34.02) and single plant yield (17.31) which indicated that the variability for these traits was mainly due to the environmental influence rather than due to genotypes (Bello *et al.*, 2012). Hence direct selection of these traits would not be preferable. The traits such as days to fifty percent flowering (1.41), plant height (9.07), kernel length (1.22), kernel breadth (1.11), length to breadth ratio (0.80) and hundred seed weight (0.49) could yield better response to direct selection due to lower values for relative differences (Ishiyaku *et al.*, 2005). The higher the value of relative differences indicates that the environment has a high influence on a particular trait, whereas the smaller the value indicates that accessions have had a strong and significant impact on detectable expression with limited environmental influence (Usman *et al.*, 2014).

Table 2. Analysis of variance for the fourteen morphological traits studied

Source of variation	Df	DFF	PH	NT	NPT	FL	FW	PL	NOG	SF	KL	KB	LBR	HSW	SPY
Replication	2	4.29	9.28	1.11	4.42	22.02	0.01	16.46	1268.40	40.36	0.002	0.002	0.005	0.002	317.87
Genotypes	59	624.03**	1378.92**	40.35**	31.87**	249.53**	0.08**	31.15**	6767.60**	70.23**	3.46**	0.57**	0.68**	1.03**	392.07**
Error	118	5.71	89.99	9.54	5.71	24.03	0.01	4.94	647.10	21.19	0.02	0.004	0.003	0.003	52.36

DFF-days to fifty percent flowering, PH-plant height, NPT-number of tillers, NPT-number of productive tillers, FL-flag leaf length, FW-flag leaf width, PL-panicle length, NOG-number of grains per panicle, SF-spikelet fertility, KL-kernel length, KB-kernel breadth, LBR-length to breadth ratio, HSW-hundred seed weight and SPY-single plant yield. **- Significant @ 1 % level.

Table 3. Estimates of mean, coefficient of variation, heritability and genetic advance as percent of mean for the studied traits

Traits	Mean	Max	Min	PCV (%)	GCV (%)	RD	h ² (%)	GAM (%)
DFF	97.70±1.37	130.00	62.00	14.90	14.69	1.41	97.31	29.86
PH (cm)	119.52±5.47	187.73	65.63	19.07	17.34	9.07	82.68	32.49
NT	17.87±1.78	31.67	11.00	24.90	17.93	27.99	51.86	26.60
NPT	14.94±1.38	26.00	8.00	25.43	19.77	22.26	60.46	31.66
FL (cm)	35.06±2.83	63.27	19.27	28.41	24.73	12.95	75.78	44.34
FW(cm)	1.22±0.06	1.70	0.93	15.28	12.68	17.02	68.88	21.67
PL (cm)	25.13±1.28	31.60	15.97	14.72	11.76	20.11	63.89	19.36
NOG	139.22±14.69	258.67	60.00	37.23	32.44	12.87	75.92	58.23
SF (%)	89.87±2.66	97.44	75.10	6.82	4.50	34.02	43.55	6.12
KL (mm)	6.60±0.10	9.70	4.00	16.40	16.20	1.22	97.58	32.96
KB (mm)	2.44±0.04	3.40	1.60	17.97	17.77	1.11	97.77	36.20
LBR	2.75±0.03	3.95	1.67	17.47	17.33	0.80	98.44	35.44
HSW (g)	2.39±0.03	3.61	0.96	24.56	24.44	0.49	98.99	50.10
SPY (g)	32.05±4.17	63.60	11.80	40.16	33.21	17.31	68.38	56.57

DFF-days to fifty percent flowering, PH-plant height, NPT-number of tillers, NPT-number of productive tillers, FL-flag leaf length, FW-flag leaf width, PL-panicle length, NOG-number of grains per panicle, SF-spikelet fertility, KL-kernel length, KB-kernel breadth, LBR-length to breadth ratio, HSW-hundred seed weight and SPY-single plant yield.

Heritability is the proportion of total genetically determined variation in phenotypic traits within each group. Broad sense heritability of the studied traits was found to be high (> 60 %) except number of tillers and spikelet fertility which belonged to moderate category (30-60 %) (Johnson *et al.*, 1955) and ranged from 43.55 % (spikelet fertility) to 98.99 % (hundred seed weight) which depicted that degree of heritability is less affected by the environment and thus help in effective selection by adopting simple selection method (Gour *et al.*, 2017; Sumanth *et al.*, 2017 and Saha *et al.*, 2019)

Genetic advance as percent of mean ranged from 6.12 % (spikelet fertility) to 58.23 % (number of grains per panicle). It is intermediate for panicle length (19.36 %) whereas low for spikelet fertility. All other traits were found to have high genetic advance in concurrence with high heritability values. Superior GCV, together with high heritability and genetic advance, offer a better indicator of selection than specific genetic matrices or measurement units (Khan *et al.*, 2020). Selection based on number of grains per panicle, flag leaf length and hundred seed weight would be the best choice to improve the accessions as it is mainly governed by additive genes (Sumanth *et al.*, 2017; Saha *et al.*, 2019; Langat *et al.*, 2019). Spikelet fertility was majorly governed by non-additive genes as it had moderate heritability along with low genetic advance (Rafii *et al.*, 2014).

Crop research has extensively employed PCA to classify characteristics and grouping of accessions. It can be used to identify characteristics with a significant impact on

genotypic variation (Gour *et al.*, 2017). In present study, the first five principal components (PC) were shown eigen value of more than one which account for 74.41 % of cumulative variation. The main components with more than one eigenvalue showed increased variation among the rice genotypes studied which could be the ideal way to select the parents (Kasanaboina *et al.*, 2022). The first PC elucidated the utmost proportion of variance (26.69 %) followed by 15.71 % variation by second PC. The relationship of 60 accessions and fourteen phenological and morphological traits depicted by PCA are furnished in **Fig. 1** and **Fig. 2** which revealed that three traits namely, spikelet fertility, kernel length, length to breadth ratio and eight traits namely days to fifty percent flowering, plant height, flag leaf width, panicle length, number of grains, spikelet fertility, length to breadth ratio and single plant yield had a positive association with PC1 and PC2 respectively. Factor loading values revealed by PCA for the studied traits are depicted in **Table 4**. Traits such as spikelet fertility, kernel length and length to breadth ratio showed significance to the PC1 while traits flag leaf width, number of grains per panicle, spikelet fertility, length breadth ratio for PC2 and number of tillers, productive tillers for PC3 and days to fifty percent flowering, flag leaf width, number of grains for PC4 and number of tillers, productive tillers, kernel length, length to breadth ratio for PC5, showed significance to the respective PCs. Traits coming together in different principal components might be given top priority for selection in any breeding programmes as it has a tendency to remain together (Chakravorty *et al.*, 2013).

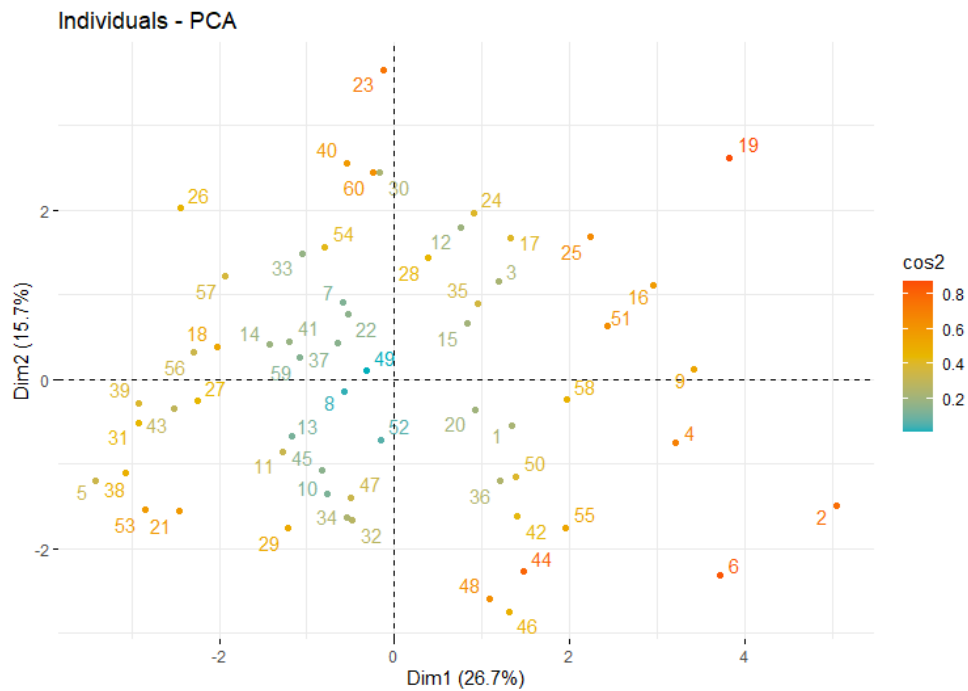


Fig 1. Clustering of genotypes based on principal components.
 Numbers indicating the corresponding genotypes listed in the Table 1.

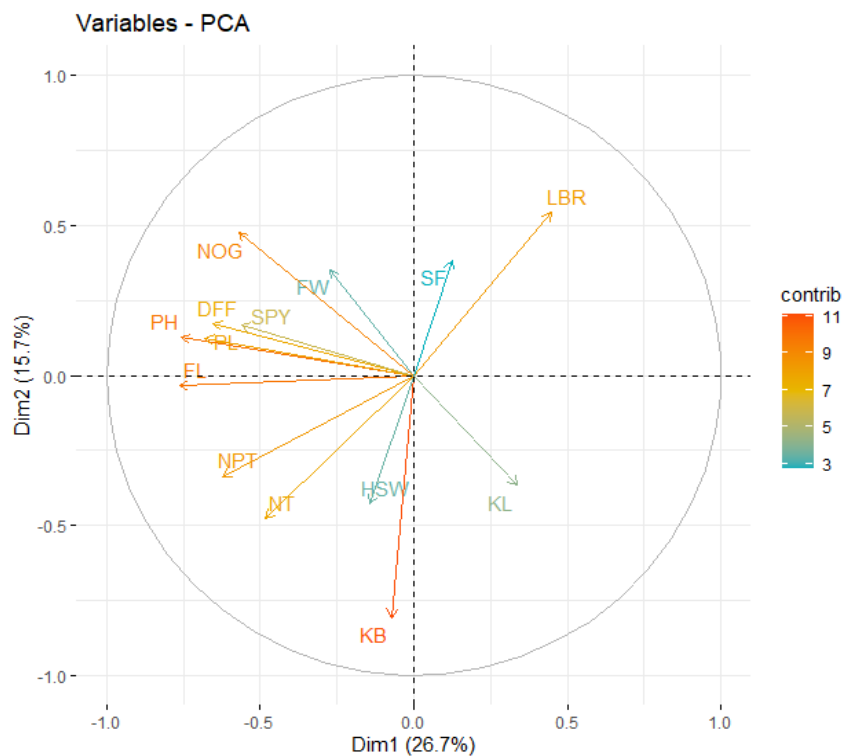


Fig 2. Clustering of variables towards principal components.

DFF-days to fifty percent flowering, PH-plant height, NPT-number of tillers, NPT-number of productive tillers, FL-flag leaf length, FW-flag leaf width, PL-panicle length, NOG-number of grains per panicle, SF-spikelet fertility, KL-kernel length, KB-kernel breadth, LBR-length to breadth ratio, HSW-hundred seed weight and SPY-single plant yield.

Table 4. Factor loadings of fourteen morphological traits to principal components

Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
EV	3.74	2.20	1.87	1.42	1.20	1.00	0.71	0.58	0.46	0.33	0.27	0.18	0.06	0.00
PV	26.69	15.71	13.34	10.11	8.55	7.13	5.07	4.17	3.27	2.33	1.89	1.26	0.44	0.02
CPV	26.69	42.41	55.75	65.85	74.41	81.54	86.60	90.78	94.04	96.38	98.27	99.53	99.98	100.00
DFF	-0.653	0.173	-0.212	0.362	-0.172	-0.334	-0.278	0.027	-0.177	0.138	-0.305	-0.075	-0.005	0.000
PH	-0.757	0.126	-0.295	-0.191	0.075	-0.032	0.019	-0.253	-0.172	-0.426	-0.029	0.066	-0.012	0.000
NT	-0.483	-0.478	0.517	0.123	0.447	-0.013	-0.131	0.089	0.026	-0.002	0.001	0.040	-0.169	-0.001
NPT	-0.623	-0.337	0.513	0.128	0.415	-0.046	-0.066	0.079	0.020	-0.027	-0.001	0.022	0.180	0.001
FL	-0.764	-0.034	-0.311	-0.336	-0.009	-0.086	0.198	-0.091	0.074	0.278	0.006	0.261	0.000	-0.001
FW	-0.273	0.352	-0.419	0.536	0.115	0.160	-0.329	-0.120	0.402	-0.028	0.115	0.035	0.001	-0.001
PL	-0.679	0.125	-0.190	-0.496	0.249	0.133	0.169	-0.008	0.218	0.064	-0.054	-0.278	-0.010	0.002
NOG	-0.571	0.476	0.035	0.396	0.081	0.194	0.187	-0.014	-0.344	0.130	0.264	-0.073	-0.011	0.001
SF	0.124	0.384	0.194	-0.419	0.113	0.615	-0.432	-0.058	-0.156	0.085	-0.091	0.057	0.009	-0.001
KL	0.337	-0.367	-0.606	0.249	0.418	0.288	0.176	0.089	-0.101	0.009	-0.120	0.012	0.010	-0.032
KB	-0.074	-0.809	-0.284	0.225	-0.152	0.390	0.050	-0.154	-0.052	0.032	-0.048	-0.025	0.005	0.036
LBR	0.448	0.544	-0.275	0.015	0.568	-0.146	0.102	0.245	-0.034	-0.027	-0.078	0.066	-0.005	0.032
HSW	-0.143	-0.430	-0.571	-0.337	-0.028	-0.176	-0.377	0.343	-0.120	-0.006	0.221	-0.032	0.009	0.001
SPY	-0.562	0.167	0.094	0.108	-0.417	0.360	0.160	0.519	0.098	-0.129	-0.077	0.060	-0.007	0.000

DFF-days to fifty percent flowering, PH-plant height, NPT-number of tillers, NPT-number of productive tillers, FL-flag leaf length, FW-flag leaf width, PL-panicle length, NOG-number of grains per panicle, SF-spikelet fertility, KL-kernel length, KB-kernel breadth, LBR-length to breadth ratio, HSW-hundred seed weight and SPY-single plant yield.

Correlation is a powerful tool and correlation coefficient is an essential measure of an index for the breeders to prefer the traits to be integrated into selection process. In the present study, significantly positive and intermediate association ($0.25 \leq r < 0.75$) was found between flag leaf length ($r = 0.3$, $p < 0.05$), panicle length ($r = 0.3$, $P < 0.05$), plant height ($r = 0.27$, $p < 0.05$), days to fifty percent flowering ($r = 0.32$, $p < 0.05$) and number of grains per panicle ($r = 0.43$, $p < 0.001$) with single plant yield (Fig. 3). Results revealed that late flowering landraces may have a higher probability of vegetative phase, which would increase the source-sink connection and enable for a higher proportion of grain numbers and yield (Manasa *et al.*, 2022). Therefore, direct selection for these characteristics can potentially boost the yield (Khan *et al.*, 2020). Similar findings were reported by Devi *et al.*, 2017; Gour *et al.*, 2017; Saha *et al.*, 2019. Negative and intermediate correlation was found between kernel length ($r = -0.28$, $p < 0.05$), length to breadth ratio ($r = -0.32$, $p < 0.05$) with single plant yield. Hence, indirect selection for these traits would improve single plant yield. Strong ($0.75 \leq r < 1.00$) and significant correlation ($r = 0.92$, $p < 0.001$) was noted between number of tillers and productive tillers. Number of grains per panicle had a positive and intermediate correlation with number of productive tillers ($r = 0.26$, $p < 0.05$), plant height ($r = 0.4$, $p < 0.01$), flag leaf length ($r = 0.29$, $p < 0.05$), panicle length ($r = 0.26$, $p < 0.05$) and days to fifty percent flowering

($r = 0.46$, $p < 0.001$) while negative and significant association with hundred seed weight ($r = -0.29$, $p < 0.05$). Days to fifty percent flowering was found to exhibit highly significant correlation with plant height ($r = 0.47$, $p < 0.001$) and flag leaf length ($r = 0.41$, $p < 0.01$) while panicle length had a highly significant positive association with flag leaf length ($r = 0.62$, $p < 0.001$) and plant height ($r = 0.72$, $p < 0.001$). Hundred seed weight detected significant ($p < 0.05$) and positive association with flag leaf length ($r = 0.31$), kernel length ($r = 0.26$), kernel breadth ($r = 0.3$), whereas negative association with number of grains per panicle ($r = -0.29$). These results indicated that panicle length, number of grains per panicle, flag leaf length were directly associated with single plant yield and while number of productive tillers had an indirect association with yield. This implied that traits panicle length, number of grains per panicle, flag leaf length and number of tillers might be important for determining yield. Similar findings were suggested in earlier studies in different varieties (Poudel *et al.*, 2020).

Cluster analysis based on D^2 values grouped 60 landraces into eight clusters. Clustering pattern revealed that Cluster I had 36 landrace, forming the largest cluster which might be due to their similar ecotype (Panda *et al.*, 2020), cluster II had 12 landrace, cluster III had four, cluster V had two landrace whereas clusters VI, VII and VIII had single landrace in each cluster (Table 5).

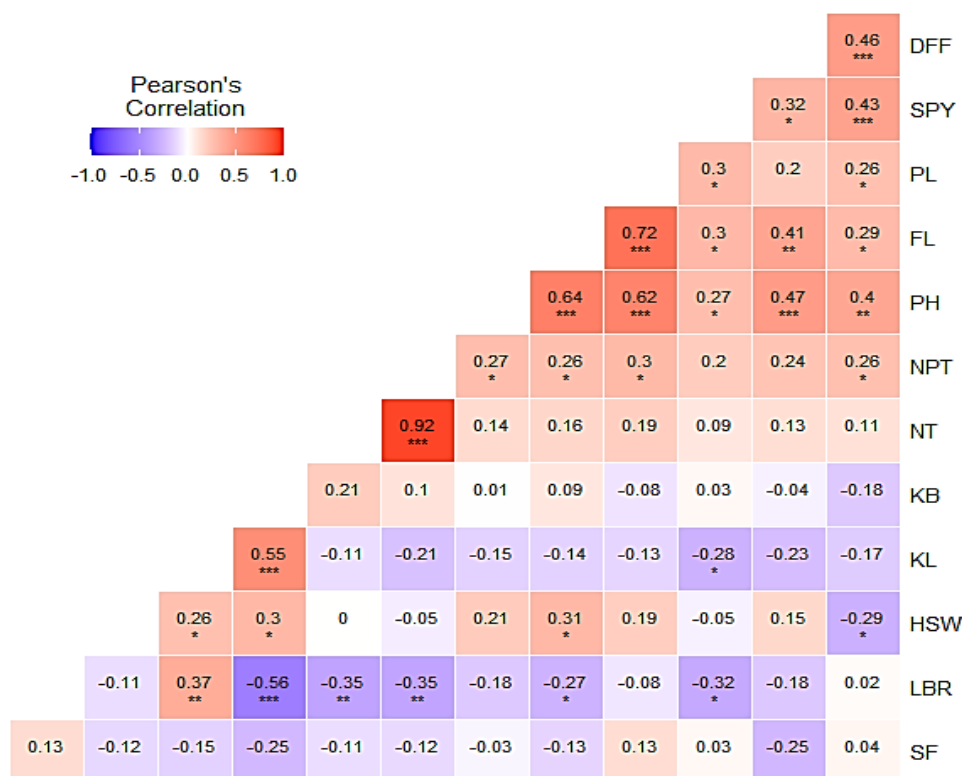


Fig. 3 Association analysis of fourteen morphological traits

DFF-days to fifty percent flowering, PH-plant height, NPT-number of tillers, NPT-number of productive tillers, FL-flag leaf length, FW-flag leaf width, PL-panicle length, NOG-number of grains per panicle, SF-spikelet fertility, KL-kernel length, KB-kernel breadth, LBR-length to breadth ratio, HSW-hundred seed weight and SPY-single plant yield.

Table 5. Clusters and its genotypes

Clusters	Genotypes
Cluster I	<i>Adukkam, Athur kichadi, Chenellu, Chinkini kar, Chithirai Kar, Chitti mutyalu, Edakkal, GEB-24, Illupai poo Samba, Iravai Pandi, Jai Sri Ram, Kuliadichan, Kaatu Ponni, Kaatu samba, Kaivara samba, Kalanamak, Kaliyan Samba, Kallundai, Kandhasali, Karunguruvai, Karuppu kavuni, Karuthakar, Kattai kar, Kattu vanibam, Kichali samba, Kichadi samba, Kullakkar, Kuthala samba, Mandamaranellu, Manjal ponni, Maranellu, Melaki, Milagu samba, Mohini Samba, Mullampunchan and Mutrina Samba</i>
Cluster II	<i>Chandai kar, Kottanel, Karuppu Nel, Kuruvai kalanjiyam, Kudavaraghai, Koduvaliyam, Karimbalan, Aarupatham kuruvai, Mattaikar, Kaan, Manvilayan and Kottara samba</i>
Cluster III	<i>Kattu yanam, Mappilai samba, Athur kichadi samba and Karudan samba</i>
Cluster IV	<i>Aanai komban, Chinna Punchai, Gedumani</i>
Cluster V	<i>Chinnar, Gandakasala</i>
Cluster VI	<i>Karnel</i>
Cluster VII	<i>Katta samba</i>
Cluster VIII	<i>Kothamalli samba</i>

Intra-cluster D^2 values ranged from 0 to 1224.16 (Table 6). The maximum intra-cluster distance was found within cluster V (1224.16) followed by cluster I (1019.80), cluster II (956.99), cluster IV (828.07) while cluster III showed a minimum intra-cluster distance (705.73). Clusters VI, VII and VIII had zero intra-cluster distance,

as they had only one landrace each. Cluster V's high intra-cluster distance indicated a high degree of genetic variation among the genotypes in the cluster. Hence, due to their higher diversity, the genotypes listed under cluster V could be employed as parents in a recombination breeding programmes (Sujata *et al.*, 2021).

Table 6. Inter and Intra cluster distance between each clusters based on D² values

Clusters	I	II	III	IV	V	VI	VII	VIII
I	1019.80							
II	3510.60	956.99						
III	8198.67	3315.43	705.73					
IV	2107.62	2750.66	8428.61	828.07				
V	3877.20	5016.90	12751.46	2458.79	1224.16			
VI	10271.84	4226.68	2525.09	8089.59	10444.75	0.00		
VII	2300.71	4973.12	13522.04	1785.47	2315.50	14660.61	0.00	
VIII	2852.32	4126.60	5019.10	6200.53	9822.92	10396.11	7040.28	0.00

Table 7 Cluster mean values for the studied traits

Clusters	DFP	PH	NT	NPT	FL	FW	PL	SPY	NOG	SF	KL	KB	LBR	HSW
I (36)	97.42	121.31	17.79	15.03	35.14	1.22	25.60	33.40	148.09	92.23	6.05	2.26	2.73	2.30
II (12)	94.42	110.71	18.06	14.69	31.34	1.18	23.06	27.83	107.19	85.57	7.54	2.97	2.54	2.63
III (4)	117.50	140.71	18.83	16.00	44.79	1.21	26.49	31.98	144.17	78.55	6.10	2.30	2.67	2.50
IV (4)	88.67	102.47	16.89	13.78	27.84	1.28	22.61	18.17	97.67	91.53	8.13	2.17	3.77	2.98
V (2)	96.00	125.20	18.33	15.67	45.75	1.25	28.45	33.23	214.83	93.20	8.85	3.10	2.86	2.28
VI (1)	109.00	121.10	14.00	12.67	33.67	1.50	25.17	43.97	234.33	77.52	8.00	2.10	3.81	1.60
VII (1)	86.00	117.30	17.00	11.67	29.83	1.17	28.37	33.43	65.67	96.45	8.00	3.10	2.58	2.44
VIII (1)	99.00	116.43	21.67	18.00	44.63	1.17	25.37	60.00	136.33	87.78	4.00	2.40	1.67	1.75

DFP-days to fifty percent flowering, PH-plant height, NT-number of tillers, NPT-number of productive tillers, FL-flag leaf length, FW-flag leaf width, PL-panicle length, NOG-number of grains per panicle, SF-spikelet fertility, KL-kernel length, KB-kernel breadth, LBR-length to breadth ratio, HSW-hundred seed weight and SPY-single plant yield.

Diversity between the clusters ranged from 1785.47 to 13522.04. Cluster III and cluster VII showed maximum inter-cluster distance (13522.04) followed by cluster III and cluster V (12751.46) which suggested that the genotypes in these clusters had a significant degree of genetic diversity and that crossings between the genotypes in these clusters would produce desirable transgressive segregants. Similar findings were reported by Sudeepthi *et al.*, 2020; Amegan *et al.*, 2020; Sujata *et al.*, 2021. Whereas the lowest inter-cluster distance was noticed between cluster IV and cluster VII (1785.47) followed by cluster I and cluster IV (2107.62), suggesting closeness among the genotypes in these clusters for most of the traits.

Cluster means of all the characters is presented in **Table 7**. Cluster III showed highest mean values for days to fifty percent flowering (117.50) and plant height (140.71). Highest mean for hundred seed weight (2.98) was exhibited by cluster IV. Cluster V showed highest mean values for flag leaf length (45.75), panicle length (28.45), spikelet fertility (93.20), kernel length (8.85) and kernel breadth (3.10) whereas solitary cluster VI having *Karnel* genotypes had highest mean values for flag leaf width (1.50), number of grains per panicle (234.33) and

length to breadth ratio (3.81). Cluster VIII, comprising of the genotype *Kothamalli samba* showed highest mean values for number of tillers (21.67), productive tillers (18.00) and single plant yield (60.00) suggesting that the genotype *Kothamalli samba* would be the good yielder whereas cluster IV comprised of poor yielding genotypes. Based on the cluster means, it was evident that cluster III possessed long duration genotypes having more number of tillers along with high grain number per panicle but low spikelet fertility percentage whereas clusters IV and VII were comprised of short duration genotypes with high spikelet fertility percentage. The results indicated the existence of high genetic diversity among genotypes in clusters III and VII; therefore, genotypes in these clusters could be used for specific trait improvement in plant breeding programmes. Similar results were explained by Muthuramu *et al.*, 2017; Sujata *et al.*, 2021.

Large numbers of agronomically important genes may be present in the native rice landraces and hence they are valued as potential source for varietal improvement programmes. Therefore, special attention should be taken on collection, conservation and utilization of the existing farmer varieties and landraces. Enormous genetic diversity present in rice and its utilization mainly

depends on the way of finding variation in a population. Major traits contributing towards maximum divergence has been identified with the help of multivariate analysis. Traits namely, number of grains per panicle, flag leaf length, kernel length, length to breadth ratio and hundred seed weight were the major determinants and contributing traits towards total diversity as explained by various multivariate analyses. Selection based on these traits would be ideal way to improve these traits in future programmes. Traditional varieties falling under cluster III and cluster VII could be utilized for the future breeding programmes to obtain higher heterotic expression in F_1 's as they were found to be more divergent. Hence the landraces *Aathurkichadi samba* for high number of tillers, *Kaatuyanam* for panicle length, *Katta samba* for high spikelet fertility, *Mappilai samba* for grain weight and *Karudan samba* for plant height could be utilized in hybridization to identify desirable recombinants for the targeted traits.

ACKNOWLEDGEMENT

The authors thank Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu Agricultural University, Tamil Nadu, India for conducting experiments. Author A. Shanmugam sincerely acknowledges the *Council of Scientific and Industrial Research (CSIR)*, New Delhi for CSIR-SRF (File No: 09/641(0174)/2019-EMR-I) fellowship support.

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