



RESEARCH ARTICLE

Scouting rice (*Oryza sativa* L.) landraces for moisture stress tolerance using morphometric diversity analysis

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Abstract

Climate-change is a major threat to sustainable agriculture. Rice is one of the staple food grains that sustain 2/3rd of global population. Therefore, developing climate-resilient rice genotypes to combat moisture stress and other climate change factors are most important to address the challenges posed by climate change. The vast availability of genetic variance among the rice genotypes for different traits favours the selection of desirable donor parents. A field investigation was carried out to characterize 21 traditional rice landraces under induced moisture stress in 2 environments including induced moisture stress (S) and non-stress (NS). The response to the varied level of environments was observed in terms of biometric and yield parameters followed by multivariate analysis and variability analysis. The study revealed higher phenotypic-coefficient of variation (PCV) and genotypic-coefficient of variation (GCV) for plant height and single plant yield in both environments. High heritability was also recorded in the moisture stressed environment for plant height (98.63 %), single plant yield (98.19 %) and productive tillers (95.12 %), whereas under NS, the heritability is more for single plant yield only (99.56 %). The genotypes formed nine clusters under the S environment, based on the Euclidean distance, of which the three CMS lines segregated in cluster III distinctly. The principal component analysis exhibited three principal components with a cumulative variance of 86.13 % and 86.40 % in the NS and S environments respectively. The traits such as days to 50 % flowering, panicle height, panicle length, grains per panicle, productive tillers, thousand-grain weight and single plant yield were the positive contributors. Spikelet fertility (%) and harvest index were positively correlated with seed yield per plant. Path-coefficient analysis was significant for grain yield, harvest index, spikelet fertility, pollen fertility and plant height and positively influenced by productive tillers plant⁻¹. The study concluded the prospect of using Mattaikar, Rajalakshmi, Mallikar and Kuli-yadichan as potential donors for developing upland rice with moisture stress resilience.

Keywords

Drought; diversity; rice landraces; variability; water- use efficiency

Introduction

More than 65 % of the global population depends on rice (*Oryza sativa* L.) as their primary staple food, providing 27 % of dietary energy and 20 % of die-

tary protein (1). Rice cultivation influences the livelihood and socio-economic well-being of several billion especially in developing countries. Hence, rice cultivation and traditions attached to it are an integral part of the world's cultural heritage as represented by the phrase, "Rice is Life". Rice is a unique crop grown under diverse ecological regions from irrigated to rainfed, lowland to upland and deep-water system. Rice productivity in rainfed ecosystem is being threatened by frequent episodes of drought stress due to unprecedented precipitation and occasional failure of monsoon. It has been estimated that 23 million hectares of rainfed rice in Asia are prone to drought, eventually affecting the irrigated low lands as well in India (2). So, there is an emerging challenge to accelerate the breeding of rice varieties for high yield potential coupled with better adaptation under drought stress is of great concern (3).

In general, drought tolerance is regarded as a complex trait governed by morphological, physiological, biochemical and molecular cascades. The agricultural heritage of India is endowed with a distinct germplasm of rice cultivars which is evident from *Sangam* literatures. The rich genetic pool could be a potential source for improving rice and its domestication across wide ecosystem. However, there is a wide knowledge gap about these valuable genetic resources, which has to be unravelled to understand the unique genes and genomes contributing for their adaptation under adverse environments. Rice landraces are known for their superior nutritional profile and sturdy nature to combat natural calamities like flood, drought, heat and salinity. Besides these facts, rice landraces received less attention owing to lower productivity and selective geographical locations. While crossing landraces and diverse clusters of rice accessions, this resulted in desirable recombinants in the subsequent segregating generations (4). Genetic diversity analysis like variability, principal component analysis (PCA), correlation and path analysis are used to explore the genetic resources for further hybridization. Recent reports on genetic variability studies such as genetic advancement, PCV, GCV and heritability showed higher variability in rice landraces concerning agronomic and phenotypic traits (5). Understanding the mechanisms and traits associated with the improved performance of rice landraces under water stress, would enable effective screening and selection of tolerant genotypes for further applications in rice improvement programs. With this background, the present study aimed to analyse the genetic variability for moisture stress tolerance and yield contributing traits in traditional rice landraces. Also, the heritability (h^2) and path coefficient were assessed for all the phenotypic traits to identify the desirable donor parents.

Materials and Methods

The present study was carried out at the Department of Plant Breeding and Genetics, AC and RI, Killikulam during Kharif 2020-21. Twenty-one local rice landraces along with checks were obtained from various agro-climatic zones, across Tamil Nadu (Table 1 and Fig. 1).

Table 1. List of genotypes used in the study.

Genotype	Type	Origin
TNAUCMS2A	A line	Tamil Nadu
TNAUCMS27A	A line	Tamil Nadu
TNAUCMS30A	A line	Tamil Nadu
Chandaikar	Landrace	Tamil Nadu
Mallikar	Landrace	Tamil Nadu
Mattaikar	Landrace	Tamil Nadu
Kuliyadichan	Landrace	Tamil Nadu
Rajalakshmi	Landrace	Tamil Nadu
Adukan	Landrace	Tamil Nadu
Anjali	Landrace	Tamil Nadu
Annada	Landrace	Tamil Nadu
Nootripattu	Landrace	Tamil Nadu
Kallurandaikar	Landrace	Tamil Nadu
Seeraga-samba	Landrace	Tamil Nadu
Virendra	Landrace	Tamil Nadu
Mulampunchan	Landrace	Tamil Nadu
CORH3	Cultivar	Tamil Nadu
CORH4	Cultivar	Tamil Nadu
IR64	Cultivar	Tamil Nadu
IR64(DRT)1	Cultivar	Andhra Pradesh
TKM13	Cultivar	Tamil Nadu

Experimental design

With 21 local landraces of rice (Fig. 1) including checks in RCBD (randomized complete block design), the experiment was replicated thrice, imposing a drought environment. The normal package of practices was followed except for the irrigation schedule. The water was withheld 21 days after transplanting (21 DAT) until maturity and only flash irrigation was given when plants exhibited wilting symptoms. Under control, regular irrigation was given without creating any stress.

Biometric parameters

Exactly 5 plants were randomly selected from each genotype and tagged for all the observations except for days to 50 % flowering (DFF). The other parameters such as plant height in cm (PH), tillers plant⁻¹ (NT), productive tillers plant⁻¹ (NPT), panicle length (PL), panicles plant⁻¹ (NPP), grains panicle⁻¹ (NGP), filled grains panicle⁻¹ (NGPP), spikelet fertility (SF), thousand grain weight (TGW) and single plant yield (SPY) were recorded (5).

Statistical analysis

The analysis of variance (ANOVA) and mean comparison were performed in INDOSTAT software. Diversity analysis was conducted in R studio (ver 4.2.2) using the package 'variability'. The genotypic and phenotypic coefficients of variation, heritability and the genetic advancement were calculated according to the previously given formulas (6, 7). Pearson's correlation coefficients were computed to evaluate the relationship among the observed variables. Genotypic correlations were partitioned into path-

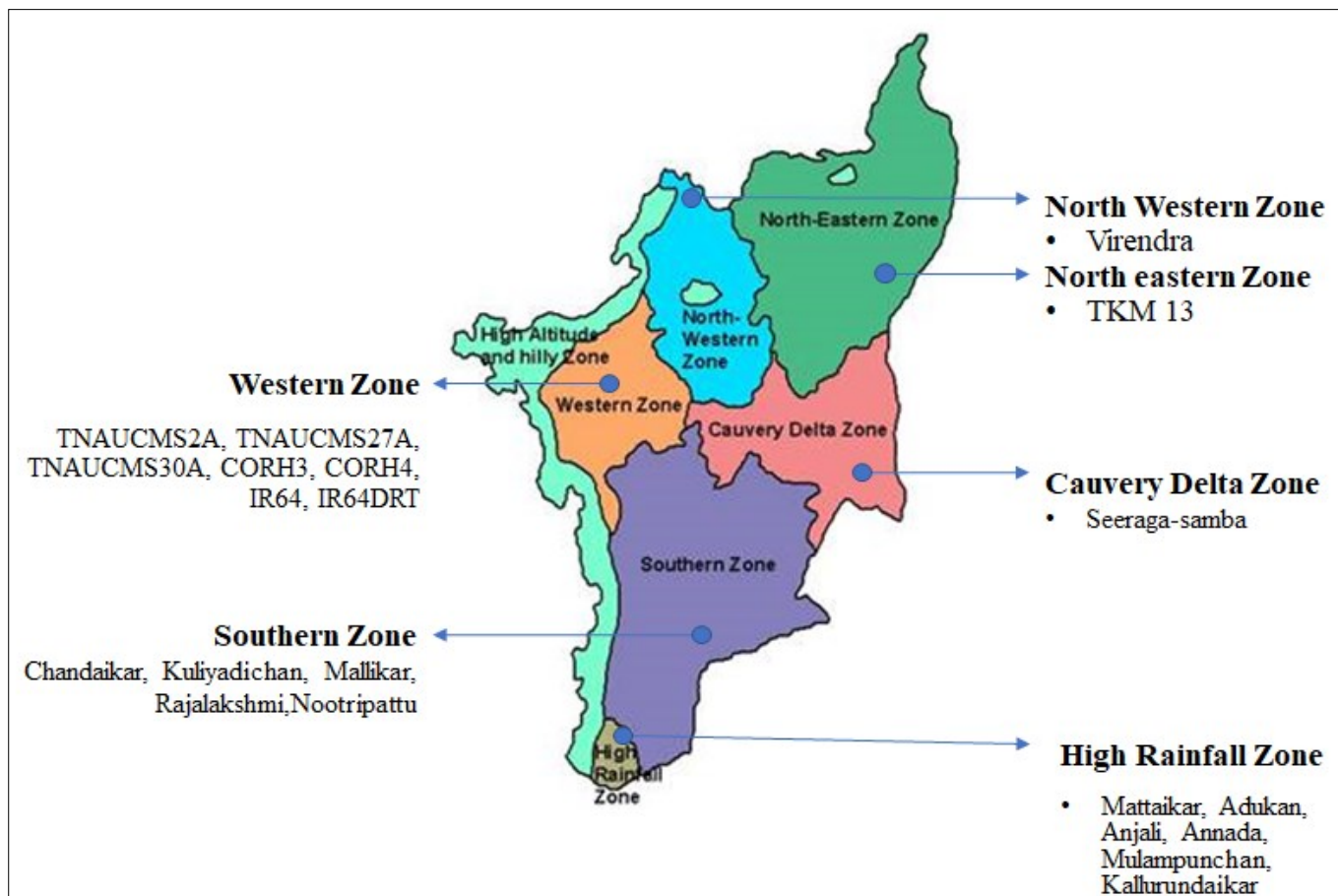


Fig. 1. Agro-climatic zones representing the collection of rice landraces.

coefficient using the technique of Dewey and his co-workers (8). Clustering was carried out by using Unweighted Pair Group with Arithmetic Mean (UPGMA) method. The correlation matrix was used to examine the percentage contribution of each trait to total genetic variation. Principal component analysis (PCA) was performed using R software.

Results

Variability components and their estimation

The genotypic (G) and environmental (E) components of phenotypic variance along with the coefficient of variation (CV) are used for the comparison among characters measured in different units (Table 1). The results showed a maximum variability level of 42.46 % and 42.36 % phenotypic and genotypic respectively under NS for plant height followed by single plant yield (PCV 41.99 % and GCV 41.89 %), number of tillers (PCV 40.53 % & GCV 38.61 %) and NPT (PCV 31.70 % and GCV 31.07 %). The minimum variability was recorded by the character panicle length (GCV 10.08 % and PCV 12.00 %). On the contrary, number of tillers exhibited maximum variability (PCV 41.45 % and GCV 38.10 %) levels under stressed environment (S) followed by single plant yield (GCV 39.60 % and PCV 39.91 %) and the number of productive tillers (GCV 34.50 % and PCV 35.37 %). The study highlighted that the environmental influence was maximum for grains panicle⁻¹, number of filled grains and spikelet fertility under NS, whereas S environment greatly influenced grains panicle⁻¹, plant height and number of tillers plant⁻¹.

Heritability (h^2) and genetic advance (GA)

The genotypes recorded high h^2 values for single plant yield (99.56 %) and plant height (99.54 %) in NS, whereas the traits PH (98.63 %) followed by SPY (98.19 %) and number of productive tillers (95.12 %) exhibited high h^2 under moisture stress (S). Genetic advance is an independent unit of measurement used for comparison among the traits under study (Table 2). The traits PH, SPY and NT showed maximum GA when raised in both NS and S environments. However, the moisture stress significantly influenced the number of productive tillers (69.30 %) when compared to the NS environment.

Cluster analysis

While clustering the 21 rice genotypes based on the Euclidean distance values under the NS environment, 4 major groups were observed at a dissimilarity coefficient value of 4.05 (Fig. 2a). Among the 21 genotypes, nine were grouped in Cluster IV (46.51 %), which is regarded as the dominant cluster. Cluster I had 6 genotypes, followed by Clusters II and III with 4 and 2 genotypes respectively. However, in the S environment (Fig. 2b), the genotypes were grouped into 9 clusters, which consisted of 46.51 % of all genotypes. Cluster III contained the 3 CMS lines and stayed separated. The genotypes Mattaikar, Rajalakshmi, Mallikar and Kuliyaichan were grouped into 2 distinct clusters such as Clusters I and II, with a cluster distance of 5.28 and 4.58 respectively.

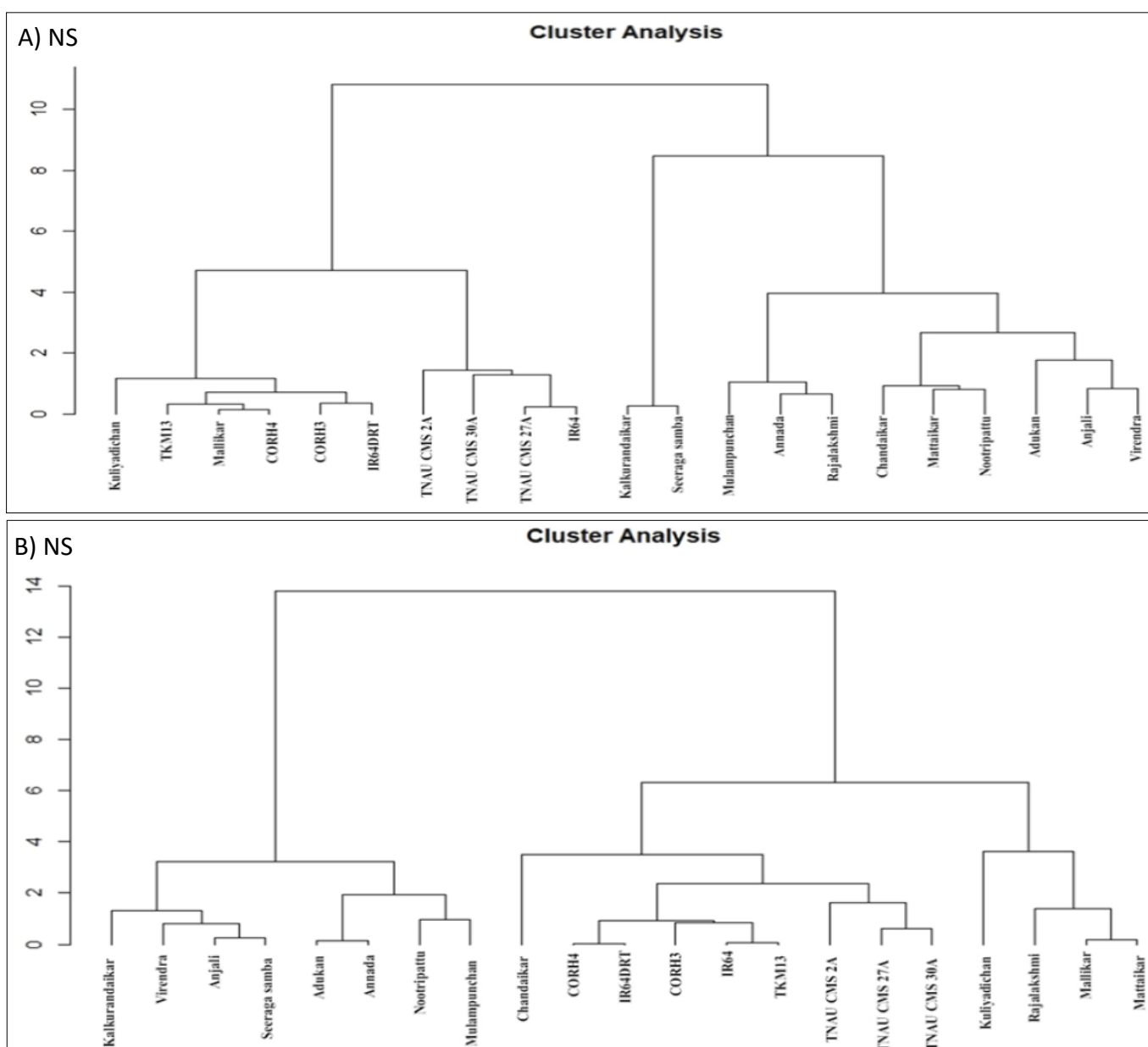
Principal component analysis

The variability for all the traits across the 2 environments,

Table 2. Components of genetic parameters for yield and yield attributing traits for non-stress and stress environments.

	GV		PV		GCV		PCV		ECV		HERT		GA (% of Mean)	
	NS	S	NS	S	NS	S	NS	S	NS	S	NS	S	NS	S
DFF (days)	91.07	67.05	101.12	73.83	9.28	11.80	9.74	12.46	2.95	3.93	90.81	90.06	18.23	23.11
PH (cm)	1003.32	3708.00	1017.20	3725	42.36	25.80	42.46	25.95	2.87	3.03	99.54	98.63	87.06	52.73
NT	62.97	106.80	74.43	117.70	38.61	38.10	40.54	41.45	12.34	16.27	90.73	84.60	75.77	72.23
NPT	42.48	55.44	44.66	57.75	31.07	34.50	31.71	35.37	6.35	7.81	95.99	95.12	62.70	69.31
PL (cm)	10.25	6.76	11.04	9.59	10.08	15.40	12.00	15.97	6.51	4.25	70.55	92.92	17.44	30.57
NPP	18.86	18.63	20.43	19.90	19.38	24.90	20.03	25.95	5.06	7.19	93.63	92.33	38.63	49.35
NGP	1489.30	1685.00	1562.60	1742	27.00	28.50	27.45	29.14	4.96	6.31	96.74	95.31	54.70	57.21
NFG	16.15	415.10	48.31	446.30	15.96	3.78	16.55	6.54	4.37	5.34	93.01	33.43	31.71	4.51
SF (%)	445.80	691.60	456.01	723.10	29.30	33.60	29.96	34.01	6.24	5.09	95.65	97.76	59.03	68.49
TGW (g)	29.60	27.15	30.28	27.53	19.40	24.20	19.54	24.43	2.31	3.67	98.60	97.75	39.69	49.20
SPY (g)	144.03	236.30	146.68	237.40	41.90	39.60	41.99	39.91	2.78	5.37	99.56	98.19	86.12	80.74

DFF- Days to fifty per cent flowering; **PH**- Plant height; **NT**- Number of tillers; **NPT**- Number of productive tillers; **PL**- Panicle length; **NPP**- Number of panicles per plant; **NGP**- Number of grains per panicle; **NFG**- Number of filled grains; **SF**- Spikelet fertility; **TGW**- Thousand grain weight; **SPY**- Single plant yield; **GV**- Genetic variance; **PV**- Phenotypic variance; **GCV**- Genotypic co-efficient of variation; **PCV**- Phenotypic co-efficient of variation; **ECV**- Environmental co-efficient of variation; **HERT**- Heritability.

**Fig. 2.** Cluster analysis of 21 rice genotypes-based yield attributing characters under **A)** non-stress and **B)** stress environment.

towards the population was computed using PCA. In the non-stress environment, the first 3 PCs accounting for 86.13 % of the total variation (eigenvalues >1), exhibited a highly significant correlation among the traits (Table 2). Among the 3 PCs, PC1, PC2 and PC3 explained about 38.96 %, 56.00 % and 86.13 % of the total variations respectively (Table 3). The traits namely, DFF (0.27), PH (0.31), PL (0.26), SF (0.23), TGW (0.36) and SPY (0.40) had positive contribution towards the overall variability and are represented by PC1. Similarly, DFF (0.1), NGP (0.49), TGW (0.01) and SPY (0.02) were the important contributing parameters of PC2.

Table 3. The eigenvalue, percentage of variation, cumulative percentage and eigenvector value for the first eleven principal components.

	PC1		PC2		PC3	
	NS	S	NS	S	NS	S
Eigen value	4.29	5.28	1.88	4.58	1.41	1.18
% Variance	38.96	49.96	17.04	14.88	12.77	10.75
Cumulative %	38.96	49.96	56.00	64.84	86.13	86.40
DFF	0.27	0.34	0.10	0.10	-0.52	-0.13
PH	0.31	0.36	-0.12	-0.10	-0.40	-0.15
NT	-0.37	-0.34	-0.33	0.30	-0.20	-0.04
NPT	-0.35	-0.26	-0.33	0.52	0.01	-0.06
PL	0.26	0.35	-0.37	0.33	-0.27	0.17
NP.P	-0.25	-0.13	-0.29	0.52	-0.08	-0.16
NGP	-0.21	0.02	0.49	0.00	-0.41	-0.87
NFG	-0.23	0.17	-0.05	0.45	-0.51	0.17
SF	0.23	-0.37	-0.55	-0.14	0.02	0.10
TGW	0.36	0.34	0.01	0.09	-0.05	0.27
SPY	0.40	0.39	0.03	0.10	0.14	-0.20

However, the PCA analysis corresponding to the stressed environment exhibited 3 reliable PCs that accounted for 86.40 % of the total variation for studied variables. Like NS, here also the 3 PCs showed a very high correlation among the traits. PC1, PC2 and PC3 contributed 49.96 %, 64.84 % and 86.40 % of the total variation respectively (Table 3). The contributing traits for the population in PC1 were DFF (0.34), PH (0.36), PL (0.35), NGP (0.02), NFG (0.17), TGW (0.34) and SPY (0.39). Likewise, for PC2, the traits namely DFF (0.10), NT (0.30), NPT (0.52), PL (0.33), NP/P (0.52), NFG (0.45), TGW (0.09) and SPY (0.10) exerted positive contribution to the overall variability in the population. The results showed that the PCAs differentiated the genotypes based on traits and exhibited substantial variability among the 21 rice genotypes in 3 clusters.

Considering the interaction among the traits in the PCA biplot, the traits namely SPY and TGW were plotted in positive PC1 and PC2 quadrants (Fig. 3). For PC1, the contributed variables in both the environments were NPT, PH, spikelet fertility, TGW, DFF and number of panicles plant⁻¹. In PC2, NPT, SPY, TGW and number of filled grains contributed positively towards the variability whereas PH and number of panicles plant⁻¹ exerted negative contribution. Therefore, the traits studied can be considered as valid selection indices for screening drought tolerant genotypes.

Correlation-coefficients between SPY and yield contributing characters, for both non-stressed and stressed environment

The genotypic correlation coefficients between SPY and other yield contributing traits, for both NS and S environment were assessed (Fig. 4a and 4b). SPY was found to be

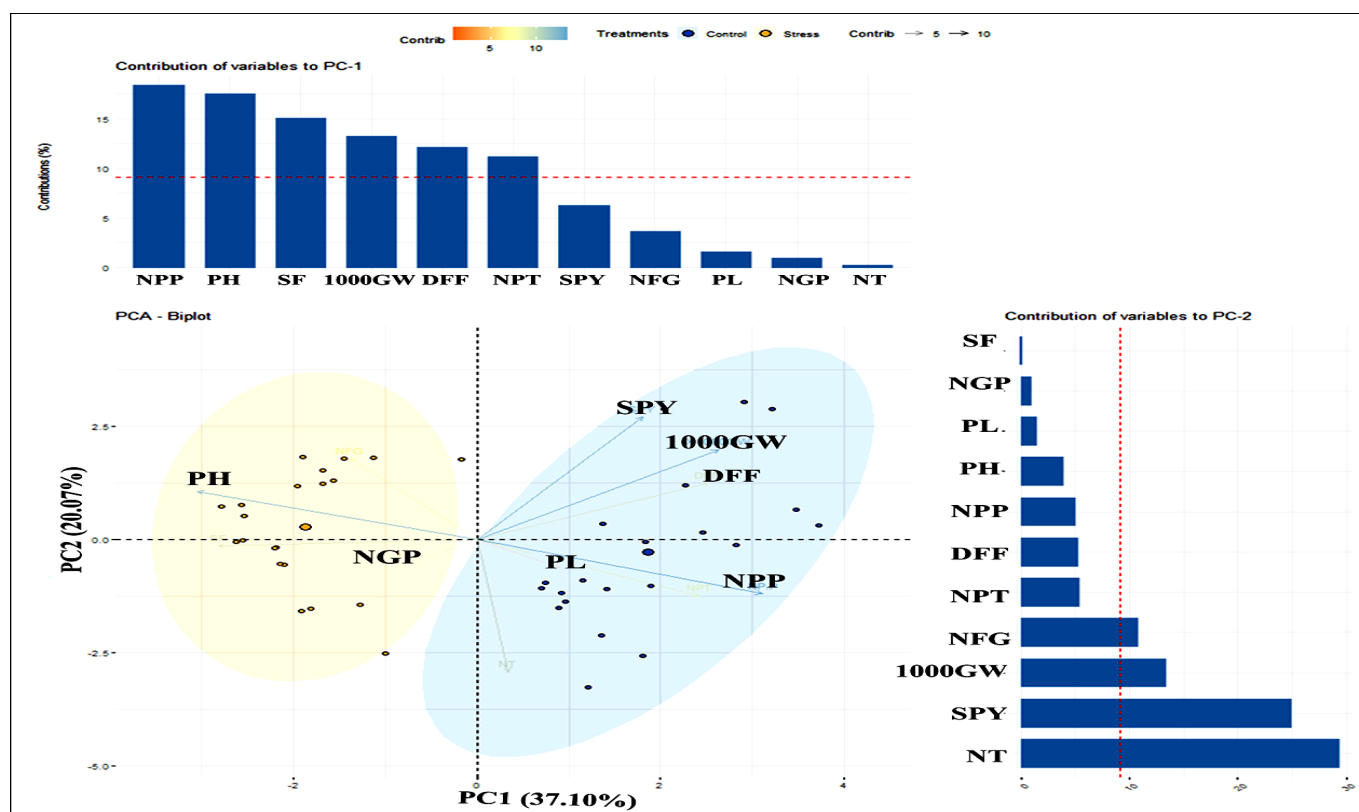


Fig. 3. PCA biplot of 21 rice genotypes-based yield attributing characters under non-stressed (NS) and stress (NS) environments.

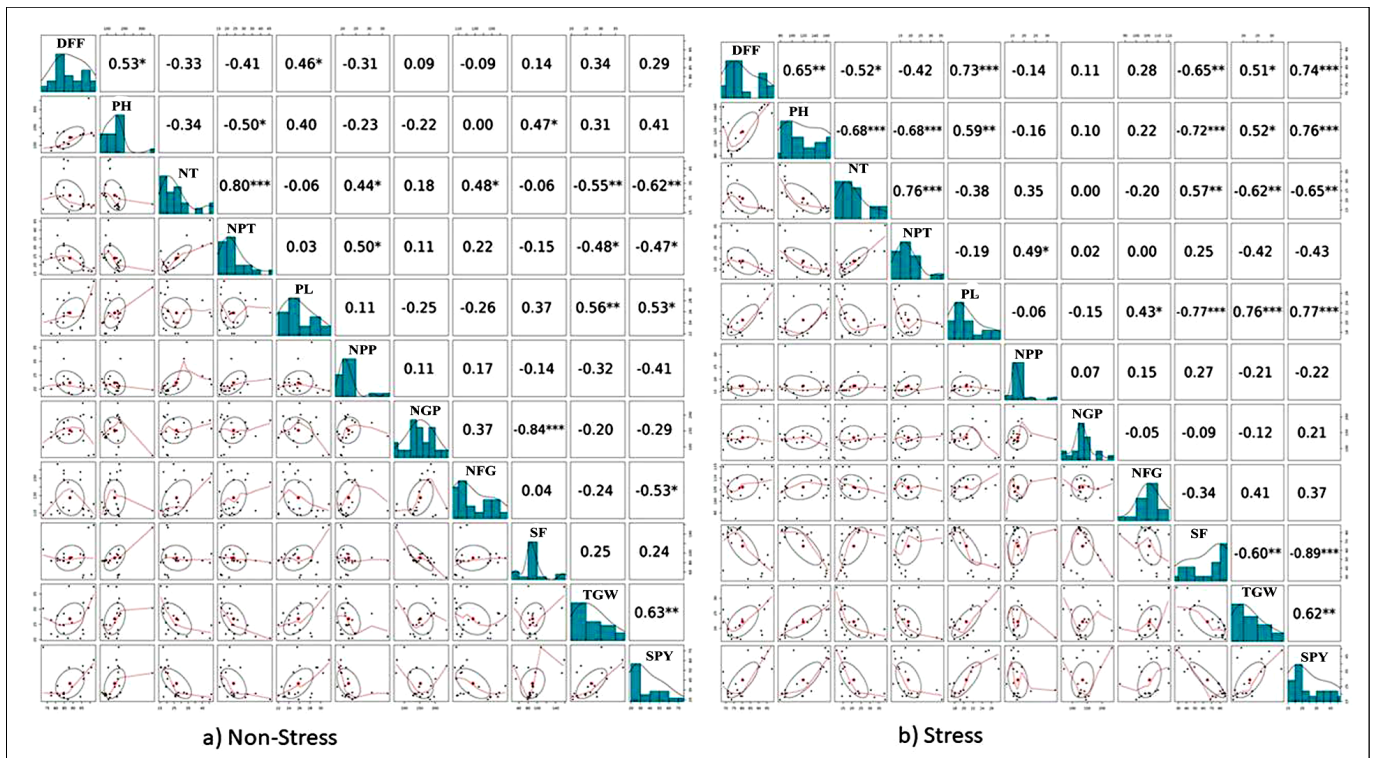


Fig. 4. Correlogram of 21 rice genotypes-based yield attributing characters under non-stressed and stress environments.

highly significant and positively correlated with thousand grain weight (0.632) followed by panicle length (0.565). PH (0.405) was positively correlated with SPY under NS. Correlation co-efficient values of the traits namely NT (-0.629), number of filled grains (-0.532) and NPT (-0.473) were negatively significant with SPY. DFF and PH were positively correlated with each other followed by PL and NPT whereas PH was correlated with panicle length and spikelet fertility. Panicle length is positively correlated with spikelet fertility and highly significant with thousand grain weight.

The moisture stressed environment revealed that, the SPY had highly significant and positive correlation with panicle length (0.765), DFF (0.759), plant height (0.745), thousand-grain weight (0.605) and number of filled grains panicle⁻¹ (0.552). The trait spikelet fertility (-0.888) and number of tillers (-0.694) had significant correlation in neg-

ative direction (Fig. 3b). DFF significantly correlated with PH, PL and TGW positively. Number of tillers and spikelet fertility was highly significant but negatively correlated. PH had significant positive correlation with PL and TGW however, negatively correlated with number of tillers, NPT tillers and SF. PL is significant and had positive correlation with NFG and TGW and negatively correlated with SF. Number of filled grains and TGW were positively correlated and was highly significant.

Path-coefficient analysis for both non-stress and stress environment

The genotypic correlation coefficient of single plant yield with other traits was further partitioned into direct and indirect effects. The results are presented in Fig. 5a and 5b.

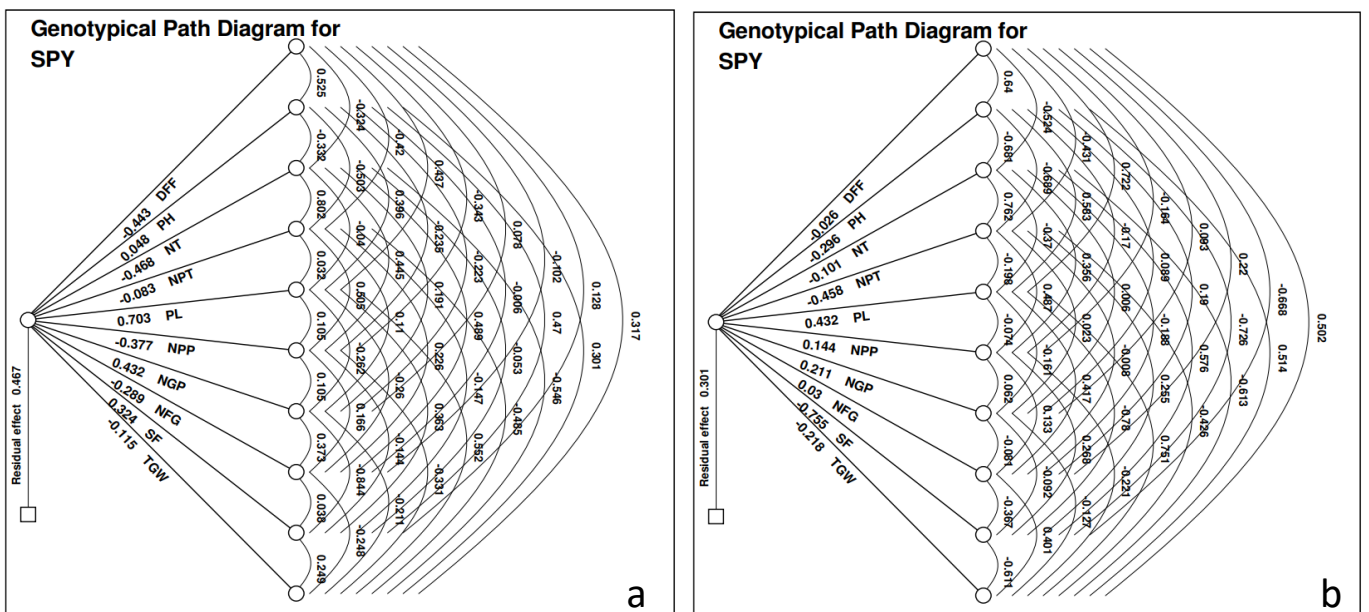


Fig. 5. Genotypical path coefficient for a) non-stressed and b) stress environments.

Direct and indirect effects of yield components on seed yield plant⁻¹

Path co-efficient analysis showed that under NS environment the residual effect was 0.2034. Among the traits studied, the panicle length (1.96) recorded very high positive effect with SPY, followed by NFG (0.44). Thousand grain weight (-0.960) and DFF (-0.8435) recorded very high negative direct effect. Under S environment, the residual effect of path analysis is 0.2313. Very high positive direct effect was recorded by PL (2.26) and number of grains panicle⁻¹ (0.580). Number of panicles plant⁻¹ (0.258) and number of filled grains (0.28) showed moderate positive direct effect. Single plant yield had high negative direct effects with all other characters under study.

Under the NS environment (Fig. 5a), DFF recorded high positive indirect effect with panicle length (0.945) and moderate effect indirectly mediated by NT (0.285), NPT (0.232) and other characters showed negligible negative indirect effect. PH recorded high positive indirect effect with PL (0.837), NPT (0.306) and moderate positive indirect effect with tillers count (0.278). Plant height exerted low, high and moderate indirect positive effect with number of panicles plant⁻¹ (0.166), DFF (-0.447), thousand-grain weight (-0.293) and spikelet fertility (-0.209) respectively. The results also showed that the NPT per plant imparted positive indirect effect as determined by thousand grain weight (0.463) and DFF (0.358). However, number of tillers (-0.658) and NPT (-0.605) possessed indirect effect. The PL recorded negligible positive indirect effect with number of tillers plant⁻¹ (0.054), number of grains panicle⁻¹ (0.048) and all other characters had negative indirect effect. The number of grains panicle⁻¹ recorded highly positive indirect effect via spikelet fertility (0.368) and high negative indirect effect via panicle length (-0.542) under NS. The number of filled grains panicle⁻¹ recorded moderate positive indirect effect via thousand grain weight (0.232) and high negative indirect effect via panicle length (-0.552) and number of tillers (-0.399). The spikelet fertility recorded high positive indirect effect via panicle length (0.777) and negative moderate and low indirect effect were recorded via thousand grain weight (-0.248), plant height (-0.130) and DFF (-0.128) respectively under NS. TGW registered highly positive indirect effect via panicle length (1.163), number of tillers (0.547) and high negative with thousand grain weight (-0.960) under NS environment.

Likewise, under stressed environment, DFF recorded high indirect effect with panicle length (1.72), tillers count (0.527) and NPT (0.518), high negative indirect effect with TGW (-0.740), PH (-0.658) and negligible negative indirect effect with number of panicles plant⁻¹ (-0.003) (Fig. 5b). PH had highly positive indirect effect via panicle length (1.276), NPT (0.836), tillers count (0.665) and SF (0.311). PH had high negative indirect effect via TGW (-0.731) and DFF (-0.683). NPT plant⁻¹ recorded high positive indirect effect via PH (0.729) followed by TGW (0.627) and DFF (0.469), whereas it exhibited high negative indirect effect through number of productive tillers (-1.155) and number of tillers (-0.703) for S environment. The panicle length registered high positive indirect effect via tillers count (0.366), and

spikelet fertility (0.346). High negative indirect effect was recorded via thousand grain weight (-1.125), DFF (-7.95) and plant height (-569). The number of grains panicle⁻¹ had moderate positive indirect effect with thousand grain weight (0.212) and high negative indirect effect with panicle length (-0.418). All other characters showed negligible positive and negative indirect effect for number of grains panicle⁻¹. On the other hand, the spikelet fertility exerted high positive indirect effect via thousand grain weight (0.881), plant height (0.698), and DFF (0.687) and high negative indirect effect via panicle length (-1.739), number of tillers (-0.565), spikelet fertility (-0.450) under stress condition. TGW showed high positive indirect effect through panicle length (1.729), number of tillers (0.585), number of productive tillers (0.493) and significant negative indirect effect with thousand grain weight (-1.471).

Discussion

Quantitative traits of the plant population and their genetic analysis are a pre-requisite for selecting desirable genotypes for breeding for specific traits. The current study suggests the existence of maximum variability both PCV and GCV for all traits in non-stressed and induced moisture stressed environments. The effect of environment on plant trait is indicated by the degree of its genotypic and phenotypic coefficients of variation (9). Genetic variability and diversity studies for drought tolerance traits are scarce for upland and lowland rice. The present study envisaged 21 rice genotypes raised across 2 environments such as NS and S and the variation of yield contributing and drought tolerance traits were assessed. Variability studies depicted considerable differences between PCV and GCV for almost all the traits explored. The results suggest the environmental influence on the genotypic expression of traits studied and the selection would be viable for future crossing programme. The variables SPY and PH exhibited high heritability (h^2) of 100 % indicating the presence of additive gene action. Thus, the selection based on these traits with exploitable amount of variation would be more effective for segregating generations in future breeding programmes. Similar variations in SPY and PH under stressed and non-stressed environments were observed by previous researchers (10, 11). They indicated that these parameters decreased with an increase in the degree of moisture stress. The traits SPY, NT and PH showed very high heritability cum genetic advance. This suggests that these traits were mainly under genetic control and their phenotypic performance could be scored. High heritability values > 60 % with more GA (genetic advance) were observed in 19 upland rice accessions for leaf chlorophyll content, productive tillers plant⁻¹, panicle weight, grains panicle⁻¹ and thousand grain weight (12). Hence, this population could be exploited in future with other rice landraces for effective selection and improvement.

The 21 rice genotypes grouped into four distinct clusters represented a similar dendrogram topology and cluster members, to those computed using PCA analysis. This confirmed the accuracy of the constructed dendro-

gram in the present study. The results are in agreement with the previously reported similar pattern of clustering for 24 genotypes (13). Further the estimated Euclidian distance showed that the clusters predominantly comprised of drought tolerant genotypes, however, the less frequent drought tolerant genotypes were present in the same cluster. The results of our study are in agreement with the recent findings (4) grouping 14 genotypes into 6 clusters based on panicle and yield related traits. The significant variations among the 21 rice genotypes were further confirmed by PCA. The first 3 reliable PCs accounted for 68.76 % and 75.58 % of the total variation in both NS and S environments respectively. The results affirmed a very strong correlation among the selected traits for drought tolerance studied. PC1, which solely contributed to the variation for NS (38.9 %) and S (49.9 %) environments, was found to be the most significant one. Accordingly, the traits DFF, PH, PL, SF, TGW and SPY were important in differentiating the genotypes due to their high loadings in PC1. Likewise, another study explained 61.2 % of the total variability from PC1 and PC2 (13, 14). In another study, 32 upland rice varieties exhibited 82.7 % of the total variation.

Genetic diversity is a key to the selection of desirable parents for further breeding programme (15). The present study also highlighted that the genotypes with drought tolerance created a broader genetic variation for yield and other yield contributing traits. The computed PCA results exhibited clear distinction among the traits measured among 21 rice cultivars in the three clusters. From the PCA biplot, SPY and TGW were placed in positive PC1 and PC2 quadrant, whereas the PC for PH and number of panicles plant⁻¹ contributed in a negative manner. Further, from the PCA biplot, it was observed that the yield attributes such as SPY, TGW, PH and NP/P were significant contributors to both PCs. Hence these traits namely SPY, TGW, PH, NPT were found to be vary among the 21 rice genotypes analyzed. Therefore, selection of these traits will be effective in rice for breeding towards moisture stress tolerance. Thus, Mattaikar, Rajalakshmi, Mallikar and Kuliyaichan could be identified as desirable genotypes for breeding towards abiotic stress. Similar contribution of these traits through PCs towards genetic variability was also reported (16).

Similarly, significant variation was observed among the 21 rice genotypes for grain yield, and yield associated traits with differential response to induced moisture stress at reproductive stage. The direct positive correlation of grain yield plant⁻¹ with thousand grain weight, PL and number of productive tillers under irrigated condition agrees with earlier reports (17-19). It was observed that TGW, number of tillers and number of panicles plant⁻¹ had high positive direct effect on grain yield plant⁻¹ in both irrigated (NS) as well as stressed environment. The results indicate that these traits were related with grain yield and direct selection for these traits will be rewarding. Besides, indirect positive correlation of grain yield plant⁻¹ with thousand grain weight, PH, tillers count, number of productive tillers plant⁻¹, number of panicles plant⁻¹ and num-

ber of filled grains panicle⁻¹ on both NS and S environment were also observed. The correlation studies suggest that these traits could be used as selection indices for yield improvement in rice under moisture stress condition. Similar results were reported by previous workers (17, 20-22). More recently, a study reported that in rice genotypes with Asian and African backgrounds, the correlation between the yield, number of panicles per plant and filled grains per panicle are significant and positively correlated (23). In rest of the traits, it was observed that the correlation was through component characters due to indirect effects. Hence, indirect selection of these traits will lead to moisture stress tolerant rice with improved yield attributes. Accordingly, genotypes Mattaikar, Rajalakshmi, Mallikar and Kuliyaichan could be selected as potential donors for developing drought tolerant rice cultivars to mitigate climate change.

Conclusion

Moisture stress is one of the abiotic stresses influencing rice productivity especially under rainfed conditions and uplands. Present investigation on 21 traditional rice genotypes across two environments (stressed and non-stressed) showed highest heritability for the traits SPY, PH, TGW and number of grains plant⁻¹. The traits identified could be successfully employed in rice hybridisation programme due to additive gene action. PH and SPY with high genetic advance imply that these traits could be used to select genotypes for uplands especially for water deficit regions. Growth and yield contributing attributes such as TGW, tillers count and number of panicles plant⁻¹ were positively correlated with grain yield per plant⁻¹ in direct and indirect means both in the irrigated and moisture stressed environments. The potential for moisture stress tolerance through indirect selection using the associated traits may be useful for developing moisture stress resilient rice cultivars. However, the traits having high positive direct effect on grain yield plant⁻¹ such as thousand grain weight, number of tillers and number of panicles plant⁻¹ in both irrigated as well as stressed environments would be highly rewarding for yield improvement cum moisture stress tolerance. Therefore, the selected rice genotypes Mattaikar, Rajalakshmi, Mallikar and Kuliyaichan may serve as potential donors for developing climate resilient rice varieties with high water use efficiency and suitable for upland cultivation.

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Authors' contributions

All the authors made substantial contributions to the successful completion of the project. AKB as principal investigator of project conceived the idea, designed the experiments and overall supervision of the work; KPK-execution of experiments and data acquisition; ST, RS-data analysis and interpretation; NF- drafting and revising the manuscript; AS, NKR- final proof reading.

Compliance with ethical standards

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

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