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Genetic Diversity Studies in Drought Tolerant Rice (*Oryza sativa* L.) Genotypes

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ABSTRACT

Background: Assessing the genetic diversity and relationship among breeding materials isan invaluable aid for any crop improvement programme. Principal component analysis (PCA) is a multivariate statistical technique attempt to simplify and analyze the inter relationship among a large set of variables in term of a relatively a small set of variables or components without losing any essential information of original data set.

Methods: The present investigation was carried out to study the genetic diversity and relationship among the sixty five rice genotypes including popular rice varieties of Tamil Nadu, drought tolerant rice varieties, aerobic rice genotypes and land races. These genotypes were raised at Rice Research Station, Tiruvallur, during *kharif,* 2015 in randomized block design with three replications under aerobic condition. Data on eight yield and yield attributing traits were recorded and subjected to principal component analysis and association analysis.

Result: In principal component analysis, PC1accounted for 22.91% and PC2 accounted for 19.53% of the total variation. The traits panicle length, no. of grains per panicle, plant height, days to 50% flowering, no of productive tillers per plant from the first two principal components accounted for major contribution to the total variability. Cluster analysis grouped the genotypes into six discrete clusters. The association analysis revealed that the traits *viz*., no. of productive tillers/plant, panicle length and hundred seed weight had positive association with higher direct effect on plot yield which could be used as selection criteria for developing high yielding rice varieties. The results of the present study have revealed the high level of genetic variation existing in the genotypes studied and explains the traits contributing for this diversity.

Key words: Aerobic condition, Association, Genetic divergence, Rice, Variation.

INTRODUCTION

Rice (*Oryza sativa L.*) is the staple food crop for more than half of the global populations. Irrigated low land is the most important ecosystem for rice in Asia which requires substantially more water (*i.e.* about 5000 liters of water/kg of rice grain). Declining water availability and increasing water scarcity has threatened the sustainability of this system all over the world including India. Aerobic system of rice cultivation is gaining momentum in recent times. The lack of varieties with stable yield under aerobic system is a major limitation in achieving the maximum yield potential under water limited conditions (Sandhu *et al*., 2019).To combat this situation, it is essential to focus the research priority towards the development of water efficient ‘aerobic rice’ varieties.

Estimation of genetic divergence is very much essential for the selection of parental lines for hybridization programme. Identifying the diverse parental combinations for creating the segregating progenies with maximum genetic variability for further selection and introgressing the desirable genes from the diverse germplasm into the available genetic base is the prerequisite for the any breeding programme.

Considering the importance of developing aerobic rice varieties, the present investigation was undertaken i) to assess the genetic diversity for identifying genetically diverse parental lines and ii) to find out the nature of the relationship among the yield and yield contributing traits by Association analysis.

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MATERIALS AND METHODS

The present experiment was conducted with 65 rice genotypes including popular rice varieties of Tamil Nadu, drought tolerant rice varieties, aerobic rice genotypes and land races at Rice Research Station, Tirur, Tiruvallur during *kharif*, 2015. The genotypes were raised in randomized block design with three replications in 3 m row length (15 rows) with the spacing of 20 x 10 cm under aerobic condition and irrigated at weekly intervals. Observations were recorded on five randomly selected plants per replication for the characters *viz*., plant height, no. of productive tillers/plant, panicle length, no. of grains/panicle, Hundred seed weight and panicle harvest index whereas, the characters like plot yield and days to 50% flowering were recorded on plot basis. Then the data were subjected to statistical analysis by following Singh and Chaudhary (1995) for correlation coefficient and Dewey and Lu (1959) for path analysis. Selection based on the detailed Principal Component Analysis was worked out through correlation matrix using PAST 3. Dissimilarity between the genotypes was calculated based on Euclidean distance and the genetic divergence was computed using Wards D minimum method of clustering through R 3.5.1 statistical package.

RESULTS AND DISCUSSION

Principal Component Analysis (PCA)

Principal component analysis reflects the importance of larger contributor to the total variation at each axis of differentiation (Sharma, 1998). Eigen values are used to determine the number of major principal components to be retained (Hailegiorgis *et al.*, 2010).

In the present study, it revealed that first five principal components in the PCA contributed to a maximum of 78.67% of the total phenotypic diversity among the 65 rice genotypes (Table 1).The first three principal components have eigen values more than one which showed cumulative variation of 56.86% of the total variation (Fig 1). Girma *et al.* (2018), Shalini Singh *et al*. (2021), Mohan *et al*. (2021) and Yugandhar *et al*., (2018) reported 64%, 86.7%, 79.12% and 71.4% of total variation explained by first three, four, five and six principal components respectively in various studies. Shivangi *et al*., 2021 reported that first eight principal components exhibited eigen value more than 1.0 and 81.84 per cent variability among the 28 traits studied in 67 rice germplasm lines. The predominant characters coming together in a particular principal component by contributing towards variability offer opportunity for its utilization in crop breeding. To assess the contribution of characters which influenced greater the PCA value, it is customary to look for individual loadings. Scree plot graph (Fig 1) obtained by plotting eigen values and principal component numbers explained the percentage of variation associated with each principal components. PC1 showed 22.91% variability with Eigen value 1.83, which then declined gradually.

The contribution of each component to total variation is presented in Table 1. The first principal component (PC1) with an eigen value of 1.83 explained 22.91% of the total variation. PC1 was associated mainly with panicle length (0.561), no. of grains per panicle (0.507), plant height (0.341), plot yield (0.327) and days to 50% flowering (0.321). In PC1, major contribution was from the yield attributing traits *viz*., panicle length and no. of grains per panicle. The second principal component (PC2) accounted for 19.53% of the total variation and was mainly related to productive tillers/plant (0.593), single plant yield (0.504) and panicle harvest index (0.378). PC3 accounted for 14.42% of the total variation and was characterized by panicle harvest index (0.574) and days to 50% flowering (0.450). The traits panicle length, no. of grains per panicle, plant height, days to 50% flowering and no of productive tillers per plant from the first two principal accounted for major contribution to the total variability.

Cluster analysis

Cluster analysis was used to determine the genetic relationship among the genotypes and find out the suitable genotypes for future breeding programme. Cluster analysis based on eight quantitative traits for 65 genotypes grouped them into six discrete and well defined clusters. Cluster III was the largest consisting of 19 genotypes (Table 2 and Fig 2) followed by the clusters I with 17 genotypes and the cluster II with 16 genotypes whereas, the smallest was cluster VI with three genotypes.

Presence of variability in the 65 genotypes was also reflected in the cluster means for the eight traits evaluated (Table 3). Cluster I comprised of seventeen genotypes

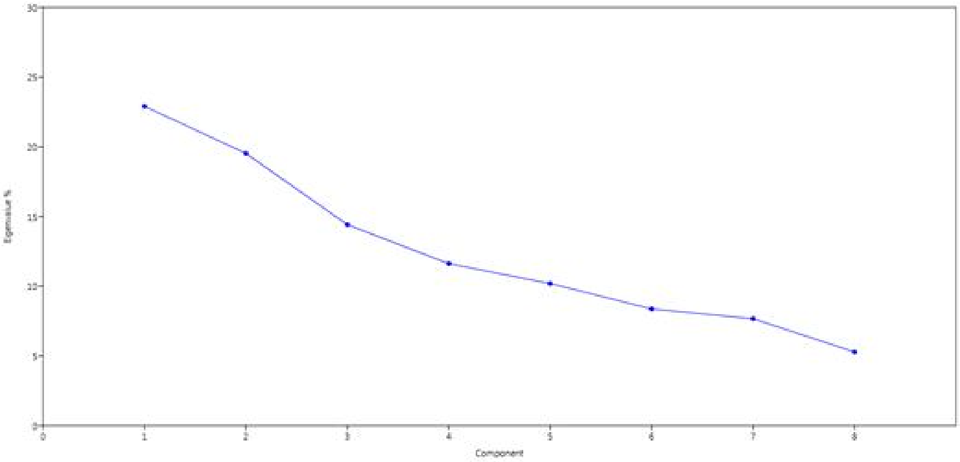

Fig 1: Scree plot showing eigen value variation for eight quantitative traits in rice.

characterized by genotypes with maximum plant height (117.7 cm), longer panicle length (26.46 cm) with more number of grains per panicle (118.38). Cluster II comprised of sixteen genotypes with semi dwarf plant types (100.7 cm) and higher panicle harvest Index (94%). Cluster III comprised of 19 genotypes predominantly early maturing, having short panicles (22.75 cm) with lesser number of grains per panicle (104). Cluster IV comprised of four genotypes which were characterized by late in attaining fifty per cent flowering (97 days), less number of productive tillers per plant (7.50) and with lesser hundred seed weight (2.67g). Cluster V comprised of six genotypes which were predominantly characterized by tall genotypes (116.87 cm) having high hundred seed weight (3.79g) with least plot yield. The cluster VI having only three genotypes *viz*., CB-06-551, CB-13-14, CB-14-112 which are early in attaining fifty per cent flowering with maximum number of productive tillers per plant which leads to higher single plant yield. Clear difference in grain yield was observed in the six clusters. Genotypes found in cluster VI recorded highest grain yield per plot (2.49 g) where as the cluster V comprised of six genotypes registered minimum single plant yield (0.45 g). Crossing between promising genotypes of cluster VI with the genotypes in V may provide superior desirable segregates for developing high yielding genotypes.

Association analysis

As genotypic correlation coefficient would give the realistic picture of relationships existing among the characters in the absence of environmental influence, the genotypic correlation coefficient was utilized in the present study. Significant and positive associations with plot yield were exhibited by the yield contributing traits *viz*., no. of productive tillers plant (0.455), panicle length (0.243) and hundred seed

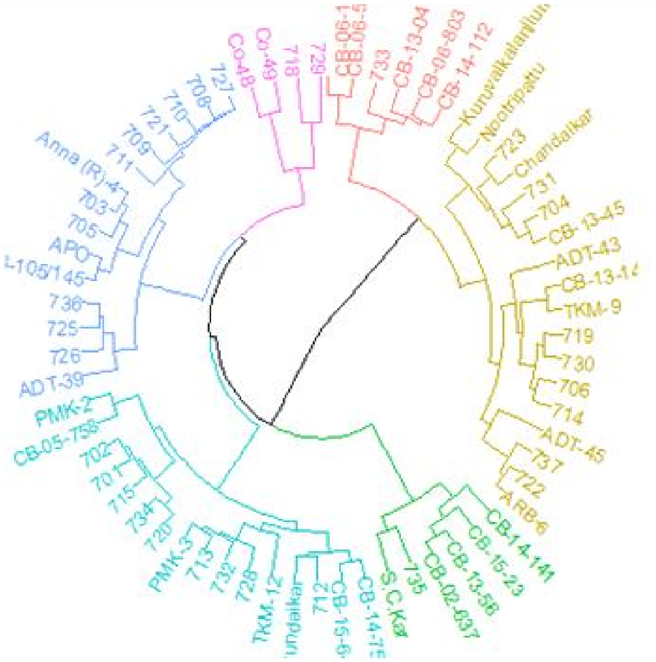

Fig 2: Circular dendrogram showing relationship among the rice genotypes based on eight quantitative traits.

Table 1: Eigen value, per cent variance and component matrix of and component matrix of rice germplasm.

PC	PC 1	PC 2	PC 3	PC 4	PC 5
Eigenvalue	1.83	1.56	1.15	0.93	0.82
Variance %	22.91	19.53	14.42	11.62	10.19
Cumulative %	22.91	42.44	56.86	68.48	78.67
			Component Matrix		
	PC 1	PC 2	PC 3	PC 4	PC 5
DFF	**0.321**	-0.314	**0.450**	**0.398**	0.060
PH	**0.341**	-0.086	-0.411	**0.441**	-0.665
NPT	0.245	**0.593**	0.145	-0.028	-0.310
PL	**0.561**	-0.156	0.020	-0.134	0.275
NGP	**0.507**	-0.207	0.206	-0.216	0.040
HSW	0.180	0.278	-0.485	**0.467**	**0.615**
PHI	-0.100	**0.378**	**0.574**	**0.466**	0.052
PY	**0.327**	**0.504**	-0.032	-0.382	0.012

weight (0.219) (Table 4). Similar results were reported earlier by Mohanty *et al*. (2012), Manohara and Singh (2015), Rukmani Devi *et al*. (2017) and Sahu *et al*. (2019) for panicle length, Sathish Chandra *et al*., 2009 and Kishore *et al*., 2015 for productive tillers/plant. Significant and positive association of these traits indicates that selection based on these traits would ultimately improve grain yield under aerobic conditions. The inter correlation among the component traits is also important in order to decide upon which traits to be given due weightage in exercising selection. The inter correlation between the yield contributing traits *viz*., days to fifty per cent flowering with panicle length (0.272) and no. of grains per panicle (0.272); plant height with panicle length (0.219); no. of productive tillers/plant with panicle harvest index (0.401); panicle length with no. of grains per panicle (0.454) and hundred seed weight with panicle harvest index (0.279) were positive and significant indicating the possibility of simultaneous improvement of these traits by concentrating on any one or two of these traits.

Information obtained from correlation study could not indicate whether the association of the yield-related traits with yield is due to their direct effect on yield or is a consequence of their indirect effect via some other traits. Path coefficient analysis is useful to understand the direct and indirect effects of each character on grain yield and the application of selection pressure in a better way for yield improvement, partitioning of correlation coefficient into direct and indirect effects. In the present study, path analysis showed that the maximum positive direct effect contributing to plot yield was exhibited by no. of productive tillers / plant (0.455) followed by panicle length (0.243) and hundred Seed weight (0.219) which implies that selection for these traits would improve the plot yield (Table 5). Similar results have been reported by Nanda *et al.* (2019) for the traits number of productive tillers/plant and hundred seed weight and Bhadru *et al*. 2012 for panicle length. Panicle harvest Index exhibited highest indirect effect on yield via no. of productive tillers per plant (0.198) followed by no. of grains per panicle *via* panicle length (0.124). This shows that selection for the traits no. of productive tillers per plant and panicle length would indirectly help in increasing the grain yield. A residual effect of 0.815

Table 2: Clustering pattern of 65 rice accessions based on dendrogram.

Cluster	No of accessions	Accessions
I	17	CB-11-701, CB-11-702, CB-11-712, CB-11-713, CB-11- CB-11-715, CB-11- CB-11-720, CB-11-728, CB-11-731, CB-11-732, CB-11-734, CB-05-758, CB-06-112, CB-15-64, ADT-39, PMK-2, PMK-3, TKM-12.
II	16	CB-11-703, CB-11-705, CB-11-708, CB-11-709, CB-11-710, CB-11-711, CB-11-721, CB-11-725, CB-11-726, CB-11-727, CB-11-736, CB-13-105/145, CB-14-75, Anna (R)-4, APO, Kallurundaikar.
III	19	CB-11-704, CB-11-706, CB-11-714, CB-11-719, CB-11-722, CB-11-723, CB-11-730, CB-11-733, CB-11-737, ARB-6, CB-06-803, CB-13-04, CB-13-45, ADT-43, ADT-45, Kuruvaikalanjium, Chandaikar, TKM-9, Nootripattu.
IV	4	CB-11-718, CB-11-729, Co-48, Co-49.
V	6	CB-11-735, CB-13-56, CB-14-141, CB-15-23, CB-02-637, Sivappuchithiraikar.
VI	3	CB-06-551, CB-13-14, CB-14-112.

Table 3: Cluster means for yield and its component traits in rice.

Cluster	DFF	PH	NPT	PL	NGP	HSW	PHI	PY
I	83	117.72	9.41	26.46	188.38	3.60	0.94	0.88
II	81	100.70	7.82	25.49	171.63	3.44	0.94	0.72
III	77	101.14	8.84	22.75	104.00	3.38	0.94	0.57
IV	97	115.75	7.50	25.90	145.74	2.67	0.92	0.52
V	78	116.87	7.83	24.78	158.94	3.79	0.88	0.45
VI	76	108.73	10.50	25.15	122.65	3.70	0.93	2.49

Table 4: Genotypic correlation coefficients of yield and yield attributing traits.

	DFF	PH	NPT	PL	NGP	HSW	PHI	PY
DFF	1.000	0.110	-0.056	0.272*	0.272*	- 0.125	0.063	-0.063
PH		1.000	0.081	0.219*	0.132	0.186	-0.278	0.033
NPT			1.000	0.020	0.114	0.183	0.401*	0.455*
PL				1.000	0.454*	0.065	-0.251	0.243*
NGP					1.000	-0.015	- 0.201	0.069
HSW						1.000	0.279*	0.219*
PHI							1.000	0.088
PY								1-000

* Significance at 0.05% probability.

Table 5: Direct and Indirect of yield and yield attributing traits.

	DFF	PH	NPT	PL	NGP	HSW	PHI	PY
DFF	-0.036	-0.013	- 0.028	0.074	-0.030	-0.021	-0.009	-0.063
PH	-0.004	0.118	0.040	0.060	-0.015	-0.031	0.040	0.033
NPT	0.002	-0.010	0.496	0.006	-0.013	0.030	-0.057	0.455*
PL	-0.010	-0.026	0.010	0.274	-0.051	-0.011	0.036	0.243*
NGP	-0.010	-0.016	0.056	0.124	-0.112	- 0.002	0.029	0.069
HSW	0.004	-0.022	0.091	0.018	0.002	0.166	-0.040	0.219*
PHI	-0.002	0.033	0.198	-0.069	0.023	0.046	-0.142	0.088

* Significance at 0.05 % probability*

Characters - DFF-(Days to 50 % flowering), PH-(plant height), NPT-(Number of branches per plant), PL-(Panicle length), NGP-(Number of grains per panicle), HSW-(100 seed weight), PHI-(Panicle harvest index), PY-(Plot yield).

implies that the casual traits explained only about 18.5% of the variability, leaving 81.5% of the variability unexplained.

It can be concluded that the traits panicle length, no. of grains per panicle, plant height, days to 50% flowering and no of productive tillers per plant from the first two principal accounted for major contribution to the total variability. The predominant characters coming together in a particular principal component by contributing towards variability offer opportunity for its utilization in the breeding programme. The traits no. of productive tillers/plant, panicle length and hundred seed weight had positive association with higher direct effect on plot yield which could be used as selection criteria for developing new rice varieties with high productivity under aerobic condition.

REFERENCES

Bhadru, D., Lokanadha Reddy, D., Ramesha, M.S. (2012). Correlation and Path analysis of yield and yield components in hybrid rice (*Oryza sativa* L.). Agricultural Science Digest. 32(3): 199-203.

Dewey, J.R. and Lu, K.H. (1959). Correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 51: 515-518.

Girma, B.T., Kitil, M.A., Banje, D.G., Biru, H.M., Serbessa, T.B. (2018). Genetic variability study of yield and yield related traits in rice (*Oryza sativa* L.) Genotypes. Advances in Crop Science and Technology. 6: 381. DOI: 10.4172/2329-8863.1000381

Hailegiorgis, D., Mesfin, M., Gangwar, S.K. (2010). Genetic divergence analysis on some bread wheat. Int J Sci Nat 1: 53-57.

Kishore, N.S., Srinivas, T., Nagabhushanam, U.,Pallavi, M. and Sameera, S.K. (2015). Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. SAARC Journal of Agriculture. 13(1): 99-108.

Manohara, K.K. and Narendra Pratap Singh. (2015). Genetic Variability, Correlation and Path Analysis in Rice (Oryza sativa L.) under Coastal Salinity Conditions of Goa. Journal of the Indian Society of Coastal Agricultural Research. 33(1): 34-39.

Mohan, S., Sheeba, A. and Kalaimagal, T. (2021). Genetic Diversity and Association Studies in Greengram [*Vigna Radiata* (L.) Wilczek]. Legume Research. 44(7): 779-784. DOI: 10.18805/LR-4176.

Mohanty, N., Sekhar, M.R., Reddy, D.M. and Sudhakar, P. (2012). Genetic variability and character association of agro-morphological and quality characters in rice. Oryza. 49(2): 88-92.

Nanda, K., D.N. Bastia and Ashutosh Nanda. (2019). Character association and path coefficient analysis for yield and its component traits in slender grain rice (*Oryza sativa L.*). Electronic Journal of Plant Breeding. 10(3): 963-969.

Rukhmani Devi, K., Satish Chandra, Lingaiah, N., Hari, Y., Venkanna, V. (2017). Analysis of variability, correlation and path coefficient studies for yield and quality traits in Rice (*Oryza Sativa* L.). Agricultural Science Digest. 37(1): 1-9.

Sahu, S, Sharma, D, Sao, R. and Rao, G.V. (2019). Association analysis of yield and yield contributing traits in traditional varieties of rice (*Oryza sativa* L). International Journal of Chemical Studies. 7(6): 848-852.

Sandhu, N., Yadaw, R.B., Chaudhary, B., Prasai, H., Iftekharuddaula, K., *et al.* (2019). Evaluating the performance of rice genotypes for improving yield and adaptability under direct seeded aerobic cultivation conditions. Frontiers in Plant Science. 10: 159.

Satish Chandra, B., Dayakar Reddy, T., Ansari, N.A. and Sudheer Kumar, S. (2009). Correlation and Path analysis for yield and yield components in rice (*Oryza sativa* L.). Agricultural Science Digest. 29(1): 45-49.

Shalini Singh, V. Rakesh Sharma, Vinay Kumar Reddy Nannuru, B. Singh, Mukesh Kumar. (2021). Phenotypic diversity of pea genotypes (*Pisum sativum* L.) based on multivariate analysis. Legume Research 44 Issue 8: 875-881.

Sharma, J.R. (1998). Statistical and Biometrical Techniques in Plant Breeding. New Age International Pvt Limited.

Shivangi, R., Yogendra Singh, Upadhyay, P.K. and Koutu, G.K. (2021). Principal Component analysis of JNPT lines of rice for the important traits responsible for yield and quality. Indian Journal of Genetics. 81(1): 127-131. DOI: 10.31742 /IJGPB.81.1.14.

Singh, R.K. and Chaudhary, B.D. (1979). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, pp. 215-218.

Yugandhar P.R., Suneetha Kota, UshaKiran, B. and Sridhar, M. (2018). Principal component analysis for agro morphological and quality characters in germ plasm of rice. International Journal of Advanced Biotechnology Research. 8(2): 268-270.