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Diversity in salt tolerant rice genotypes based on multivariate analysis

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ABSTRACT

Forty four salt tolerant genotypes of rice from different geographic regions were used to assess diversity among them by Mahalanobis D^2 and principal component analysis (PCA). D^2 statistics grouped genotypes into 12 distinct clusters and exhibited maximum intercluster distance between cluster IX and X (144.91) followed by clusters II and X (131.87) and clusters VII and X (126.27). PCA revealed axis 1 and 2 accounted for 82.88% and 11.14% of variance, respectively with positive correlation to number of grains panicle^{-1}. Similar to D^2 analysis PCA grouped the genotypes, which have similar phenotypic performance and attain meaningful grouping of genotypes. Both the statistical analysis revealed that genetic diversity was based on pedigree and independent of geographical origin.

Key words: *rice, genetic diversity, salt tolerance, principal component analysis*

The presence of excess salt is one of the most widespread soil problems in many rice growing areas. In India, it accounts for 8.5 million hectares of land and the yield reduction is estimated to the tune of 30-50% (Babu *et al*. 2005). Success of any breeding programme depends on available genetic divergence in the crop. Rice has good source of salt tolerant genes in a large number of varieties with variation in salt tolerance (Yeo and Flowers, 1982). A narrow genetic base among released cultivars and the practice of using elite line x elite line crosses has been implicated in slowing the rate of genetic advance for yield (Lal and Rana, 2000). Divergent parents in a cross has the greater scope of obtaining heterotic F_1's and broad spectrum of variability in the segregating generations in any varietal improvement programme. Hence, analysis of genetic relationships among extant genotypes is an important component of crop improvement program, as it provides information about genetic diversity and helps to stratify breeding populations.

Clustering germplasm into various groups using hierarchical or non-hierarchical algorithms based on multivariate statistical techniques and sampling from within discrete groups is a common method for maximizing diversity. Thus, the present investigation was designed to investigate the extent of genetic diversity in saline tolerant rice genotypes and to identify promising genotypes for future utilization in hybridization for developing saline tolerant genotype with high yield, and to estimate the nature and magnitude of relationship among quantitative traits associated with yield under saline environment.

MATERIALS AND METHODS

Forty four genetically diverse salt tolerant genotypes of rice from different region of India, were used in the present study (Table 1). These genotypes were grown in saline soil with soil and irrigation water EC of 2.83 and 0.86 dSm^{-1}, respectively during the dry season of 2006 and 2007, at the experimental farm of Plant Breeding, Annamalai University, Tamil Nadu. The seeds were sown in a raised nursery bed with good irrigation water; 25 day old seedlings were transplanted in the field. The experiment was laid out in a randomized block design with three replications, using 20 x 20 cm spacing, in 10 sq.m plots. The standard cultural practices were followed to ensure normal crop stand. Observations were recorded on ten randomly selected plants in each replication for the characters viz., days to 50% flowering, plant height, number of productive tillers, panicle length, number of grains panicle^{-1}, yield plant^{-1} and survival percentage. The data from the two years

were pooled in the analysis and subjected to Mahalanobis D^2 analysis (Mahalanobis, 1936) to estimate genetic divergence. The genotypes were grouped on the basis of minimum generalised distance using Tocher's method as described by Rao (1952) and principal component analysis was worked out.

RESULTS AND DISCUSSION

On the basis of D^2 analysis, the genotypes could be grouped into 12 clusters (Table 1). Cluster I comprised 19 genotypes, whereas cluster II had nine genotypes. Genotypes from few states (Andhra Pradesh, Haryana, Maharastra, Odishaand Uttar Pradesh) or with similar pedigree were grouped in the same cluster, as revealed by cluster I and II. In contrast, genotypes from different states (Andhra Pradesh, Maharastra and West Bengal) were grouped in the same cluster, such as cluster V that contained four genotypes (Sinha *et al*. 2001). On the other hand, genotypes from different states were scattered into monogenic clusters viz., III, IV, VI, VII, IX and XII. This suggested that geographical distribution did not necessarily be related to genetic divergence (Sarawgi and Shrivastava, 1996). The scattering of genotypes from same geographic region to different clusters might be due to heterogeneity, genetic architecture and history of selection (Murty and Arunachalam, 1966). The clusters VIII, X and XI were comprised of two genotypes each. The genotypes belonging these three clusters were from three states (Haryana, Odishaand Uttar Pradesh). These findings were in general agreement with Rathore *et al.* (2001) and Arun Sharma *et al.* (2008) in rice. The grouping of genotypes from different states into a single cluster might be due to unidirectional selection practice by breeders or free exchange of germplasm among the breeders.

The intracluster distance varied from 0.00 to 40.16 (Table 2). It was maximum for cluster XI (40.16) followed by cluster V, cluster X, cluster VIII), cluster I and cluster II. The clusters III, IV, VI, VII, IX and XII each contained only one genotype. The minimum intercluster distance was obtained between clusters III and IV (24.95) followed by clusters III and V, whereas, it was maximum between cluster IX and X (144.91) followed by clusters II and X and clusters VII and X (126.27). The inter cluster distances were higher than that of intracluster distances which indicated substantial diversity among the genotypes in the present study

Table 1. Clustering pattern of rice genotypes based on D^2 analysis

Cluster No.	No. of Genotypes	Parentage of genotypes
I	19	CSR 21 x CSR 10 (G18), IR 64 x IR 4630-22-2-5-1-3 x IR 9764-45-2-2 (G19), CST 7-1 (G42), CSRL-01-IR 75 (G36), CSR-01-IR 97 (G37), Usar 1 x Mahsuri (G16), IR 28 x Chakrakonda (G22), IET 9993 (MS) x N 52 (G31), Bipasa x Kalojira (G27), IET 9993 (MS) x BM 47 (G38), TCCP 266-249-B-B-3 x IR 262-43-8-1 (G6), CSR 3 x Kasturi (G32), Jaya x Lunishree (G25), IR 55182-3B-14-3-2-2- x IR 4499-29-2-2-2 (G7), IR 64 x PNL 2 (G20), Nonabokra x IR 36 (G29), CSR 3 x Kasturi (G33), Jaya x CSR 23 (G12), IR 68661-16-8 x NDR-2-B-2-1 (G15).
II	9	IR 72 x CSR 23 (G13), Mutant of IR 4630-22-2-5-1-3 x Pokkali (G30), Mahsuri x Chakrakonda (G23), IR 70804-9-NDR-3-7-91 (G8), Savithri x Lunishree (G2), KDML 105 x IR 4630-22-2-5-1-3 x IR 20925-33-3-1-28 (G1), PNL 2 x IET 8320 (G10), IET 8320 x PNL 1 (G9), CSR 23 x CSR 10 (G26)
III	1	CSR 3 x Kasturi (G34)
IV	1	Savithri x Lunishree (G4)
V	4	IET 13845 x GJ 11 (G21), Pankaj x SR 26B (G39), Pankaj x SR 26B (G28), TN1 x T141(G43)
VI	1	CSRL-04-2366 (G35)
VII	1	IR 578-172-2-2 x BR-1-2-B-19 (G44)
VIII	2	Mahsuri x Ormundakan (G5), Selection from Kalanamak (G17)
IX	1	PNL -2 x IET 8320 (G11)
X	2	Jaya x Lunishree (G3), Nona Bokra x IR 5657-33-2 (G41)
XI	2	Jaya x Lunishree (G24), CSR 1 x Basmati 370 x CSR 5 (G40)
XII	1	Mahsuri x Madhukar 105 (G14)

Table 2. Intra and inter cluster distances for 12 clusters in rice

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	34.54	50.78	45.41	45.29	72.73	42.05	52.85	83.55	53.75	107.78	88.69	56.33
II		33.73	76.01	67.73	106.60	51.08	79.09	102.46	60.36	131.87	114.45	69.51
III			0.00	24.95	38.99	45.35	55.74	55.38	78.51	80.15	75.68	63.18
IV				0.00	53.40	39.18	59.44	46.03	76.88	89.43	92.01	73.74
V					37.12	74.93	68.17	66.15	99.13	79.23	78.03	85.53
VI						0.00	76.54	66.54	79.01	97.62	92.84	49.80
VII							0.00	99.00	41.83	126.27	101.35	79.91
VIII								35.90	119.79	75.67	104.30	102.87
IX									0.00	144.91	112.82	82.60
X										36.16	66.05	116.27
XI											40.16	93.27
XII												0.00

(Table 2). Higher genetic distance between the clusters, suggested wide diversity between the genotypes. The crosses made between the genotypes from the above clusters may give useful transgressive segregants (Sharma and Bhuyan, 2004). The genotypes belonging to clusters having maximum intercluster distance were relatively closer to each other; such analysis helps to avoid selection of parents from genetically homogeneous clusters, and reduces narrow genetic bases. Besides high genetic divergence, the performance of genotypes for characters with maximum contribution towards genetic divergence should also be given due consideration. The differences among the genotypes for number of grains panicle^{-1}, grain yield plot^{-1} and survival per cent were more pronounced as compared to other traits (Table 3). Therefore, the character number of grains panicle^{-1} seems to be most important as its per cent contribution was maximum (42.07%) towards genetic divergence followed by grain yield plant^{-1} and survival per cent (De and Rao, 1987 and Chaturvedi and Maurya, 2005).

Considering the cluster means (Table 3) of various characters in different clusters revealed that the genotypes in cluster XII took minimum number of days to 50% flowering and genotypes in cluster III took short plant height, whereas the genotypes in cluster IX and VIII took maximum number of days to 50%

Table 3. Mean performance of different clusters with respect to different traits in rice

Cluster	Days to 50% flowering	Plant height (cm.)	No. of productive tillers plant^{-1}	Panicle length (cm.)	No. of grains panicle^{-1}	Grain yield plot (g)	Survival per cent
I	86.86	104.02	19.33	29.20	109.91	5.28	61.37
II	85.63	92.47	17.46	25.52	78.41	1.91	61.34
III	86.33	87.22	14.83	28.10	166.33	6.15	62.00
IV	92.00	110.17	17.33	28.13	165.00	4.06	66.34
V	87.79	113.56	21.96	29.25	190.58	8.70	62.77
VI	77.17	121.53	27.50	28.45	132.67	2.39	61.17
VII	96.67	109.16	16.50	25.03	110.33	9.51	72.28
VIII	90.75	134.84	17.33	26.14	220.75	2.12	64.30
IX	97.83	94.30	22.83	26.48	59.00	7.71	66.78
X	85.58	131.38	17.67	30.21	222.33	5.13	34.85
XI	82.67	113.90	24.83	26.13	144.33	9.12	31.33
XII	60.33	93.85	20.50	26.50	102.33	5.78	60.67
% contribution to diversity	7.08	1.16	1.59	0.42	42.07	29.81	17.86

flowering and plant height, respectively. Cluster means for number of productive tillers plant^{-1} was the highest for cluster VI. However, genotypes from cluster X had the longest panicles, maximum number of grains panicle^{-1}, highest survival percentage high grain yield plant^{-1}. In this cluster, these characters were recorded by the genotypes G3 and G41. Parents for crossing programme should belong to diverse clusters characterized by large intercluster distance. Such genotypes have genes with different magnitude of effects and the chances to obtain recombinants outside the range of parents are greater. Therefore, the lines belonging to clusters X, IX, II and VIII can be used in hybridization programme to obtain useful recombinants.

The genotypes G3 and G41 in cluster X were found to be high yielding and medium duration type whereas, the genotype G14 in cluster XII was found promising for early flowering. The genotype G35 from cluster VI had the highest productive tillering plant. Thus, hybridization between these genotypes could be useful in developing early maturing rice varieties for saline environmental condition.

The graphical representation of PCA analysis was applied to identify the genetic diversity among genotypes and the traits responsible for main source of the variability. The first and second principal component (PC) accounted for 82.88% and 11.14% of the variance respectively (Table 4). Since the first two PC accounted for about 94.02% of the total variability, a two dimensional representation of the relative position of the varieties in the biplot graph was found adequate.

The 82.88% of variation by first PC was mainly due to the variation in number of grains per panicle. The first PC was positively correlated with all characters except plant survival per cent. The 11.14% variation in second PC mainly resulted from the variation in plant height. The second PC was positively correlated with number of grains panicle^{-1}, plant survival per cent and grain yield plot^{-1}.

Clusters were distinctly delineated to their respective positions similar to their position in D^2 analysis (Tyagi *et al*. 1999) (Fig. 1). The genotypes G3 and G41 of cluster X and G11 of cluster IX were situated opposite to each other indicating considerable divergence between them. Similar to D^2 analysis, PCA also clustered genotypes based on pedigree and not by geographic origin. Thus, it suggests that, selection of lines for hybridization based on genetic diversity rather than geographic distance.

Table 4. Principal components for rice genotypes based on seven characters

Parameters	PC1	PC2	PC3	PC4
Eigen values	102366	13755	3934	1717
Percentage variance (%)	82.88	11.14	3.19	1.39
Cumulative variance (%)	82.88			
Character	Latent vectors (loadings)			
Days to 50% flowering	0.009	-0.010	0.150	0.979
Plant height	0.218	-0.972	0.080	-0.023
Productive tillers plant^{-1}	0.005	-0.009	-0.013	-0.127
Panicle length	0.016	-0.003	0.029	0.000
No. of grain panicle^{-1}	0.974	0.222	0.034	-0.013
Grain yield plot^{-1}	0.014	0.004	-0.041	0.065
Survival percentage	-0.053	0.073	0.984	-0.145

Hierarchical or non-hierarchical algorithms based on multivariate statistical techniques is a common method for breeders to identify diverse genotypes for developing suitable varieties for target environment. Thus it provides chance to obtain recombinants resulting from recombination of favourable genes. In the present study, the results indicated that genotypes selected from clusters X, IX, II and VIII could be used in hybridization programme. Since the genotypes from these clusters exhibited maximum diversity in respect to the aggregate effect of the characters examined. Thus, the segregants

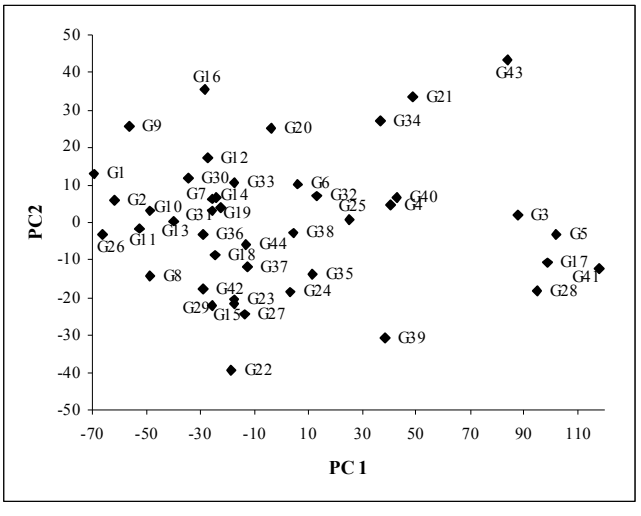

Fig. 1. Spatial distribution of 44 rice genotypes for first two principal components

from the above clusters would yield promising genotypes for salt affected soil with high survival percentage and yield.

The PCA and D^2 statistic exhibited high level of variability among the genotypes and allowed to select highly diverse genotypes which differ in phenotype performance.

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