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Multivariate Analysis Under Drought in Rice (*Oryza sativa* L.)

A Siva Prasad, K V Seetharamaiah, J V Ramana and B Vijaya Lakshmi
Department of Genetics and Plant Breeding, Agricultural College, Bapatla 522101, Andhra Pradesh

ABSTRACT

Genetic diversity of 37 genotypes of rice were evaluated for drought tolerance using Mahalanobis' D^2 statistic, principal component and cluster analyses. The pattern of distribution of 37 genotypes obtained from different agro-ecological regions was 6 clusters in case of D^2 analysis and 7 clusters incase of cluster analysis. The best clusters with regards to grain yield and drought tolerance were cluster IV and VI in case of D^2 analysis where as cluster V and IV in cluster analysis. The principal component analysis explained 92.069 variability among the genotypes studied. Days to 50% flowering, chlorophyll content index and stomatal conductivity are major contribution towards genetic diversity under drought tolerance.

Key words : Cluster Analysis,D^2 Analysis, Principal Component Analysis, Rice

In the crop improvement programme, genetic diversity is essential prerequisite for hybridization. Inclusion of diverse parents in hybridization helps in isolation of superior recombinants. Several methods for multivariate analysis such as D^2 analysis, principal component analysis have been shown to be useful in selecting genetically distant parents for hybridization. The present investigation was to identify the extent of diversity among 37 genotypes of rice for drought tolerance using D^2, principal component and cluster analyses.

MATERIAL AND METHODS

The germplasm known to have drought tolerance was obtained from various sources *viz.,* CRRI Cuttack, NBPGR and DRR, Rajendranagar, Hyderabad, along with the low land cultivars (Table1) was evaluated during *kharif* 2006 at Andhra Pradesh Rice Research Institute (APRRI) and Regional Agricutural Research Station (RARS) Maruteru, West Godavari. The experiment was laid out with two replications in randomized complete block design. The plot size was 5x5m and the material was sown adopting the inter- and intra-row spacing of 10x10cm. Plants were watered daily up to 40 DAS and later stress was imposed by not giving irrigation for fifteen days at tillering stage and at weekly intervals at flowering stage. Observations were recorded on five plants selected at random in each entry and on plot basis in each replication. D^2 statistics (Mahalanobis, 1928), principal component analysis (Jackson, 1991) and hierarchical cluster analysis (Anderberg, 1993) were carried out using SPSS computer programme.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant difference among the genotypes for 15 characters. This difference indicated the existence of significant amount of variability among the genotypes for drought tolerant characters studied.

The 37 genotypes were grouped into 6 clusters in D^2 analysis (Table 2) whereas 7 in Ward's method(Table 3 and Fig 1) the variation in the composition of individual clusters with regard to number of genotypes indicated the presence of large amount of diversity in the population. The results have clearly indicated that there is no parlleism between the geographic diversity and genetic diversity in rice as also reported by Nayak and Reddy (2005).

On the basis of D^2 analysis the maximum intra-cluster (D^2 values) was observed in cluster II (397.20) and it was zero for cluster III, V and VI, while on the basis of cluster analysis the maximum intra-cluster distances was observed in VII (621.05) and zero in cluster IV.

Maximum inter-cluster distances (3915.00) was found between cluster II and VI while minimum distance (712.89) was found between clusters V and cluster III on the basis of D^2 analysis(Table 4). The maximum inter-cluster distance between VI and IV (8409.96) while minimum divergence was found between II and III (1075.56) on the basis of cluster analysis (Table5). The hybridization between genotypes from the medium inter-cluster distances should give rise to heterotic hybrids.

The D^2 analysis indicated that the days to 50% flowering (40.24%), chlorophyll content index

Table 1. List of rice (Oryza sativa L.) genotypes studied

S.No	Genotype	Pedigree	Origin
1	Accession no.11103	Land race	NA
2	Accession no.11982	Land race	Chattisgarh
3	Accession no.10989	Land race	NA
4	Rudrama	HR 19 / TN 1	Rudrur, Andhra Pradesh
5	Prabhat	IR 8 / MTU 3	Maruteru, Andhra Pradesh
6	Putikabari	NA	NA
7	Naveen	NA	CRRI, Cuttack, Orissa
8	Anjali	PR-19-2/RR-149-1129	CRRI. Cuttack, Orissa
9	Prasanna	IRAT 8 / N 22	DRR, Hyderabad, Andhra Pradesh
10	Varalu	WGL 20471 / CR 544-1-2	RARS, Warangal, Andhra Pradesh
11	MTU 1006	Pure line selection from oodasannalu	Maruteru, Andhra Pradesh
12	Nagina 22	Selection from Rajbhog	Uttarpradesh
13	Govind	IR 20/ IR 24	CRRI, Cuttack, Orissa
14	Rasi	TN Z(1) / CO 29	DRR, Hyderabad, Andhra Pradesh
15	Bhadraj	Land race	Orissa
16	Dular	Land race	West Bengal
17	Tulasi	Rasi/fine Gora	DRR, Hyderabad, Andhra Pradesh
18	Mudhol Tellalu	NA	Rudrur, Andhra Pradesh
19	Accession no.11053	Land race	NA
20	Accession no.11091	Land race	NA
21	Heera	CR 404-48 / CR 289-1208	CRRI, Cuttack, Orissa
22	Accession no.11111	Land Race	NA
23	Swarna	Vasista / Mashuri	Maruteru, Andhra Pradesh
24	Aditya	M 63-83 / Cauvery	DRR, Hyderabad, Andhra Pradesh
25	Ravi	M63-83 / RP 79-5 / Rikotu Norin 21	DRR, Hyderabad, Andhra Pradesh
26	Chennangi	Land race	Ananthapur, Andhra Pradesh
27	NLR 145	CICA-4 / IR-625-23-3-1 /Tetap	Nellore, Andhra Pradesh
28	TN 1	Peta / Dee-geo-Woo-gen	NA
29	Azucena	Tropical joponica upland cultivar	Philippines
30	Lalnakanda-41	Land race	Punjab
31	Cottondora	Krishnaveni / IR 64	Maruteru, Andhra Pradesh
32	IR 64	IR 5857-33-2-1 / IR 2061-465-1-5-5	Philippines
33	Vijetha	Vajram / MTU 7014	Maruteru, Andhra Pradesh
34	Vandhana	C22 / Kalakari	DRR, Hyderabad, Andhra Pradesh
35	Salumpikit	Traditional Philippine dryland cultivar	Philippines
36	Annada	MTU 15 / Waikoku	CRRI, Cuttack, Orissa
37	Moroberekan	Japonical upland	Philippines

NA = not available

Table 2. Clustering of 37 genotypes of rice (*Oryza sativa* L.) by Tocher's method

Cluster No.	No. of genotypes	Name of genotypes (S)
I	21	Dular, Aditya, 10989, Lalankanda -41, Vandhana, Prasanna, 10982, Salumpekit, Putikabari, Varalu, Chennangi, Rudrama, N22, Ravi, Govind, Rasi, Annada, Tulasi, Anjali, Naveen, 11103
II	11	MTU 3626, MTU 1001, Cottondora Sannalu, Mudhol-Tellalu, Bhadraj, Swarnamukhi, IR 64, 11053, Swarna, 11091, TN 1
III	1	Acc.No.11111
IV	2	Azucena, Moroberekan
V	1	MTU 1006
VI	1	Heera

Table 3. Clustering of 37 rice (*Oryza sativa* L.) genotypes by Ward's minimum variance method.

Sl.No	No.of genotypes	Name of genotypes (S)
I	4	11103, 11111, Rudrama, Tulasi
II	7	Naveen, Ravi, Govind, Rasi, Annada, Anjali, MTU1006
III	12	Putikabari, Salumpekit, 10982, N22, Chennangi, Prasanna, Vandhan, Varalu,Dular, Aditya, 10989, Lanankanda-41
IV	1	Heera
V	2	Azucena, Morobereken
VI	8	MTU3626,MTU1001, Cottondora Sannalu, Bhadraj, Mudhlo-Tellalu, Swarna, Swarnamukhi, IR64
VII	3	1053, TN1, 11091

Table 4. Intra-and inter- cluster Mehalanobis' D^2 mean values in rice (*Oryza sativa* L.)

Cluster	I	II	III	IV	V	VI
I	**380.64**	1284.50	712.89	1130.98	723.61	1293.84
II		**397.20**	1588.82	2368.76	809.97	3915.00
III			**0.00**	2383.88	1044.25	1319.86
IV				**284.25**	1582.45	2649.16
V					**0.00**	2266.71
VI						**0.00**

Bold values indicate intra-cluster distances

Table 5. Intra- and inter -cluster average values of 7 clusters based on Ward's minimum variance method from 37 genotypes of rice (*Oryza sativa* L.)

Cluster	I	II	III	IV	V	VI	VII
I	**551.54**	10.83.58	1075.56	2545.58	3764.95	2765.11	1506.32
II		**495.36**	1101.41	3930.82	2503.80	1535.06	1054.26
III			**516.01**	1983.47	1886.24	3634.99	2296.30
IV				**0.00**	5298.61	8409.96	6279.17
V					**568.80**	5099.69	3769.70
VI						**582.82**	1063.20
VII							**621.05**

Bold values indicate intra-cluster distances

Table 6. Contribution of different characters towards genetic divergence in 37 genotypes of rice (*Oryza sativa* L.) based on D^2 values

Source	Rank	Contribution %
Days to 50% flowering	1	40.24
Grains panicle^{-1}	8	1.80
100 Grain weight	5	8.41
L/B ratio	4	9.16
Yield M^{2-1}	10	1.50
Root volume	6	5.86
Leaf water potential	9	1.65
Stomatal conductivity	3	10.66
Relative water content	7	2.40
Chlorophyl content index	2	17.87

(17.87%), stomatal conductivity (10.66%), L/B ratio (9.16%) and test weight (8.41%) contributed towards genetic diversity (Table 6). These results are in accordance with Gupta *et al.* (2003).

In the present investigation, principal component (PC) method was used to extract the principal factor (PF) as it does not require the assumption of normal distribution of population. The PCs with eigen values >1 were retained and <1 were considered non-significant (Legendre and Legendre, 1984). The first three PC's showed eigen values more than one and they together explained 88.18% of variability (Table 7). The first PC explained 61.37% of total variability in all the varities three PCA scores in the set of varieties and remaining ones accounted for progressively lesser and lesser amount of variation.

Principal factor scores (PF scores) for all the 37 genotypes were estimated in all the 3 PC's and utilized to construct precise 3D plot (Fig 2). Genotypes of same cluster *viz.,* Putikabari, 10989, Aditya and Dular of cluster III fall nearer to each other on the positive axis of PCI. Cottondora Sannalu, MTU3626 of cluster VI fall nearer to each other, while genotypes Moroberken and Azucena away from each other indicate the specificity in clustering.

Both D^2 and cluster analyses revealed a single concept of non-correspondence of genetic diversity and geographical diversity. In broad sense

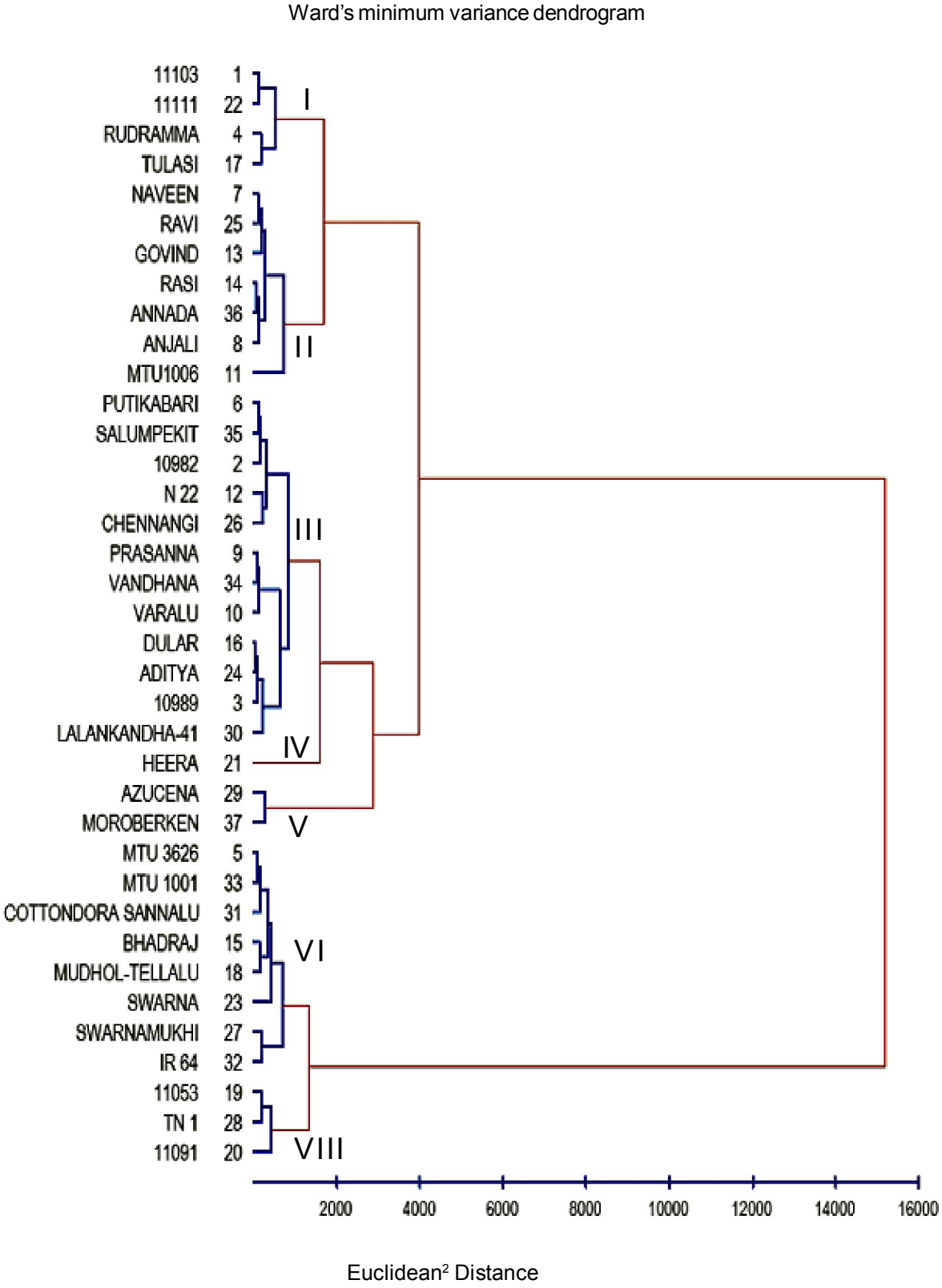

Fig 1. Ward's minimum variance dendrogram of rice (*Oryza sativa* L.) based on Euclidean^2 distance during *kharif* 2006

Fig.2. Three dimensional scattered diagram showing genotypes of rice (*Oryza sativa* L.) based on PCA scores during *kharif* 2006(genotypes as per Table 1)

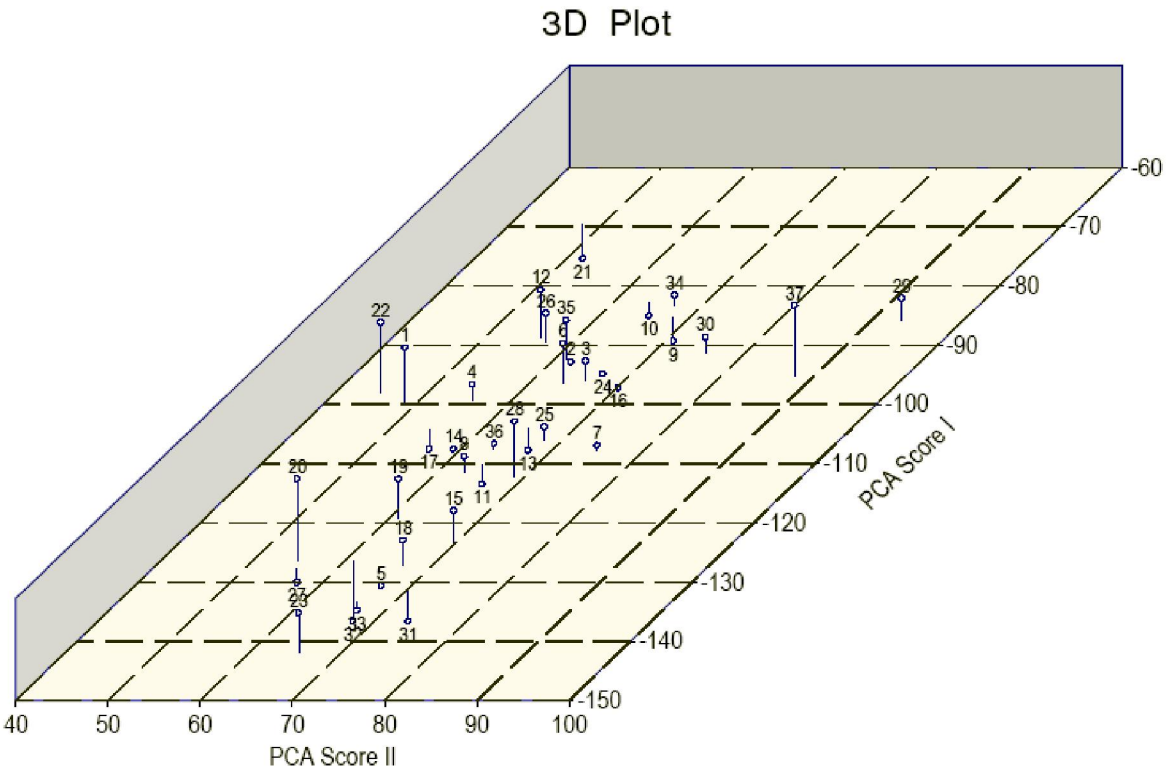

Table 7. Eigen values, proportion of total variance represented by four principal components, cumulative per cent variance and component loading of different characters in rice (*Oryza sativa* L.) during *kharif* 2006.

Character	PCI	PCII	PCIII	PCIV
Eigene value(Root)	10663.93	3227.36	1429.66	675.25
% variance explained	61.37	18.57	8.23	3.88
Cumulative variance explained	61.37	79.95	88.18	92.07
Plant height (cm)	0.01598	0.1083	0.2329	0.2232
Days to 50% flowering	-0.6141	0.2508	0.1235	-0.0636
Ear bearing tillers	-0.0066	0.0267	-0.1104	-0.0081
Panicle length (cm)	-0.1794	0.1175	0.0934	0.0766
Filled grains per panicle	-0.2652	0.1342	0.01898	-0.1152
Grains per panicle	-0.2616	0.2292	0.04205	-0.1208
Test weight (g)	0.2621	0.2481	-0.3428	-0.3883
L/B ratio	-0.0509	0.3008	-0.5843	0.5636
Yield/m^2	-0.0221	0.1131	0.0724	-0.3024
Root length (cm)	-0.0377	0.1997	0.1996	0.4063
Root volume (cc)	0.3965	0.1185	0.2048	0.1620
Leaf water potential (-Mpa)	-0.1149	-0.2789	0.2068	-0.1705
Stomal conductivity (mmol/sec/m^2)	-0.3700	-0.1546	-0.4559	-0.1327
Relative water content (%)	-0.1358	0.3634	0.3309	0.0681
Chlorophyl content index (CCI)	0.2290	0.6225	-0.0336	-0.3309

both the methods of classifying genotypes into different groups is equally useful but cluster analyses gave an additional advantage of indentifying sub-clusters of the major groups at different levels so that each small group can be critically analysed. Moreover characters like days to 50% flowering, chlorophyll content index and stomatal conductivity are major contribution towards genetic diversity under drought. Thus these characters could therefore, form the basis for selection of parents from distantly placed clusters to obtain high heterotic combinations.

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