

# Electronic Journal of Plant Breeding



## Research Article

### Genetic uniformity of varieties and an assessment on the diversity among the elite varieties of rice (*Oryza sativa* L.)

Neethu Francis<sup>1\*</sup> and D. Packiaraj<sup>2</sup>

<sup>1,2</sup>Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

\*E-Mail: neethufaloor@gmail.com

#### Abstract

The concern that artificial selection for crop improvement leads to loss of genetic diversity, has been debated over the past. The knowledge about the diversity present within the released varieties was important for the direction of future breeding programmes. This experiment was conducted utilizing thirty two elite rice varieties released by Tamil Nadu Agricultural University and that are available in the Breeder's Seed Production chain of Tamil Nadu. The study was conducted at the Paddy Breeding Station of Tamil Nadu Agricultural University. The contribution of characters to divergence and clustering of varieties accordingly were estimated using Mahalanobis'  $D^2$  statistics and PCA analysis. Time to maturity, single plant yield and days to 50 per cent flowering contributed maximum to the genetic diversity as given by the per cent contribution to divergence. The varieties were grouped into seven diverse clusters. According to Principal Component analysis first three components contributed to 77.3 per cent variability. First component was partitioned among single plant yield, the number of panicles per plant and time to maturity which made 40.6 per cent variability. This study shows that the genetic diversity are being preserved in different varieties indirectly in breeding for different consumer preferences, ecosystems and climatic conditions.

#### Key words

varieties, rice, diversity, d square, pca, clustering

#### INTRODUCTION

Rice breeding have evolved over the years and contributed for the food security by the way of several varieties developed to feed the people across the world (Bardenas and Chang, 1965). Rice being the staple food crop are always subjected to introgression processes to achieve improvement over the existing promising varieties. Plant breeders generally concentrate on increasing yield while developing varieties and as a result of concentrate on alleles contributing to it. This approach may end up in loss of diverse alleles in varieties which is termed as genetic bottlenecking. This loss of alleles eventually will end up in genetic erosion. Though recently thrust has been given on inter-specific multi parental approaches, it is being hindered greatly by cross compatibility issues and latent linkage drags. Hence the inclination towards preserving

the hard earned favourable allelic combinations present in the varieties developed (McCouch *et al.*, 2007). In Tamil Nadu the varieties developed were mainly to suit different agro climatic conditions, seasons, durations and consumer preferences.

Present study is aimed at finding the diversity in the already existing rice varieties in the seed production chain among the varieties which can give an advantage over genetic erosion. Mahalanobis  $D^2$  statistics has been used as an efficient statistical tool to distinguish the varieties into different clusters based on their genetic distance (Hoque *et al.*, 2015, Tripathi *et al.*, 2017, Palaniyappan *et al.*, 2020). Grouping of varieties based on their divergence can help in preliminary distinction of varieties. The use

of Principal Component Analysis (PCA) would help to strengthen the findings from the  $D^2$  analysis and also provide the principal contributors towards variability between the genotypes (Mahajan and Mehan, 1980, Sheela et al., 2020). Principal component analysis is used to reduce large datasets and finds a small number of important independent variables. It replaces the  $p$  original variables by a smaller number,  $q$ , of derived variables, mostly retaining the original variability (Jolliffe, 2002). Based on these two methods the total diversity existing among the varieties of Tamil Nadu has been detected.

### MATERIAL AND METHODS

The present study was carried out at the Paddy Breeding Station of Tamil Nadu Agricultural University, Coimbatore among thirty two varieties of the Breeder Seed Production chain. The field experiment was laid out in RBD with three replications. The observations were recorded on nine quantitative characters *viz.*, days to 50 per cent flowering, plant height, leaf length, the number of panicles per plant, panicle length, the number of grains per panicle, 1000 grain weight, time to maturity and single plant yield. ANOVA for the characters showed significant differences among the varieties studied. Genetic diversity analysis with Mahalanobis'  $D^2$  statistics (Mahalanobis, 1928) was carried out using GenRes statistical software. Based on the degree of divergence ( $D^2$  values) between

any two genotypes, grouping of genotypes was done by using Tocher's method (Rao, 1952). The results of D square analysis were confirmed by carrying out Principal Component Analysis using MINITAB® 17.1.0 Software.

### RESULTS AND DISCUSSION

Variability studies revealed significant differences for nine quantitative characters *i.e.*, days to 50 per cent flowering, plant height, leaf length, the number of panicles per plant, panicle length, the number of grains per panicle, 1000 grain weight, time to maturity and single plant yield (Neethu-Francis *et al.*, 2018).  $D^2$  analysis for the characters among the 32 rice cultivars studied revealed the per cent contribution of each character towards divergence (Table 1). The character that contributed highest to the divergence according to  $D^2$  statistical analysis was time to maturity with a per cent contribution of 23.79 percent, followed by single plant yield with 20.36 percent. Days to 50 per cent flowering gave 16.53 per cent contribution towards divergence. Number of grains per panicle contributed least to divergence (0.20%), followed by leaf length (0.40%). Bose and Pradhan (2006) published results in accordance with the findings of the present study. Days to 50 per cent flowering and single plant yield were the major contributors to divergence in his study on deep water rice genotypes.

**Table 1. Contribution of each character towards divergence based on  $D^2$  square analysis**

Character	No. of first rank	% Contribution
Days to 50 percent flowering	82	16.5323
Plant height	40	8.0645
Leaf length	2	0.4032
No. of panicles per plant	78	15.7258
Panicle length	3	0.6048
No. of grains per panicle	1	0.2016
1000 grain weight	71	14.3145
Time to maturity	118	23.7903
Single plant yield	101	20.3629
TOTAL	496	100

Clustering based on the Critical  $D^2$  value was used to form various clusters among the thirty two varieties studied. The critical value used for cluster formation was 141.76. Seven different clusters were formed among the 32 cultivars (Table 2). Tripathi *et al.*, (2017) and Seetharam *et al.*, (2009), furnished similar clustering of rice genotypes into seven and six clusters respectively, using  $D^2$  analysis. Maximum number of cultivars (7) was grouped under cluster 6 and minimum under clusters 2, 3 and 7 with two cultivars in each. ASD16, ASD18, ASD19, MDU6, TRY1, ADT 43 were grouped under cluster one. CR1009 and CR1009 Sub1 were grouped under cluster two. TKM 9 and ADT 36 formed cluster three. TRY 3, TPS 5, Anna 4, IR 20, ADT 39 and ADT 42 formed cluster four. TKM 13, TKM 14, IR 36, ADT 38 and ADT 47 were under cluster five. ADT 37, ADT 46, ADT 45, ADT 49, ADT 50,

CO 50 and CO 49 formed cluster six. CO 48 and CO 51 were grouped under the seventh and last cluster.

Inter and intra cluster distances were also estimated using D square analysis (Table 3). Maximum intra cluster distance (10.22) was observed for cluster 7, followed by cluster 1 (9.9). Minimum intra cluster distance was estimated for cluster 2 (2.28). Distance between cluster 5 and cluster 7 was the highest estimated inter cluster distance (14.48). Next highest distance was between cluster 2 and cluster 7 (14.43). The closest clusters were cluster 3 and 5 with an inter cluster distance of 6.70.

Hence for the diversity and seven different clusters formed the main contributors are: time to maturity, single plant yield, days to fifty per cent flowering and the number of

grains per panicle. It is evident from the separate grouping of CR1009 and CR1009 *sub 1*, which are long duration, bold grain and high yielding varieties. The cluster diversity

is clear depiction of the presence of genetic diversity among the varieties which is mainly from the contribution of diverse parents.

**Table 2. Clustering of cultivars based on critical D<sup>2</sup> value**

CLUSTER 1	ASD 16, ASD 18, ASD 19, MDU 6, TRY 1, ADT 43
CLUSTER 2	CR1009, CR 1009 Sub 1
CLUSTER 3	TKM 9, ADT 36
CLUSTER 4	TRY 3, TPS 5, Anna 4, IR 20, ADT 39, ADT 42
CLUSTER 5	TKM 13, TKM 14, IR 36, ADT 38, ADT 47, IR 50
CLUSTER 6	ADT 37, ADT 46, ADT 45, ADT 49, ADT 50, CO 50, CO 49, CO 43
CLUSTER 7	CO 48, CO 51

**Table 3. Inter and intra cluster distances**

CLUSTER	I	II	III	IV	V	VI	VII
I	9.907	10.795	7.427	9.36	10.432	9.654	12.692
II		2.281	10.383	9.99	10.803	9.328	14.432
III			2.382	7.721	6.704	8.257	12.311
IV				9.617	10.023	9.361	11.557
V					7.796	10.045	<b>14.489</b>
VI						9.674	12.432
VII							10.229

The different morphological characters that contributed to the total variability, among the cultivars studied were calculated for each principal component. The first three components contributed 77.3% of the variability (**Table 4 and Fig.1**). Eigen values of the other PCs (PC4-5) dropped below 1. Similar results were three principal components contributing to major variability were reported by Radhamani *et al.*, (2015). Eigen value of the first principal component (PC1) was 3.65, followed

by second component with Eigen value of 2.01 and third with 1.28 Eigen value. The first component showed a variability percentage of 40.6% followed by 22.4 % for second component and 14.3 % for the third component. The major contributors to the principal components were determined from the loading factor values (**Table 5**). The first component contributed highest to variability and was partitioned mainly among single plant yield (0.42), the number of panicles per plant (0.37) and time to maturity

**Table 4. Eigen values of Principal Component Analysis**

Eigen value	3.6509	2.0177	1.2834	0.8562	0.558	0.3116	0.1767	0.0752	0.0703
Per cent variance	40.6	22.4	14.3	9.5	6.2	3.5	2	0.8	0.8
Cumulative (%) variance	40.6	63	77.2	86.8	93	96.4	98.4	99.2	100

**Table 5. Loading factor values of different variables to first three principal components**

	PC1	PC2	PC3
Days to 50 percent flowering	0.28	-0.36	-0.53
Plant height	0.26	0.42	-0.13
Leaf length	0.34	0.25	-0.08
No. of Panicles per Plant	0.37	-0.26	0.32
Panicle length	0.33	0.47	-0.04
No. of Grains per Panicle	0.35	-0.33	0.33
1000grain weight	0.18	0.41	0.13
Time to Maturity	0.36	-0.16	-0.54
Single plant yield	0.42	-0.11	0.39

(0.36). Maji and Shaibu, (2012) furnished similar data for the number of grains per panicle being part of principle component one. Panicle length (0.47), plant height (0.42) and thousand grain weight (0.41) were major contributors to component two. The variation of PC 3 was primarily due to time to maturity (-0.54), days to fifty per cent flowering (-0.53) and single plant yield (0.39). Caldo *et al.* (1996)

reported results in contrast for the number of components contributing to divergence in ancestral lines in rice, where ten principal components together contributed to the 67 per cent of total variation. The lesser number of components in the present study could be attributed to the lesser variability among the study material *i.e.*, varieties in comparison with the diverse ancestral lines.

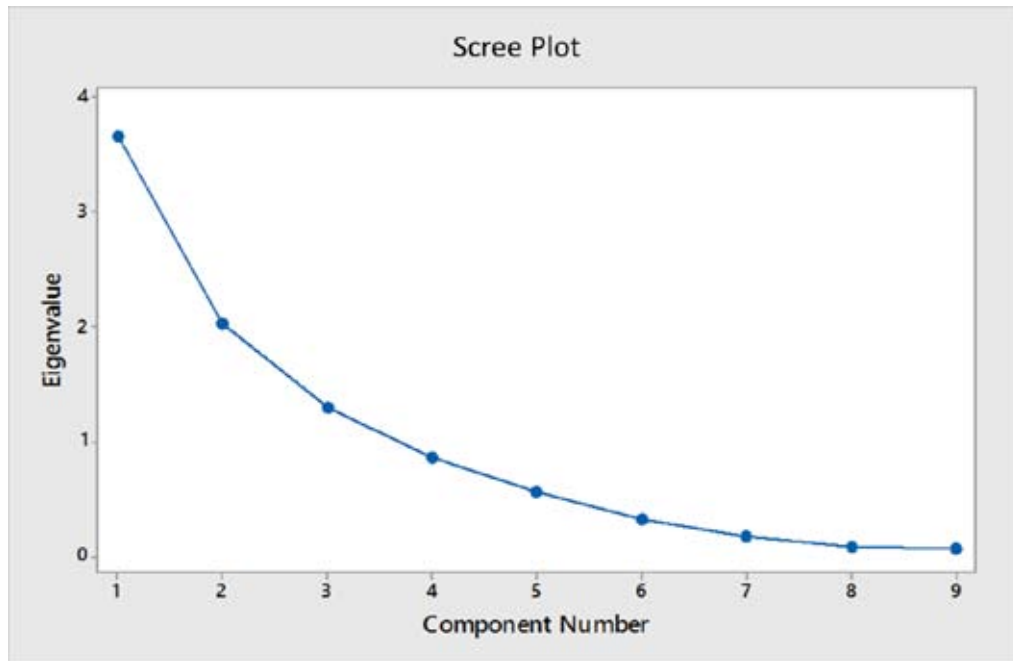


Fig. 1. Scree plot showing eigen value variation of different principal components

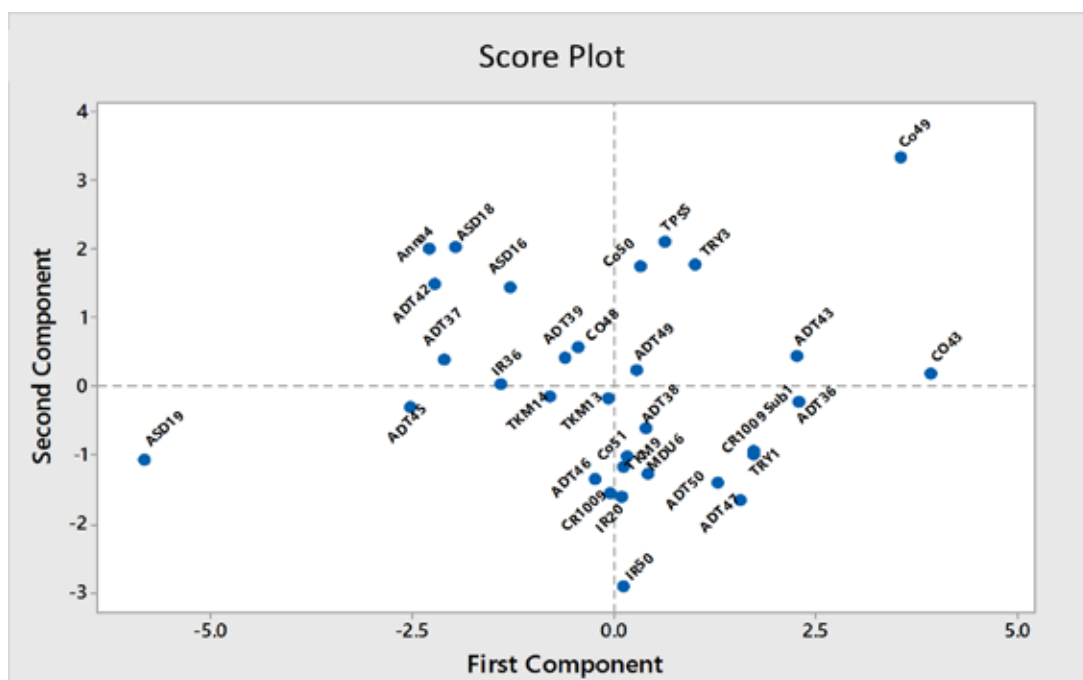


Fig. 2. Score plot for the first two principal components

The score plot of 32 cultivars using the first two principal components are presented in **Fig. 2**. Cultivar CO 43 recorded extremely high PC1 value and CO 49, followed by CO 43 showed high PC 2 value. ASD 19 gave very low value for both components indicating the poor performance for characters contributing to variation and yield.

## REFERENCES

- Annual report 2067-17. GOI. [www.agricoop.nic.in](http://www.agricoop.nic.in)
- Bardenas, E.A. and T.T. Chang. 1965. Morphology and Varietal Characteristics of the Rice Plant. *The Int. Rice Res. Inst.*, (4)
- Bose Kumar, L. and S. Pradshan. 2006. Genetic divergence in deepwater rice genotypes. *J. Cent. Europ. Agric.*, **6**:635-640
- Caldo, R., L. Sebastian and J. Hernandez. 1996. Morphology-based genetic diversity analysis of ancestral lines of Philippine rice cultivars. *Philippine J. Crop Sci.*, **21**:86-92.
- Hoque, Ahasanul, S. N. Begum, A. H. K. Robin, and L. Hassan. 2015. Partitioning of Rice (*Oryza sativa* L.) Genotypes Based on Morphometric Diversity. *American J. Exp. Agric.*, **7** (4): 242-250. [\[Cross Ref\]](#)
- Jolliffe, I. 2002. Principal component analysis, Wiley Online Library.
- Mahajan, R. and D. Mehan. 1980. Principal component analysis in rice. *Crop Improv.*, **7**:83-87.
- Mahalanobis, P. 1928. Statistical study of the Chinese head. *Man in India*. **8**:107-108p.
- Maji, A. T., and Shaibu, A. A. 2012. Application of principal component analysis for rice germplasm characterization and evaluation. *Journal of Plant Breeding and Crop Science*, **4**(6), 87-93. [\[Cross Ref\]](#)
- McCouch, S. R., M. Sweeney, J. Li, H. Jiang, M. Thomson, E. Septiningsih, ... and Tai, T. 2007. Through the genetic bottleneck: *O. rufipogon* as a source of trait-enhancing alleles for *O. sativa*. *Euphytica*, **154**(3): 317-339. [\[Cross Ref\]](#)
- Neethu-Francis, D. Packiaraj, S. Geethanjali and K. Hemaprabha. 2018. Correlation and Path Coefficient Analysis for Yield Contributing Characters in Rice (*Oryza sativa* L.) Cultivars. *Int.J.Curr.Microbiol. App.Sci.* **7**(06): 2292-2296. [\[Cross Ref\]](#)
- Palaniyappan, S., Arunachalam, P., Banumathy, S., Mini, M. L., & S. Muthuramu, 2020. Genetic divergence and clustering studies in advanced breeding lines of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **11**(2):499-504. [\[Cross Ref\]](#)
- Radhamani T.,D. Sassikumar, D. Packiaraj, R.Saraswathi and V. Ravi. 2015. Principal Component Analysis of variation among the induced mutants of rice (*Oryza sativa* L.) *Res. On Crops* **16**(4): 698-703. [\[Cross Ref\]](#)
- Rao, C.R. 1952. Advanced statistical methods in biometric research, John Wiley & Sons, New York.
- Seetharam, K., S. Thirumeni and K. Paramasivam. 2009. Estimation of genetic diversity in rice (*Oryza sativa* L.) genotypes using SSR markers and morphological characters. *African J. Biot.*, **8** (10): 2050-2059
- Sheela, K. R. V., Robin, S. and S. Manonmani, 2020. Principal component analysis for grain quality characters in rice germplasm. *Electronic Journal of Plant Breeding*, **11**(1):127-131. [\[Cross Ref\]](#)
- Tripathi, A., S. Kumar, M. K. Singh, A. Kumar, and M.K. Karnwal, 2017. Phenotypic assessment of rice (*Oryza sativa* L.) genotypes for genetic variability and varietal diversity under direct seeded condition. *J. Applied and Natural Sci.*, **9**(1): 6-8. [\[Cross Ref\]](#)