



# Genetic Diversity Analysis for Yield Associated and Quality Traits in Promising Rice Varieties of Tamil Nadu

M. Vinod Kumar Naik<sup>1\*</sup>, M. Arumugam Pillai<sup>2</sup> and S. Saravanan<sup>3</sup>

<sup>1</sup>Dept. of Genetics and Plant Breeding, S.V. Agricultural College, Acharya NG Ranga Agricultural University (ANGRAU), Tirupati (517 502), India

<sup>2</sup>Dept. of Genetics and Plant Breeding, AC& RI, Tamil Nadu Agricultural University (TNAU), Killikulam (628 252), India

<sup>3</sup>Dept. of Genetics and Plant Breeding, AC& RI, Tamil Nadu Agricultural University (TNAU), Killikulam (628 252), India

## Open Access Corresponding Author

M. Vinod Kumar Naik

e-mail: [vinod.naik2014ag@gmail.com](mailto:vinod.naik2014ag@gmail.com)

**Citation:** Naik et al., 2021. Genetic Diversity Analysis for Yield Associated and Quality Traits in Promising Rice Varieties of Tamil Nadu. *International Journal of Bio-resource and Stress Management* 2021, 12(4), 361-369. [HTTPS://DOI.ORG/10.23910/1.2021.2300](https://doi.org/10.23910/1.2021.2300).

**Copyright:** © 2021 Naik et al. This is an open access article that permits unrestricted use, distribution and reproduction in any medium after the author(s) and source are credited.

**Data Availability Statement:** Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

**Conflict of interests:** The authors have declared that no conflict of interest exists.

**Acknowledgement:** The Agricultural College and Research Institute, Tamil Nadu Agricultural University (TNAU), Killikulam-628252, to conduct present work as part of M.Sc agriculture thesis, is duly acknowledged.

## Abstract

An experiment was conducted with 55 rice varieties to assess the genetic diversity by using Mahalanobis D<sup>2</sup> Statistical and characterization of genotypes using principal component analysis. All genotypes exhibited a wide and significant variation for 19 traits, by cluster analysis grouped into ten clusters. The maximum genotypes were included in Cluster 6 (16) followed by cluster 4 (10), cluster 3 (8), cluster 2 (7), cluster 5 (5), cluster 8 (4), cluster 1 (2), with 29.09, 18.18, 14.54, 12.72, 9.09, 7.27 and 3.63 proportion respectively, the rest of three clusters had one genotype each. Maximum cluster distance obtained between cluster V constituted by single entry (Pusa Basmati) showed highest inter cluster distance from cluster V (20727.37), VII (18414.79), I (17228.89) and cluster III (17010.24) are having very high inter cluster distance and also by cluster IX from cluster VIII (8852.36), VI (7559.67), I (7444.68) and cluster VII (6666.83) followed by cluster VI from cluster V (6225.95). The lowest inter cluster distance was observed between cluster II and cluster IV III and VI followed by between cluster I and cluster VIII, XI, II, VI and cluster IV. The intra cluster D<sup>2</sup> values ranged from Zero (Cluster VII, IX, X) to 2233.91 (Cluster VIII). Contribution of amylose content was highest towards genetic divergence (23.43%) by taking 348 times ranked first followed by days to 50% flowering (23.37%) by 347 times, single plant yield (23.3%) by 346 times. The PCA analysis showed that first eight principal components accounted for about 85.4%.

**Keywords:** Cluster mean, D<sup>2</sup> analysis, PCA, rice, variability

## 1. Introduction

Rice (*Oryza sativa* L.) is one of the major staple foods for over half of the world's population. Almost 90% of the world's rice is cultivated and consumed in Asia, where 50% of the population depends on rice for food reported by Tenorio et al., 2013. It occupies almost one-fifth of the total land area covered under cereals reported by Gaballah et al., 2020. Rice crop is cultivated in extremely different situations ranged from flooded wetland to rain fed dry land reported by Degenkolbe et al., 2009. Irrigated rice which accounts for 55% of the global rice area provides 75% of the production and consumes about 90% of the freshwater resources used for agriculture in Asia reported by Wu et al., 2020. The development of

## Article History

RECEIVED on 22<sup>nd</sup> April 2021

RECEIVED in revised form on 29<sup>th</sup> July 2021

ACCEPTED in final form on 19<sup>th</sup> August 2021



high yielding varieties widely adapted pure line rice varieties together with advances in production technology has enabled us to meet with the demand of rice to a satisfactory level. However rapidly increasing demand due to ever-increasing Indian population has put on us to search for another quantum jump in rice production. The projection of India's rice production target for 2030 A.D is 120 million tonnes which can be achieved only by increasing the rice production by over 2.0 million tonnes /year in the coming decade reported by Viraktamath and Shobha Rani, 2008. Genetic diversity is a prerequisite for any crop improvement program and helps in development of superior segregants reported by Bhandari et al., 2017. The study of the level and patterns of genetic divergence in the rice genotype provides knowledge and idea of the genetic variability reported by Bhati et al., 2015. The significance of genetic diversity in selecting parents to get better transgressive segregants has been repeatedly reported by many workers (Devi et al., 2016). The crosses among parents with maximum genetic divergence are better responsive in genetic improvement (Govindaraj et al., 2014). The multivariate analysis developed by Mahalanobis (1936), has been found to be most suitable method to quantify the degree of divergence in different germplasm.

The existence of genetic variability for morphological, yield associated components and quality traits are fore most important for identification and development of desirable genotypes. To improve any trait is always depend on the sum of genetic variability present in the experimental material. Genetic diversity represents heritable variation within and between populations and the correlation between genetic distances is most important for determining breeding strategies, to classify the parental lines, defining heterotic groups, and predicting future hybrid performance reported by Acquah, 2012. Genetic distance estimates for population grouping can be estimated by different methods as it is crucial to understand the usable variability existing in the population panel reported by Nachimuthu et al., 2014. Multivariate statistical tools consist of Principal Component Analysis (PCA), Cluster analysis and discriminate analysis reported by Oyelola, 2004. Principal component analysis (PCA) analyses data consisting of several intercorrelated quantitative dependent variables as observations reported by Mahendran et al., 2015. The primary benefit of PCA is to quantify the significance of each dimension for relating the variability of a dataset (Shoba et al., 2019). Principal Component Analysis (PCA) could be used to reveal patterns and eliminate redundancy in data sets and variations routinely occur in crop species for yield and grain quality reported by Maji and Shaibu, 2012. Principal components are generally estimated using the correlation matrix.

## 2. Materials and Methods

The present experiment was conducted during *Kharif*, (May to July) 2016 at Agricultural College and Research Institute

located in 8°46' N latitude and 77°42' E longitude and at an altitude of 40 m above Mean Sea Level (MSL), Killikulam, Tamil Nadu Agricultural University, Tamil Nadu, India. The experimental material comprised of 55 rice genotypes collected from department of Genetics and plant breeding and laid out in randomized block design with two replications. Each plot consists of 3 rows of 2 m length. Eighteen days aged seedlings were transplanted with a spacing of 20 cm between rows and 15cm between plants with the application of fertilizers NPK at the rate of 120:60:40 kg ha<sup>-1</sup> respectively and the recommended agronomic practices were followed to raise a healthy crop. A combination of 10 plants from the middle row avoiding border plants was used to record observations on the plants for yield associated components like days to 50% flowering, plant height (cm), Number of productive tillers, panicle length (cm), Number of filled grains panicle<sup>-1</sup>, 1000 grain weight (g) and single plant yield (g).

Physicochemical and cooking quality characters the data was recorded for viz., milling percent (%), head rice recovery (%), grain length (mm), grain width (mm), length/breadth ratio, Grain length after cooking (mm), Grain breadth after cooking (mm), Linear elongation ratio, Breadth wise elongation ratio, alkali spreading value (ASV), Gel consistency (mm) and Amylose content. Observations of hulling cum milling were taken with the help of Satake Company make laboratory huller cum polisher, data on head rice recovery was recorded. Kernal length and kernel width of 10 whole milled rice were measured by means of graph sheet and length and breadth ratio was computed as per Murthy and Arunachalam (1967). Observations of the length and breadth of cooked Kernels and elongation ratio were recorded with the help of graph sheet to quantify cooking traits, while the volume expansion ratio, alkali spreading, gel consistency and amylose content value by following the standard procedures.

The analysis of variance, Cluster analysis and principal component analysis were performed to detect the diversity of genotypes and the contribution of traits to total divergence respectively using the software Indostat Version 9.2.

## 3. Results and Discussion

The analysis of variance revealed highly significant differences for all 19 characters studied (Table 1) indicating the existence of considerable amount of variability among the genotypes. The examination of results revealed that all the 55 genotypes were grouped into 10 clusters (Table 2; Figure 1) based on D<sup>2</sup> values. The distribution of genotypes indicated that the geographical and genetic diversities were not related to each other and thus forces other than geographical separation, such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation existed which were responsible for diversity. Cluster analysis using average linkage methods based on their similarity through quantitative traits grouped 55 rice genotypes into 10 clusters. Maximum genotypes were included in Cluster 6 (16) followed

Table 1: Analysis of variance (mean squares) for grain yield and quality traits in rice (*Oryza sativa* L.)

Sl. No.	characters	Replication (d.f=1)	Treatments (d.f=54)	Error (d.f=54)
1.	Days to 50% flowering	0.009	580.009**	0.565
2.	Plant height	1.841	358.399**	0.876
3.	No. of productive tillers	1.493	37.645**	0.801
4.	Panicle length	2.660	24.292**	0.076
5.	No. of filled grains	0.073	2146.292**	9.642
6.	1000 grain weight	2.910	10.533**	0.118
7.	Single plant yield	3.231	937.407**	1.036
8.	Milling percentage	2.576	70.126**	0.985
9.	Head ricer recovery	3.834	109.338**	0.370
10.	Grain length	1.089	0.910**	0.002
11.	Grain breadth	0.013	0.105**	0.003
12.	Length/ breadth ratio	0.907	0.611**	0.009
13.	Grain length after cooking	0.138	2.614**	0.011
14.	Grain breadth after cooking	4.759	0.386**	0.004
15.	Linear elongation ratio	1.620	0.028**	0.000
16.	Breadth wise expansion ratio	0.146	0.082**	0.007
17.	Alkali spreading value	0.815	2.088**	0.100
18.	Gel consistency	3.556	191.131**	0.668
19.	Amylose content	0.256	61.953**	0.103

\*: Significant at ( $p=0.05$ ) level; \*\*: Significant at ( $p=0.01$ ) level

by cluster 4 (10), cluster 3 (8), cluster 2 (7), cluster 5 (5), cluster 8 (4), cluster 1 (2), with 29.09, 18.18, 14.54, 12.72, 9.09, 7.27 and 3.63 proportion respectively, the rest of three clusters had one genotype each. These clustering did not follow any pattern with respect to origin.

Table 2: Clustering composition with distribution of 71 genotypes in rice by Tocher method

Cluster No	No of genotypes / Entry no	Genotypes
I	(2) - 42, 44	JGL 1798, IR 20
II	(7) - 15, 25, 21, 2, 45, 12, 24	ASD 20, IR 50, ASD 9, CO 33, ASD 14, ADT 43, ASD 18.
III	(8) - 9, 14, 11, 4, 5, 1, 40, 35	ADT 45, ADT 41, ADT 37, ADT 47, IR 64, IR 64, ADT 38, CO 45.
IV	(10) - 16, 19, 47, 50, 10, 18, 49, 23, 48, 17	MDU 5, TPS 4, IR 72, IRR1 104, Anjali, ASD 7, POKKALI, ASD 1, IR 28, ASD 2.
V	(5) - 52, 54, 55, 53, 13	BRNS (WP) 5, BRNS (WP) 22-2, Krishna Hemavathi (K.H), ASD 19, ADT 48.
VI	(16) - 33, 43, 34, 22, 46, 32, 37, 29, 41, 38, 31, 36, 27, 26, 30, 39	ADT 49, CO 43, JGL 3855, Annada, Jaya, Kavva, CR 1009, CO 50, JGL 3844, CO 49, ADT 46, Abhya, ADT 39, BPT 5204, CO 39, Swarna.
VII	(1)-28	ADT 19
VIII	(4) - 3, 7, 6, 20	ASD 16, ADT 36, ASD 17, TN 1.
IX	(1)-51	TPS 3
X	(1)-8	Pusa Basmati

The discrimination of genotypes into 10 clusters suggested presence of high degree of genetic diversity in the germplasm studied due to presence of substantial genetic diversity among the germplasm lines screened in the present experiment indicates presence of many reserve and good source of traits used in hybridization programmes aimed to isolate desirable segregants for grain yield and for important quality traits. Additionally, the selection and choice of parents mainly depends upon the contribution of characters reported by Devi et al., 2016. The selection of highly diversified genotypes based on genetic divergence analysis would be more successful rather than the choice based on the geographical distances.

These findings are in conformity with the earlier reports advocating lack of parallelism between genetic and geographical diversity in rice the number of clusters formed and genotypes within the cluster indicated that possibility of genetic improvement for yield and quality component reported by Cheema et al., 2004. The probability of obtaining good segregants by crossing the modest diverse genotypes belonging to same cluster are very low.



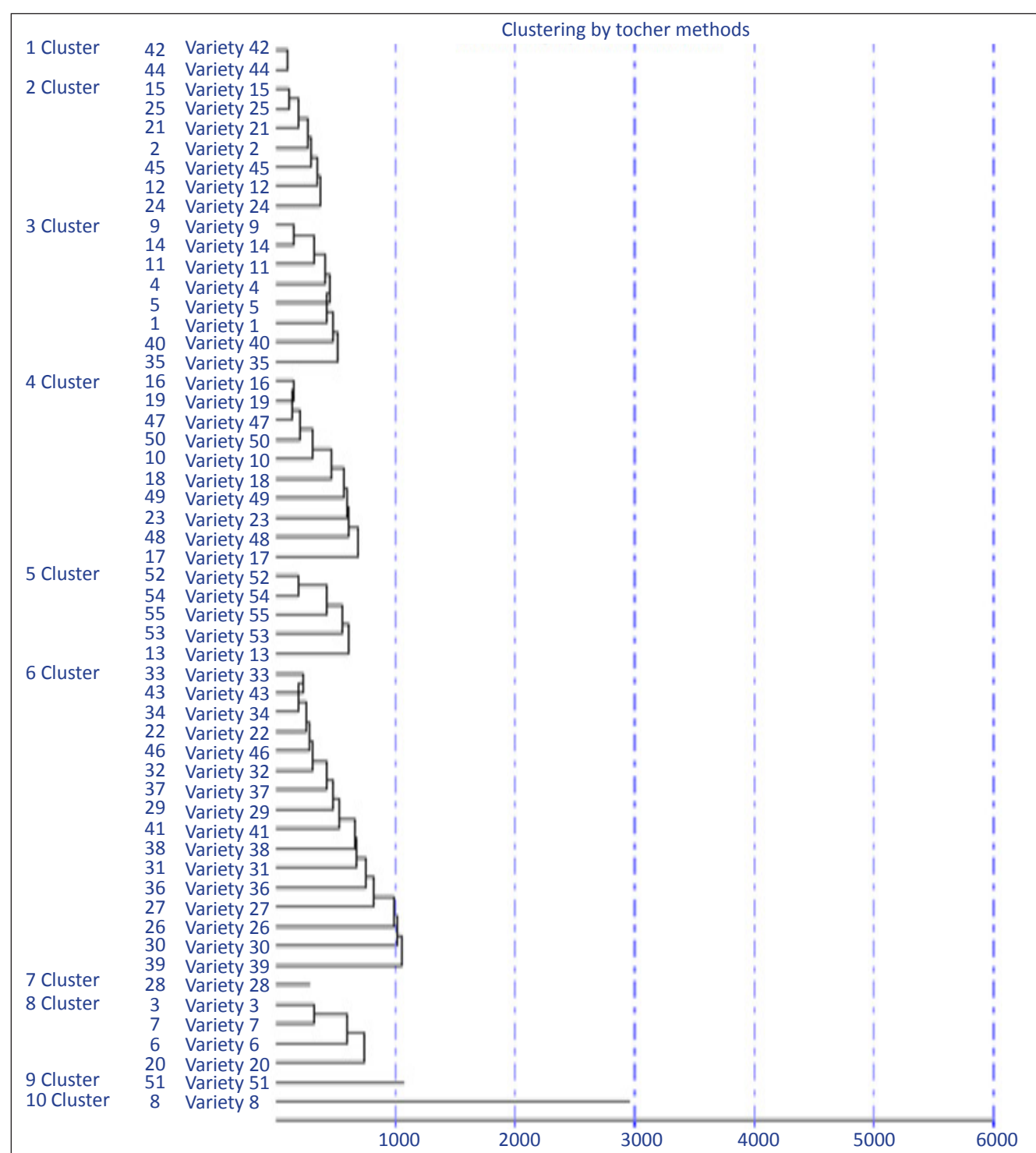


Figure 1: Clustering pattern of 55 Promising varieties in Rice according to Tocher method

The estimates of average intra and inter cluster distance for ten clusters revealed that the genotypes present in a cluster had little genetic divergence from each other with respect to aggregate effect of 19 characters under study while much more genetic diversity was observed between the genotypes belonging to different clusters. The intra and inter cluster distances among the 55 varieties studied were of

varying magnitude (Table 3). The maximum cluster distance was obtained between cluster X constituted by single entry (Pusa Basmati) which showed highest inter cluster distance from cluster V (20727.37), cluster VII (18414.79), cluster I (17228.89) and cluster III (17010.24) are having very high inter cluster distance. High inter-cluster distances were also shown by cluster IX from cluster VIII (8852.36), cluster VI (7559.67),



Table 3: Intra-Inter cluster distances among ten clusters in 55 genotypes of rice (*Oryza sativa* L.)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	257.34	2425.75	3088.01	2615.26	3016.27	2424.39	2311.24	2328.58	7444.68	17228.89
Cluster II		1000.52	2197.13	2134.64	3803.03	2738.9	4736.6	4411.77	4368.3	12640.83
Cluster III			1426.09	3625.75	4947.89	3182.95	4299.66	3185.67	5824.75	17010.24
Cluster IV				1578.62	3265.27	3688.09	3965.84	4421	4387.79	15063.1
Cluster V					1789.75	6225.95	4465.19	4889.02	4538.22	20727.37
Cluster VI						2138.1	3594.83	4122.25	7559.67	12870.08
Cluster VII							0	2462.73	6666.83	18414.79
Cluster VIII								2233.91	8852.36	22336.1
Cluster IX									0	15102.47
Cluster X										0

cluster I (7444.68) and cluster VII (6666.83) followed by cluster VI from cluster V (6225.95).

Greater the distance between two clusters wider the genetic diversity between the genotypes of those clusters and such highly divergent high performing genotypes are useful in recombination breeding programme consecutively to get high heterotic recombinants. The lowest inter cluster distance was observed between cluster II and cluster IV (2134.64), III (2197.13) and VI (2738.9) followed by between cluster I and cluster VIII (2311.24), XI (2328.58), II (2425.75), VI (2424.39) and cluster IV (2615.26) indicates the genotypes included in them were closely related. Selection of parents from genetically homogeneous clusters should be avoided to maintain relatively broad genetic base. To get maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters, however not only high heterosis but also quality characters is important objective for a plant breeder.

Keeping in view it is indicated that hybridization between the genotypes of clusters X i.e., Pusa Basmati of cluster V with BRNS (WP) 5, ASD 19, BRNS (WP)22-2 and Krishna Hemavathi (K.H), cluster VII with ADT 19, cluster I with JGL 1798 and IR 20 and cluster III with 8 genotypes. Cluster IX with cluster VIII ASD 16, ASD 17 and TN 1 genotypes, cluster VI with 16 genotypes, with JGL 1798 and IR 20 of cluster I genotypes, ADT 19 of cluster VII and cluster VI with 5 genotypes of cluster V are expected to produce highly heterotic hybrids. The genotypes of these high divergent clusters can be used as parents in the crossing programme to generate breeding material with high genetic diversity.

The intra cluster  $D^2$  values ranged from Zero (Cluster VII, IX, X to 2233.91 (Cluster VIII). Maximum intra cluster distance was observed in cluster VIII (2233.91) followed by Cluster VI (2138.1), cluster V (1789.75), cluster IV (1578.62) and cluster III (1426.09) indicating that some genetic diversity still exist among the genotypes within each of the clusters.

Cluster mean analysis shown a wide range of variation for all 19 traits under study (Table 4). The minimum and maximum cluster means were distributed in relatively distant clusters. Cluster VIII recorded highest cluster means for number of filled grains and grain breadth after cooking and second highest cluster means for single plant yield, 1000 grain weight and grain breadth. Cluster X recorded higher cluster means for days to fifty % flowering, plant height, panicle length, grain length, L/B ratio, grain length after cooking, linear elongation ratio and alkali spreading value, while cluster IX for number of productive tillers, 1000 grain weight, breadth wise expansion ratio and amylose content and second highest mean for milling percentage, head rice recovery, grain length, L/B ratio and alkali spreading value. Cluster V desirable for early flowering, recorded high cluster mean for milling percentage and grain breadth, second high cluster mean for breadth wise expansion ratio and number of productive tillers.

Cluster III was characterised by high single plant yield (77.8) and moderate means for rest of characters. Cluster VII recorded high mean cluster for head rice recovery, second highest cluster mean for panicle length, number of filled grains, grain length after cooking with medium gel consistency and low amylose content. Cluster IV observed early flowering with second high cluster mean for grain breadth after cooking, cluster VI recorded second highest cluster mean for days to fifty % flowering and plant height traits, cluster II showed high cluster mean for gel consistency (98.04) and second high cluster mean for amylose content, low milling percentage. Cluster I recorded lowest cluster means for number of productive tillers, panicle length, 1000 grain weight, grain length, alkali spreading value, second highest cluster mean for linear elongation ratio and gel and moderate mean values for rest of the characters.

The utility of  $D^2$  statistics is a potential tool to enumerate the extent of genetic diversity in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to

Table 4: Estimation of mean values to ten clusters by Tocher's method for 55 genotypes of rice for yield and quality traits (*Oryza sativa* L.)

	DFF	PH	NPT	PL	NFG	1000GWT	SPY	MP	HRR	GL
Cluster 1	107.5	101.84	10.1	20.43	133.32	19.98	28.21	65.02	60	4.68
Cluster 2	96.64	95.13	16.38	24.31	136.49	20.95	47.44	60.01	52.58	5.29
Cluster 3	103.94	98.15	17.5	25.36	144.55	22.17	77.8	68.71	63.12	5.22
Cluster 4	84.25	108.97	13.17	24.02	105.34	22.72	30.27	68.07	62.39	5.57
Cluster 5	81.7	78.96	19.84	20.62	95.98	21.68	28.04	72.97	68.44	5.43
Cluster 6	121.72	111.56	13.87	26.35	128	21.64	42.63	64.24	56.21	5.14
Cluster 7	114	98.09	13.45	28.73	155.74	21.7	41.4	76	72.15	5.3
Cluster 8	107.75	97.91	16.24	22.37	156.88	23.13	67.08	71.18	63.7	4.84
Cluster 9	85	92.7	27.5	23.3	124	27.35	47.1	72.85	69.5	6.8
Cluster 10	124	119.1	11.95	30.7	86	21.35	21.11	61.8	45.65	8.85

Table 3: Continue...

	GB	LB	GLAC	GBAC	LER	BER	ASV	GC	AC
Cluster 1	1.68	2.79	7.23	2.88	1.55	1.72	2.5	95.38	22.1
Cluster 2	1.99	2.68	7.59	3.34	1.44	1.7	4.86	98.04	30.4
Cluster 3	1.91	2.76	7.52	3.24	1.45	1.73	4.25	95.43	27.97
Cluster 4	2.11	2.66	7.73	3.64	1.39	1.72	4.55	92.98	27.12
Cluster 5	2.18	2.54	6.48	2.7	1.18	2.07	3.7	88.76	23.53
Cluster 6	1.86	2.8	7.5	3.17	1.47	1.71	4.38	89.79	26.22
Cluster 7	1.65	3.25	7.75	3.05	1.45	1.85	4	59	14.8
Cluster 8	2.16	2.24	7.05	3.69	1.46	1.71	3.38	86.25	16.84
Cluster 9	2.1	3.35	7.15	2.75	1.04	2.49	5	56.35	33.15
Cluster 10	1.5	5.72	14.7	2.05	1.67	1.33	6	93.85	25.1

total genetic divergence reported by Devi et al., 2016. The appearance of number of times that each of 19 characters appeared in first time and its respective present contribution towards genetic divergence is presented in Table 5. Contribution of amylose content was highest towards genetic divergence (23.43%) by taking 348 times ranked first followed by days to 50% flowering (23.37%) by 347 times, single plant yield (23.3%) by 346 times, head rice recovery (5.86%) by 87 times, plant height (5.32%) by 79 times, gel consistency (5.19%) by 77 times, grain length (4.51%) by 67 times, panicle length (3.97%) by 59 times, grain length after cooking (1.82%) by 27 times, grain breadth after cooking (1.28%) by 19 times, 1000 grain weight (1.01%) by 15 times, number of filled grains (0.61%) by 9 times. Number of productive tillers, milling percent, grain breadth, Length/breadth ratio exhibited zero contribution and linear elongation ratio (0.7%), breadth wise expansion ratio (0.13%) and alkali spreading value (0.13%) exhibited low contribution.

The PCA analysis showed that the first eight principal components accounted for about 85.4% of the total variation and exhibited very high correlation among them (Table 6). The first, to eighth principal components explained about

Table 5: Contribution of different characters towards genetic divergence in 55 genotypes of rice (*Oryza sativa* L.)

Sl. No.	Source	Timesranked 1 <sup>st</sup>	Contribution %
1.	DFF	347	23.37
2.	PH	79	5.32
3.	NPT	-	-
4.	PL	59	3.97
5.	NFG	9	0.61
6.	1000GWT	15	1.01
7.	SPY	346	23.3
8.	MP	-	-
9.	HRR	87	5.86
10.	GL	67	4.51
11.	GB	-	-
12.	LB	-	-
13.	GLAC	19	1.28
14.	GBAC	27	1.82

Table 5: Continue...



Sl. No.	Source	Timesranked 1 <sup>st</sup>	Contribution %
15.	LER	1	0.07
16.	BER	2	0.13
17.	ASV	2	0.13
18.	GC	77	5.19
19.	AC	348	23.43

23.9, 39.7, 51.5, 60.7, 68.7, 75.6, 81 and 85.4 of the variation obtained in the Eigen vector analysis. In the first PC, days to 50% flowering, Plant height, panicle length, l/b ratio, grain length after cooking and linear elongation ratio were more important contributing traits. Similarly, number of filled grains per panicle, grain breadth after cooking and linear elongation ratio for second PC, while third PC was characterized by 50% flowering, number of filled grains per panicle, single plant yield, milling percentage, head rice recovery and grain

breadth were important parameters. Number of productive tillers, number of filled grains panicle<sup>-1</sup>, single plant yield, alkali spreading value and amylose content were important contributing characters in PC4. In PC 5 1000 grain weight and grain breadth after cooking were important traits. In PC6 milling percentage, head rice recovery, grain length after cooking, breadth wise expansion ratio and gel consistency were contributing important traits. Plant height, milling percentage, head rice recovery and amylose content were important traits in PC7, in PC8 number of productive tillers, panicle length and milling percentage were important contributing traits. Similarly, days to 50% flowering, grain length after cooking and linear elongation ratio in PC1, PC2, single plant yield in PC3, PC4, number of filled grains per panicle, single plant yield, milling percentage, head rice recovery and grain breadth after cooking traits were contributed by PC3 Based on the principal components mean genotypic scores were computed. Principal factor scores for all the 55 genotypes were utilized

Table 6: Eigen vectors and eigen values of first eight principal components of 19 traits of in rice (*Oryza sativa* L.)

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen values	4.538	2.997	2.249	1.749	1.53	1.294	1.025	0.853
Proportion	0.239	0.158	0.118	0.092	0.081	0.068	0.054	0.045
Cumulative Proportion	23.9	39.7	51.5	60.7	68.7	75.6	81	85.4
DFF	0.268	0.133	0.291	-0.103	0.014	-0.172	0.266	-0.216
PH	0.286	0.09	-0.133	-0.123	0.223	-0.112	0.539	0.096
NPT	-0.229	-0.125	0.115	0.367	-0.162	-0.315	-0.094	0.413
PL	0.246	0.046	0.003	-0.114	0.079	-0.453	-0.058	0.55
NFG	0.069	0.247	0.374	0.384	0.132	0.093	-0.026	-0.21
1000GWT	-0.022	-0.088	-0.078	0.139	0.617	-0.148	0.229	-0.138
SPY	0.004	0.18	0.347	0.533	0.099	0.068	-0.051	0.117
MP	-0.263	-0.174	0.266	-0.141	0.125	0.341	0.29	0.291
HRR	-0.309	-0.159	0.233	-0.07	0.069	0.284	0.365	0.24
GL	0.157	-0.48	-0.104	0.083	0.191	0.143	-0.17	0.018
GB	-0.285	0.132	-0.36	0.038	0.261	0.066	-0.139	0.14
LB	0.29	-0.42	0.147	0.018	-0.029	0.046	-0.062	-0.055
GLAC	0.349	-0.285	0.004	0.018	0.145	0.252	-0.198	0.096
GBAC	-0.053	0.364	-0.23	0.007	0.374	0.18	-0.165	0.043
LER	0.343	0.255	0.177	-0.068	-0.013	0.184	-0.024	0.113
BER	-0.285	-0.227	0.004	0.066	-0.03	-0.26	0.121	-0.445
ASV	0.154	-0.181	-0.22	0.425	0.148	0.003	0.072	-0.013
GC	0.13	0.115	-0.303	0.176	-0.338	0.439	0.149	0.009
AC	0.093	-0.012	-0.325	0.347	-0.293	-0.061	0.439	0.086

Where DFF: Days to 50% flowering; PH: Plant height; NPT: Number of productive tillers; PL: Panicle length; NFG: Number of filled grains; 1000 GWT: 1000 grain weight; SPY: Single plant yield; MP: Milling percentage; HRR: Head rice recovery; GL: grain length; GB: Grain breadth; L/B ratio: Length/ breadth ratio; GLAC: Grain length after cooking; GBAC: Grain breadth after cooking; LER: Linear elongation ratio; BER: Breadth wise expansion ratio; ASV: Alkali spreading Value; GC: Gel consistency; AC: amylose Content



to construct precise 3D plot (Figure 2) all the genotypes were plotted for PC1, PC2, PC3, PC4, PC5, PC6, PC7 and PC8 which completely explained 85.4% variability which accounts for all 19 characters. In component based genotypic scoring ASD 20, MDU 5 in PC1, Krishna hemavathi (K.H) in PC3 showed maximum score while TPS 3 in PC6 and BRNS (WP) 22-2 in PC8 recorded minimum score. The genotypes Pusa Basmati,

BRNS (WP) 5, ASD 19, BRNS (WP) 22-2 and Krishna Hemavathi (K.H), having maximum genetic divergence with high mean values for yield contributing characters and quality traits can be utilized in the breeding programmes. However, crossing of the genotypes with diverse local and popular cultivars may also give potential transgressive segregants with high yield.

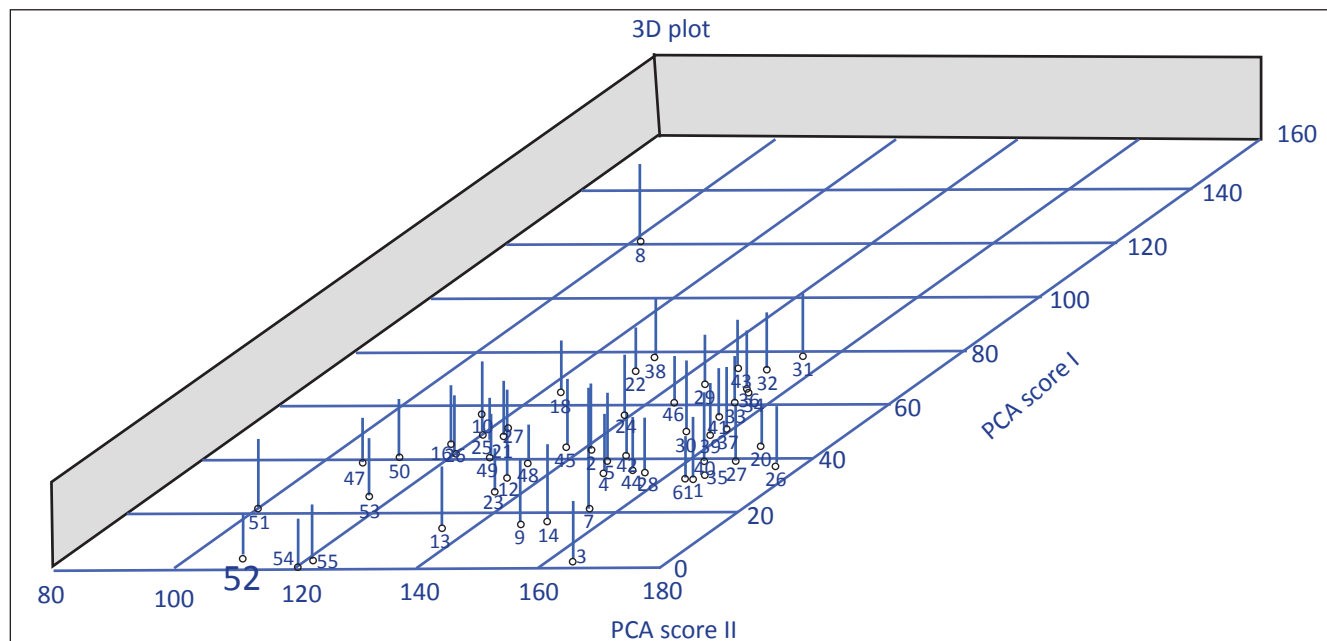


Figure 2: Three-dimensional graph of 55 promising varieties in Rice based on yield and quality traits (principal component analysis)

#### 4. Conclusion

The parents for hybridization programme should be selected based on the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance having maximum heterosis. Pusa Basmati, BRNS (WP) 5, ASD 19, BRNS (WP) 22-2 and Krishna Hemavathi (K.H), having maximum genetic divergence with high mean values for yield contributing characters and quality traits could be utilized in the breeding programmes.

#### 5. Acknowledgement

The Agricultural College and Research Institute, Tamil Nadu Agricultural University (TNAU), Killikulam-628252, to conduct present work as part of M.Sc agriculture thesis, is duly acknowledged.

#### 5. References

- Acquaah, G., 2012. Principles of plant genetics and breeding. Second edition. Wiley-Blackwell publications, 127–129.
- Bhati, P.K., Singh, K.S., Dhurai, S.Y., Sharma, A., 2015. Genetic divergence for quantitative traits in rice germplasm. *Electronic Journal of Plant Breeding* 6(2), 528–534.
- Cheema, A., Rashid, A., Ashraf, M., Qatar, Z.U., 2004. Genetic divergence in rice collection. *Pakistan Journal of Botany* 36(3), 557–566.
- Degenkolbe, D.O., Zuther, P.T., Repsiber, T., Walther, E.D., Hinch, G.D.K., Kohl, K.I., 2009. Expression profiling of rice cultivars differing in their tolerance to long term drought stress. *Plant Molecular Biology* 69, 133–153.
- Devi, R.K., Parimala, K., Cheralu, C., 2016. Assessment of genetic diversity and other genetic parameters in exotic germplasm of rice. *Bioinfolet* 13(18), 190–196.
- Gaballah, M.M., Azza, M.M., Milan, S., Hassan, M.M., Marian, B., Abagh, E.L.A., Fayed, M.A., 2020. Genetic diversity of selected rice genotypes under water stress conditions. *Plants* 10(1), 27. <https://doi.org/10.3390/plants10010027>.
- Bhandari, H.R., Bhanu, A.N., Srivastava, K., Singh, M.N., Shreya, Hemantaranjan, A., 2017. Assessment of genetic diversity in crop plants - an overview. *Advances in Plants Agriculture Research* 7(3), 279–286.
- Govindaraj, G., Vetriventhan, M., Srinivasan, M., 2014. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics Research International*, 15(15), 1–15.



- Mahalanobis, P.C., 1936. On the generalized distance in statistics. Proceedings of national academy of sciences India 2, 49–55.
- Mahendran, R., Veerabhadhiran, P., Robin, S., Raveendran, M., 2015. Principal component analysis of rice germplasm accessions under high temperature stress. International Journal of Agricultural Science and Research 5(3), 355–360.
- Maji, A.T., 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.
- Murthy, B.R., Arunachalam, V., 1966. The nature of genetic diversity in relation to breeding system in crop plants. Indian Journal of Genetics 26, 188–198.
- Nachimuthu, V.V., Robin, S., Sudhakar, D., Raveendran, M., Rajeswari, S., Manonmani, S., 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. Indian Journal of Science and Technology 7(10), 1555–1562.
- Oyelola, B.A., 2012. The Nigerian statistical association preconference workshop, University of Ibadan, 20–21.
- Shoba, D., Vijayan, R., Robin, S.I., Manivannan, N., 2019. Assessment of genetic diversity in aromatic rice (*Oryza sativa* L.) germplasm using PCA and cluster Analysis. Electronic Journal of Plant Breeding 10(3), 1095–1104.
- Tenorio, F.A., Ye, C., Redona, E., Sierra, S., Laza, M., Argayoso, M.A., 2013. Screening rice genetic resources for heat tolerance. Sabrao Journal of Breeding and Genetics 45(3), 371–381.
- Viraktamath, B.C., Shobha Rani, N., 2008. Rice: Pivotal position achieved by contribution of factors. The Hindu survey of Indian Agriculture 5, 22–24.
- Wu, X.H., Wang, W., Yin, C.M., Hou, H.J., Xie, K.J., Xie, X.L., 2017. Water consumption, grain yield, and water productivity in response to field water management in double rice systems in China. PLoS ONE 12(12), e0189280.

