GENETIC DIVERSITY STUDIES IN RICE LANDRACES (*Oryza sativa* L.) BASED ON MAHALANOBIS D^2 DISTANCE

ABSTRACT

The present investigation was carried out to assess the genetic diversity present among 66 rice landraces along with 4 checks for 14 different quantitative traits. All the genotypes were grouped into 5 clusters by performing Tocher's clustering method using Mahalanobis D^2 distance. Cluster I was the largest, comprising of 34 genotypes, followed by Cluster II with 28 genotypes. The maximum genetic distance (D^2) was observed between cluster V an III (6243.98), followed by clusters II and III (6166.44), clusters IV and II (6022.47), clusters I and IV (4544.26) and clusters IV and III (4161.67). The results revealed the highest contribution of plant height (25.50%) towards total diversity, followed by days to 50% flowering kernel (3.18%), grain yield per plant (2.42 %) and days to maturity (2.06). The rice genotypes belonging to the clusters III , IV and V were found to be the most divergent, and hence can be utilised in the recombination breeding programmes to exploit maximum heterosis.

KEY WORDS: *Cluster, Genetic diversity; Mahalanobis D^2 statistics, Rice, Landrace.*

1. INTRODUCTION

India's main food crop is rice (Oryza sativa L.). It belongs to the Oryzoideae subfamily of the Gramineae. Oryza sativa and Oryza glaberrima are two of the 23 species in the genus, according to D. Chatterjee [1], 21 of which are wild. In India, rice is referred to as "Prana," which means "breath of life." 700 million tonnes of rice are produced annually on 158 million hectares of land worldwide. 114 of the 193 countries in the world's population grow it. But more than 90% of the world's rice is produced and consumed in

Asia. More over half of the world's rice-growing acreage and 56% of its rice production are in China and India (Patra) [2]. With an area, production, and productivity of 43.80 million ha, 118.88 million tonnes, and 2650 Kg ha-1, respectively, India is one among the world's top producers of rice. Nearly all of the states in India, including Telangana, Andhra Pradesh, Bihar, Uttar Pradesh, Maharashtra, and West Bengal, cultivate rice. Out of these, West Bengal and Uttar Pradesh generate the most rice. The production and productivity of rice in Telangana State, however, is 60.50 million tonnes and 3550 kg ha-1 on an area of 1.8 million ha. With an increasing area of 55.50 lakh acres in kharif and 54.30 lakh acres in rabi, Telangana is gradually becoming known as the "Rice Bowl of India".

The first and most important step in any crop improvement programme is genetic diversity analysis. There are several important applications for genetic diversity among genotypes in crop improvement. This information can be used to classify germplasm for cultivar identification, assist in parent selection for hybridization, and reduce the number of genotypes required to sample a wide range of genetic variability. A genetically diverse parent is required to increase the likelihood of selecting better segregants for various characters. Multivariate analysis, such as Mahalanobis [3] D^2 statistics, is extensively used in genetic divergence research findings to group genotypes so that more diverse genotypes are grouped into the most distant clusters. It is also useful in determining the relative contribution of each trait to total divergence.

1. MATERIAL AND METHODS

The material used in the present investigation comprised of 70 genotypes which included 66 rice land races and 04 Standard check varieties (Chittimutyalu, DRR Dhan 45, BPT5204 and Zincorice). The experiment was carried out during *kharif*, 2021, at Agricultural College, Aswaraopet, which is situated at an altitude of 64 m above mean sea level on 18°

80' N latitude and 7° 55' E longitudes in Northern Zone of Telangana State. The experimental material was planted in a Augmented block design, Standard check varieties replicated into 3 times. Each replication consisted of three rows of 1 m length with a spacing of 20 cm between the rows and 15 cm between the plants. All required precautions were taken to ensure a uniform plant population in each treatment per replication. Five plants were selected at random and observations were recorded from each replication. The characters studied were Days to 50% flowering, Days to maturity, Plant height (cm), Panicle length (cm), Number of panicles per plant, Number of filled grains per panicle, Grain length (mm), Grain width (mm), 1000 grain weight (g), Kernel length (mm), Kernel breadth (mm), Grain iron content (ppm), Grain zinc content (ppm) and Grain yield per plant (g).The recorded data was subjected to analysis of variance and Mahalanobis D^2 statistics were used for genetic divergence analysis. Analysis of variance for Augmented Block Design was performesd as per the method suggested by Federer [4]. The genotypes were clustered by using Tocher's method. The intra- and inter-cluster distances were calculated and were used to describe the genotype relationship with the help of the formula proposed by Singh RK and Chaudhary BD [5]. All the above mentioned analyses were performed using INDOSTAT software.

2. RESULTS AND DISCUSSION

Diversity in crops is essential in plant breeding as it provides the basis for selection to sustain high level of production to meet the current demands. Because, the diversity plays an important role in the finding of parents with huge variation for different characters. Genetic diversity is commonly measured by genetic distance or genetic similarity, both implore that there are differences or similarities at the genetic level.The amount of diversity available in a crop determines the success of any crop development program. It is important

to understand the diversity spectrum, as well as the assemblage and assessment of divergence in the germplasm. In the current study, 66 genotypes along with 4 checks used to measure genetic diversity.

3.1 Grouping of genotypes into various clusters

Based on the D^2 analysis using Tocher's method (Rao) [6] genotypes were grouped into 5 clusters (Table 2 and Figure 2). Which cluster I was the largest comprising of 34 genotypes followed by II (28), III (5), IV (2) and V (1) indicating high degree of heterogeneity for those genotypes. Cluster I showed Chittimutyalu, Zincorice and Cluster II showed BPT-5204, DRR Dhan 45.

3.2 Average Intra and inter cluster distances

The average D^2 values within (intra) and between (inter) clusters are given in Table. 1 and Figure. 1 The inter cluster distances were higher than the average intra cluster distances, which indicated wide diversity among the genotypes of different groups than those of the same cluster. Similar results were reported in the studies of Hoque et al. [7].

Maximum differences among the genotypes within the same cluster were shown by cluster IV (897.33) followed by cluster I (875.93), cluster III (861.62) and cluster II (675.59). Solitary cluster (V) showed zero intra cluster distances. Lowest intra cluster value for cluster II indicated that the genotypes included in the group showed closeness between them as compared to the genotypes included in cluster IV which showed maximum divergence within the group. It was reported that genotypes with in a cluster with high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance with regard to yield, provided that there is an adequate complementation.

The inter cluster D^2 values ranged from 2119.94 to 6243.98. Maximum inter cluster D^2 values were observed between cluster III and V (6243.98), cluster II and III (6166.44) and cluster II and IV (6022.47) As, the cluster V is a solitary one, cluster cluster II and III (6166.44) and cluster II and IV (6022.47) were preferred.

The greater the distance between two clusters, the more is the genetic diversity between genotypes. The genotypes in the most divergent clusters may be able to take advantage of the maximum heterosis. It is indicated that hybridization between the genotypes (Haladichudi, Agmakunda) of cluster IV and cluster V (Bhajana), cluster V (Bhajana) and cluster III (Karamguruvay, Esakarvad, Hemberbag, Bahurupi, Mudimurangi), cluster IV (Haladichudi, Agmakunda) and cluster III (Karamguruvay, Esakarvad, Hemberbag, Bahurupi, Mudimurangi), cluster III (Karamguruvay, Esakarvad, Hemberbag, Bahurupi, Mudimurangi) and cluster IV (Haladichudi, Agmakunda). In view of this, genotypes from clusters IV and V, clusters V and III, and clusters IV and III may be used as parents in a hybridization programme to provide breeding material with significant genetic diversity.

Cross combinations with parents from the most divergent clusters are likely to have the most heterosis. The greater the genetic diversity between genotypes, the further apart two clusters are. In view of this, it is indicated that hybridization between the genotypes (Karamguruvay, Esakarvad, Hemberbag, Bahurupi, Mudimurangi) of cluster III with (Haladichudi, Agmakunda) of cluster IV , genotypes(Haladichudi, Agmakunda) of cluster IV with (Bhajana) of cluster of V, (Karamguruvay, Esakarvad, Hemberbag, Bahurupi, Mudimurangi) of cluster III with cluster V (Bhajana), are expected to produce encouraging results. The genotypes of these clusters could be used as parents in a breeding programme to provide high-diversity breeding material.

3.3 Cluster means of the character

From the results of cluster mean generated by Tocher method (Table 3), it can be concluded that considerable differences existed for all the studied traits among the clusters. Cluster mean data indicates days to 50% flowering scoring was highest in cluster IV (101.00) and lowest in cluster V (75.00), days to maturity reading recorded highest in cluster I (129.03) and lowest in cluster V (110.00), plant height reading recorded highest in cluster IV (141.20) and lowest in cluster I (81.58), panicle length was recorded highest in cluster V (23.54) and lowest in cluster II (19.55), number of panicles per plant was recorded highest in cluster I (9.85) and lowest in cluster II (6.18), number of filled grains per panicle was recorded highest in cluster III (129.60) and lowest in cluster II (57.25), grain length was highest in cluster II (8.46) and lowest in cluster IV (7.47), grain width was recorded highest in cluster V (3.83) and lowest in cluster II and III (2.69), 1000 grain weight was recorded highest in cluster IV (23.70) and lowest in cluster V (17.40), kernel length was highest in cluster V (7.11) and lowest in cluster II (6.61), kernel breadth was highest in cluster V (2.14) and lowest in cluster II (1.89), iron content was highest in cluster III (10.68) and lowest in cluster IV (4.75), zinc content was highest in cluster III (20.48) and lowest in cluster IV (11.35) and grain yield per plant was highest in cluster III (25.48) and lowest in cluster IV (15.20). Hence the genotypes from these clusters with suitable trait means can be selected to use in crossing programme to create desirable variations in the breeding material for yield improvement.

3.4 Relative contribution of characters towards genetic divergence

The contribution of different characters towards the total genetic diversity is presented in Table 4. Number of filled grains per panicle (1532 out of 2457 total numbers of combinations) by contributing 63.40 percent to the total divergence of genotypes. This

was followed by plant height (25.50%) by 616 times, days to 50% flowering kernel (3.18%) by 77 times, grain yield per plant (2.42 %) by 60 times, days to maturity (2.06) by 50 times, 1000 grain weight (1.61%) by 39 times, panicle length (1.15) by 28 times, zinc content (0.33) by 9 times, iron content (0.16) by 4 times, kernel breadth (0.06) by 3 times, kernel length (0.05) by 3 times, grain width (0.04) by 3 times, number of panicles per plant (0.03) by 2 times and grain length (0.01) by 1 time ranked least, contributed very less towards divergence. These results are in conformity with the reports given by Banumathy et al. [8] and Vennila et al. [9].

CONCLUSION:

The 70 rice genotypes were grouped into five different clusters based on D^2 values and reported the presence of significant amount of genetic diversity among the genotypes. Cluster I comprising of 34 genotypes was the largest followed by cluster II, III, IV and V. The maximum inter-cluster distance was noticed between cluster III and cluster V (6243.98) followed by cluster II and cluster III (6166.44) and between cluster II and cluster IV (6022.47). Maximum intra cluster differences among the genotypes were observed in cluster IV followed by cluster I, III, II, and V. grain yield per plant, days to 50% flowering, days to maturity, panicle length, number of filled grains per panicle, number of panicles per plant, grain yield per palnt and 1000 grain weight and quality traits *viz.,* grain length, grain width, kernel breadth, kernel length, grain iron content and grain zinc content contributed maximum towards genetic divergence, which can be used in future hybridization programme to obtain transgressive segregants among the nine clusters.

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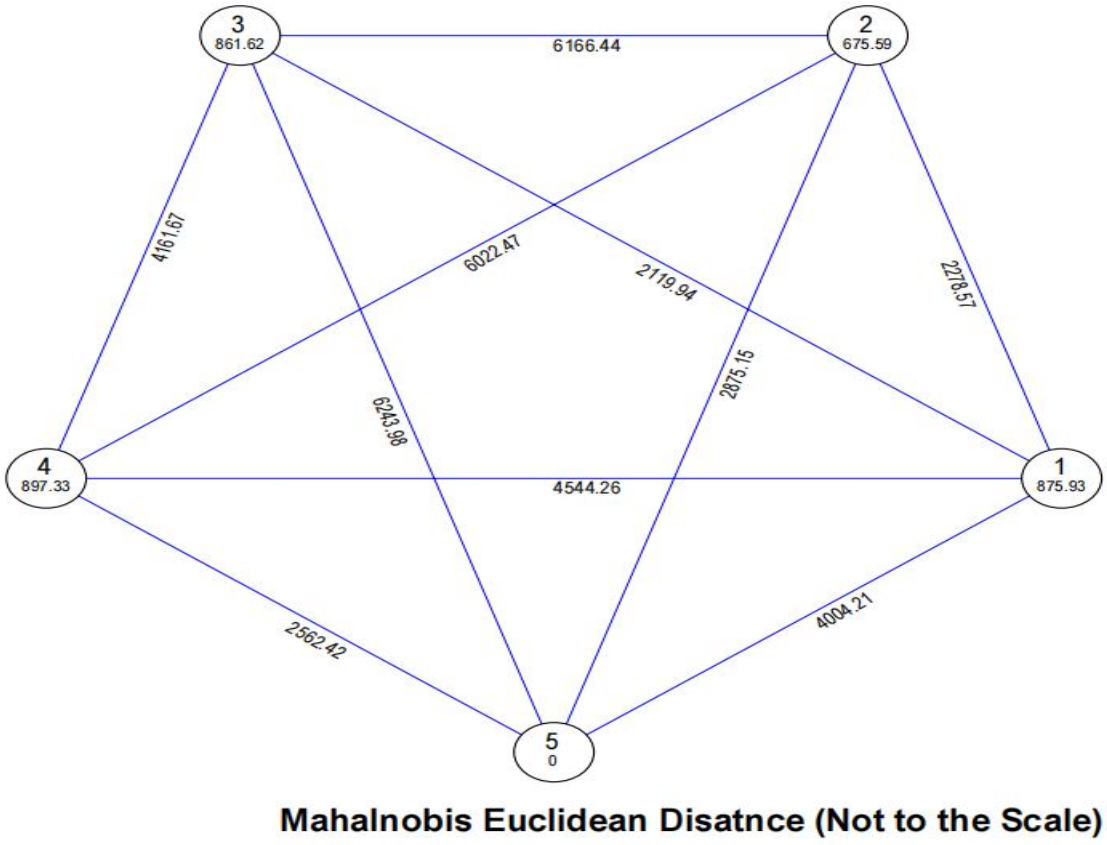

Figure 1. Cluster diagram of 70 rice genotypes based on D^2 values by Tocher method

Table. 1 Average intra (Bold values) and inter-cluster D^2 values for Fourteen characters in 66 genotypes of rice

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	**875.93**	2278.57	2119.94	4544.26	4004.21
Cluster 2		**675.59**	6166.44	6022.47	2875.15
Cluster 3			**861.62**	4161.67	6243.98
Cluster 4				**897.33**	2562.42
Cluster 5					**0.00**

Table. 2 Clustering pattern among 70 rice genotypes

Cluster Number	Number of genotypes in the cluster	Names of the Genotypes
I	34	Panchatantra, Kakirekkalu, , Assamchudi, Bammagutni, , Thonda, Zeerashankar, Kalabatta, Sughandi, Radhajigil, Dhimidi, Kumargorla, Saphari, Jajudhana, Kalalangad, Javapoola, Kudrath, Sonamali, Kundadam, Budamalu, Indrani, Kujipabali, Pohaki, Chinthabarisannalu, Red jasmine, Ambemohar-2, Kouthrimaharaj, Sidhasanna, Ramkul, Vedurusanna, Nagara, Manipur black, Chandrogadah, Chittimutyalu, Zincorice
II	28	Kanthamuguni, Hallabatta, Sannajajulu, Baludhudium, 302, Tikkimisri, Aasudhi, Tarang, DRR Dhan-45, Barhavahi, Latisali, Ghalima, Kandasagar, Raktasali, Daddiga, Gadakodimamahi, Illapusamba, Kistampetasannalu, Gedikahiye, Kalimuch, Kalajeel, Redrice, Rahikanda, BPT-5204, Methimahal, Ramjeera, Birodlu, Ambemohar.
III	5	Karamguruvay, Esakarvad, Hemberbag, Bahurupi, Mudimurangi
IV	2	Haladichudi, Agmakunda
V	1	Bhajana

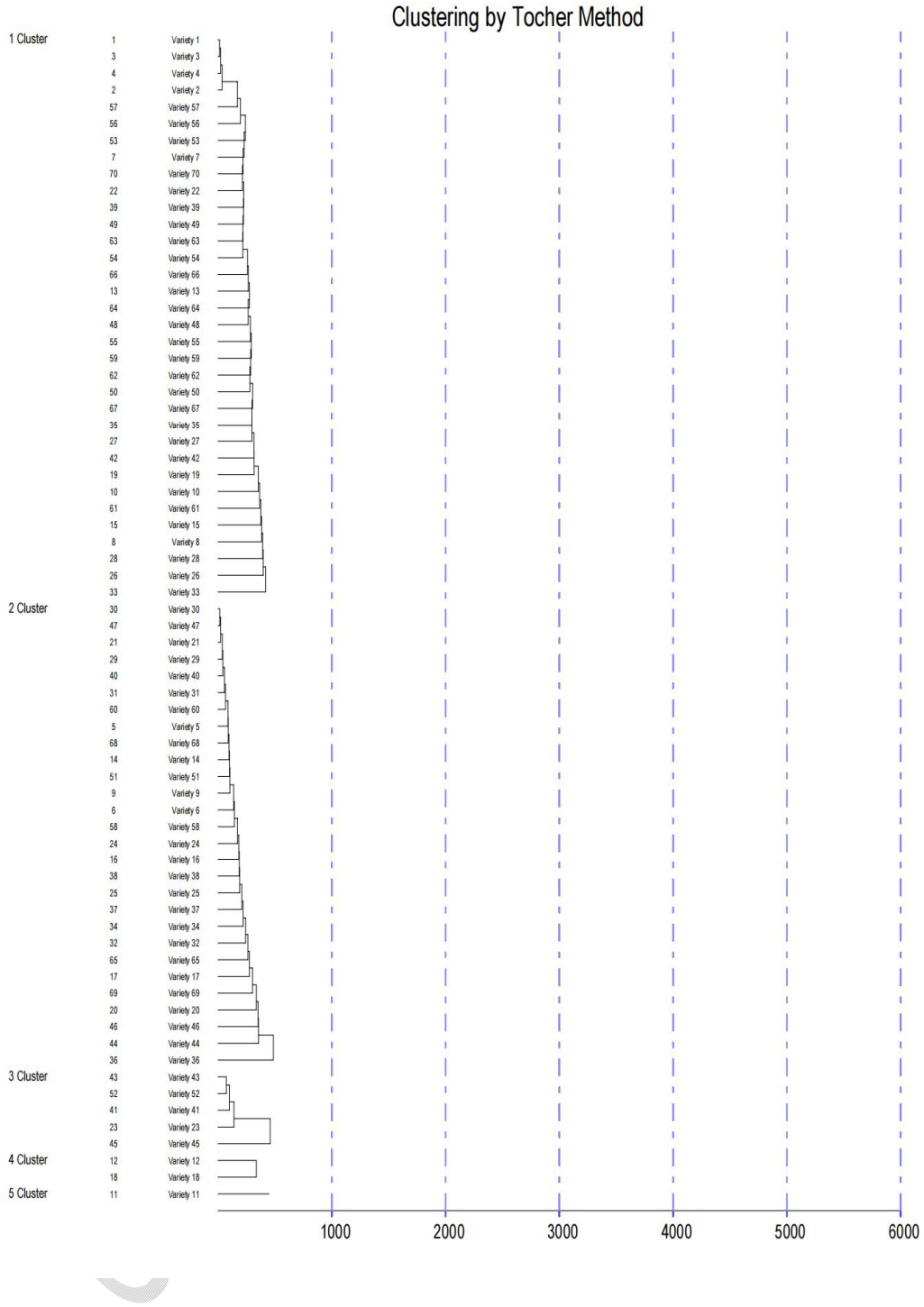

Figure. 2 Clustering of 70 rice genotypes

Table.3 Clusters means of 66 rice genotypes for 14 traits

Clusters	DFF	DM	PH	PL	NPP	NFP	GL	GW	TGW	KL	KB	FE	ZN	GYP
Cluster 1	90.21	129.03	81.58	21.75	9.85	95.47	8.35	2.89	21.37	6.66	2.08	9.27	17.44	24.90
Cluster 2	89.29	128.29	81.89	19.55	6.18	57.25	8.46	2.69	21.06	6.61	1.89	9.34	16.31	18.14
Cluster 3	88.20	128.80	94.50	23.33	9.80	129.60	8.16	2.69	21.64	6.91	2.36	10.68	20.48	25.48
Cluster 4	101.00	122.00	141.20	23.11	7.50	98.50	7.47	2.92	23.70	6.64	2.03	4.75	11.35	15.20
Cluster 5	75.00	110.00	125.60	23.54	9.00	64.00	7.78	3.83	17.40	7.11	2.14	7.50	13.70	20.50

DFF- Days to 50% flowering, **DM-** Days to maturity, **PH-** Plant height, **PL-** Panicle length, **NPP-** Number of panicles per plant, **NFP-** Number of filled grains per panicle, **GL-** Grain length, **GW-** Grain width, **TGW-** 1000 grain weight, **KL-** Kernel length, **KB-** Kernel breadth, **FC-** Fe (iron) content, **ZC-** Zn (zinc) content, **GYP-** Grain yield per plant.

Table.4 Relative contribution of different characters towards total genetic divergence

S.No.	Character	No. of times ranked first	Contribution (%)
1.	Days to 50% flowering	77	3.18
2.	Days to maturity	50	2.06
3.	Plant height	616	25.50
4.	Panicle length	28	1.15
5.	Number of panicles per plant	2	0.03
6.	No. of filled grains per panicle	1532	63.40
7.	Grain length	1	0.01
8.	Grain weight	3	0.04
9.	1000 grain weight	39	1.61
10.	Kernel length	3	0.05
11.	Kernel breadth	3	0.06
12.	Iron content	4	0.16
13.	Zinc content	9	0.33
14.	Grain yield per plant	60	2.42