



GENETIC DIVERGENCE IN MEDIUM DURATION GENOTYPES OF RICE (*ORYZA SATIVA* L.)

M. Anbarasu*, S. Thirugnanakumar and R. Eswaran

*Department of Genetics & Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar-608002 (Tamil Nadu), India

Abstract

Genetic divergence of twenty six medium duration rice (*Oryza sativa* L.) genotypes were studied through Mohalanobis's D^2 and principal component analysis for thirteen characters. The genotypes were grouped into seven clusters. The cluster V were comprised of the maximum number of genotypes eleven followed by cluster I with four genotypes followed by cluster IV with three genotypes each followed by clusters II, III, VI and VII with two genotypes. Highest inter cluster distance was observed between cluster IV and VII (569.188) followed by cluster I and VII (495.652), whereas highest intra cluster distance was found in the cluster VII (146.736) followed by cluster V (136.444) indicating closeness and diversity between the clusters respectively. Among the thirteen characters studied, maximum contribution was made by grain yield per plant (39.0769%), harvest index (25.2308%), hundred seed weight (20.000%), total dry matter production (6.7692%) and grain length (6.4615%) were found to be the maximum contributors towards the total divergence after plot yield.

Key words: Genetic Divergence, Mohalanobis's D^2 , Rice, Cluster analysis, Inter and intra cluster, Maximum contribution.

Introduction

Rice, *Oryza* species is a grass belonging to the poaceae family. The plant is annual with the height of about 36 – 150 cm. There are about 20 different species, of which the cultivated varieties are *Oryza sativa* and *Oryza glaberrima* (Vaughan *et al.*, 2003). The rice crop in India accounts for about 22 per cent of the total cropped area under cereals, and about 31 per cent of the total area under food grains (Singhal, 2003).

About half of the world's population depends on rice for their survival. Rice is being cultivated in around 113 countries of the world. The present world area, production and productivity under rice is 159.17 million hectares, 472.16 MMT and 4.42 metric tons per hectare (World Agricultural production, USDA, 2015-16). In India, rice is being grown in an area of 43.5 million hectares with a production of 104.41 MMT and productivity of 3.60 metric tons per hectare (World Agricultural production, USDA, 2015-16).

Genetic divergence among the genotypes play an

important role in selection of parents having wider variability for different traits (Nayak *et al.*, 2004). The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype.

Diverse growing conditions have led to immense variability among rice cultivars. Initiation of a hybridization programme for improvement of rice requires knowledge of genetic diversity in order to get greatest likelihood of recovering promising segregants. Genetic variability present in the base population should be useful for effective selection and recombination breeding. In the present study an attempt was made to assess the genetic divergence using mahalanobis D^2 statistics and different clustering procedures, based on yield and quality characters. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different yield and quality characters (Sarawgi and Binse, 2007).

*Author for correspondence : E-mail : anbarasu.madhu@gmail.com

Materials and Methods

The experimental material for this genetic divergence study comprised of twenty six genotypes collected from various places. The details of the materials are presented in table 1.

Methods

Field plot technique

Seeds of the twenty six rice genotypes were sown in raised nursery beds during Samba 2016. In each genotypes, one seeding per hill was transplanted in the main field after 25 days with the spacing of 20 cm between rows and 15 cm between

plants in 3 m long rows. The experiment was carried out in Randomized Block Design with three replications in season. A uniform population of 20 plants in a row was maintained.

Observations recorded

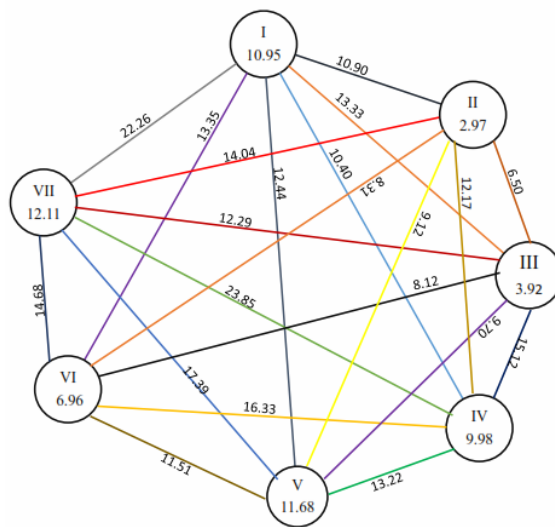
The data were recorded from five randomly selected plants for each genotypes from each replication leaving the first two border rows from all the four sides, in order to avoid the sampling error. The observations were recorded as per the following procedure. Readings from five plants were averaged replication wise and the mean data was used for statistical analysis for the 13 characters *viz.*, days to 50% flowering, plant height (cm), number of tillers per plant, number of productive tillers per plant, panicle length (cm), number of grains per panicle, grain length, grain breadth, grain L/B ratio, hundred seed weight (g), total dry matter production, harvest index (%), grain yield per plant (g). genetic diversity analysis was done following the D² statistics proposed by Mahalanobis (1936).

Table 1: List of genotypes studied.

S. No.	Name of the Genotype	Origin
1.	AD08-142	Tamilnadu Rice Research Institute, Aduthurai
2.	AD06207	Tamilnadu Rice Research Institute, Aduthurai
3.	AD07312	Tamilnadu Rice Research Institute, Aduthurai
4.	ADT- 46	Tamilnadu Rice Research Institute, Aduthurai
5.	ADT- 49	Tamilnadu Rice Research Institute, Aduthurai
6.	CB05-031	Tamilnadu Rice Research Institute, Aduthurai
7.	CN1744-313-19-19-8-8	Tamilnadu Rice Research Institute, Aduthurai
8.	CN1755-9-7-5-MLD-20	Tamilnadu Rice Research Institute, Aduthurai
9.	CO-43	Plant breeding station, Coimbatore
10.	CO-49	Plant breeding station, Coimbatore
11.	CO-50	Plant breeding station, Coimbatore
12.	CR2643-1-4-3-1	Tamilnadu Rice Research Institute, Aduthurai
13.	CR3299-11-	Tamilnadu Rice Research Institute, Aduthurai
14.	HKR08-1-1-1-1	Tamilnadu Rice Research Institute, Aduthurai
15.	HUR1204	Tamilnadu Rice Research Institute, Aduthurai
16.	KJT15-1-36-5-28-1	Tamilnadu Rice Research Institute, Aduthurai
17.	MTU1158	Tamilnadu Rice Research Institute, Aduthurai
18.	NDR359	Tamilnadu Rice Research Institute, Aduthurai
19.	OR1895-2	Tamilnadu Rice Research Institute, Aduthurai
20.	OR2163-14	Tamilnadu Rice Research Institute, Aduthurai
21.	PAU3835-62-5-1	Tamilnadu Rice Research Institute, Aduthurai
22.	RNR2448	Tamilnadu Rice Research Institute, Aduthurai
23.	RNR2836	Tamilnadu Rice Research Institute, Aduthurai
24.	UPR3330-9-12	Tamilnadu Rice Research Institute, Aduthurai
25.	WGL536	Tamilnadu Rice Research Institute, Aduthurai
26.	WGL633	Tamilnadu Rice Research Institute, Aduthurai

Results and Discussion

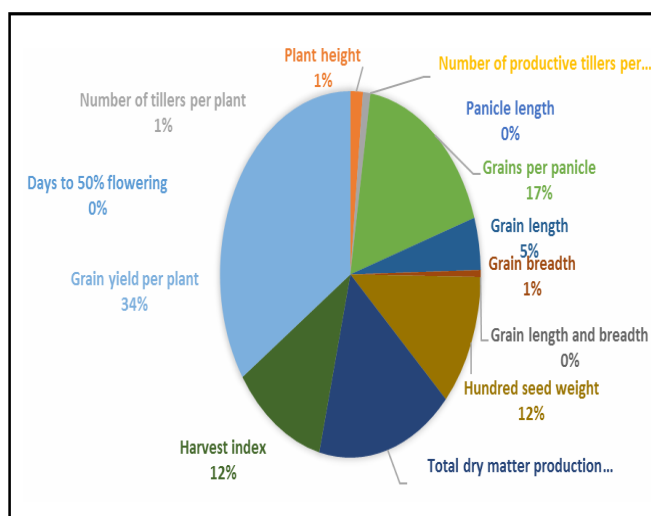
The analysis of variance revealed significant difference among the twenty six genotypes for all the thirteen traits indicating the existence of high genetic variability among the genotypes for all the traits. The results obtained here are in confirmation with the results reported by Sabesan (2005) and Rajasekaran (2006). The variability could be used in distinguishing different genotypes based on their morphology.



Cluster distance diagram of 26 rice genotypes

Table 2: Cluster composition of 26 rice genotypes.

Clusters	Number of genotypes	Name of genotypes
I	4	AD 08-142, AD 06207, CO-50, HKR 08-1
II	2	CN 1755-9-7-5-MLD-20, HUR 1204
III	2	MTU 1158, RNR 2448
IV	3	AD 07312, CO-49, WGL 633
V	11	ADT-43, ADT-49, CB 05-031, CN 1744-313-19-19-8-8, CO-43, CR 2643-1-4-3-1, CR 3299-11-1-1-1, KJT 15-1-36-5-28-1, NDR 359, OR – 1895 – 2, OR – 2163 - 14
VI	2	RNR -2836, UPR 3330-9-12
VII	2	PAU 3835-62-5-1, WGL536



Contribution of different traits to genetic divergence

Table 3: Inter cluster and intra cluster (diagonal) average of D^2 and D values (parenthesis) of 26 rice genotypes.

Clusters	I	II	III	IV	V	VI	VII
I	120.008 (10.955)	118.903 (10.904)	177.775 (13.333)	108.307 (10.407)	154.745 (12.440)	178.210 (13.350)	495.652 (22.263)
II		8.873 (2.979)	42.331 (6.506)	148.237 (12.175)	84.923 (9.215)	69.061 (8.310)	197.302 (14.046)
III			15.424 (3.927)	228.749 (15.124)	94.080 (9.700)	65.988 (8.123)	151.223 (12.297)
IV				99.615 (9.981)	174.898 (13.225)	266.824 (16.335)	569.188 (23.858)
V					136.444 (11.681)	132.598 (11.515)	302.607 (17.396)
VI						48.492 (6.964)	215.570 (14.682)
VII							146.736 (12.113)

Based on the relative magnitude of D^2 values, twenty six genotypes were grouped into seven clusters. Cluster composition of twenty six rice genotypes in Table 2. Among the clusters, cluster V eleven genotypes followed by cluster I four genotypes, IV three genotypes, II, III, VI and VII two genotypes.

The Inter and intra cluster D^2 values presented twenty six genotypes in table 3. Maximum inter cluster distance cluster IV and VII (569.188) followed by cluster I and VII (495.652). Minimum inter cluster distance was found in between the cluster II and III (42.331) followed by cluster III and VI (65.988). Maximum intra cluster distance cluster VII (146.736) followed by cluster V (136.444). Minimum intra cluster distance cluster II (8.873).

The cluster means of thirteen yield component characters presented in table 4. The cluster II recorded highest mean value for plant height (105.36) and harvest index (38.22), cluster III highest mean value for number of tillers per plant (21.16), number of productive tillers per plant (11.36), panicle length (23.95) and grain breadth (2.90), cluster IV highest mean value for grains per panicle (174.46), grain yield per plant (20.74) and total dry matter production for (66.66), cluster VI recorded highest mean value for days to 50% flowering (102.10), cluster VII highest mean value for grain length (9.81), grain L/B ratio (3.47) and hundred seed weight (2.21).

The relative contribution of individual character towards the expression of genetic diversity estimated over character wise D^2 value analysis are furnished in table

Table 4: Cluster means of 13 yield component characters.

Clusters	Days to 50% flowering	Plant height (cm)	No. of tillers per plant	No. of productive tillers per plant	Panicle length (cm)	Grains per panicle	Grain length (mm)	Grain breadth (mm)	Grain L/B ratio	100 seed weight	Total dry matter production	Harvest index	Grain yield per plant (g)
I	99.51	97.77	18.18	8.51	23.56	170.90	7.90	2.65	3.04	1.50	50.04	37.06	18.18
II	100.23	105.36	17.36	8.200	23.03	173.467	8.53	2.51	3.41	1.85	46.56	38.22	17.51
III	96.86	100.67	21.16	11.36	23.950	160.93	8.71	2.90	3.00	1.96	59.30	30.64	17.58
IV	100.20	99.56	17.48	8.86	23.80	174.46	7.94	2.42	3.33	1.49	66.66	36.46	20.74
V	99.21	100.80	18.98	9.19	23.86	161.70	8.54	2.76	3.13	1.74	63.14	30.83	18.14
VI	102.10	101.45	19.40	8.13	22.48	150.86	8.48	2.76	3.07	1.77	55.03	23.15	12.59
VII	101.70	98.35	19.16	9.86	23.17	166.53	9.81	2.81	3.47	2.21	45.85	32.77	15.06
No. of 1 st rank	0	2	0	0	1	1	21	2	2	65	22	82	127
Contribution%	0.000	0.615	0.000	0.000	0.307	0.307	6.461	0.615	0.615	20.00	6.769	25.230	39.076

4. Maximum contribution was made by grain yield per plant (39.0769%), harvest index (25.2308%), hundred seed weight (20.000%), total dry matter production (6.7692%), grain length (6.4615%) were found to be the maximum contributors towards the total divergence after plot yield.

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