GENETIC ANALYSIS OF RICE (*Oryza sativa* L.,) GENOTYPES FROM DIFFERENT GEOGRAPHICAL REGIONS UNDER COASTAL SALINE ENVIRONMENT

K.PALANIRAJA* R. PARTHASARATHI, AND S. VENNILA

*Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Chidambaram – 608 002, Tamil Nadu, India.

Department of Microbiology, Faculty of Agriculture, Annamalai University, Chidambaram – 608 002, Tamil Nadu, India.

Abstract:

The present investigation was conducted at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. The nature and magnitude of genetic divergence were estimated in 30 rice genotypes using Mahalanobis D^2 statistics by considering 11 economic characters. In D^2 analysis 30 genotypes were grouped into six clusters with cluster I and III constituted maximum number of genotypes (i.e.) 13 and 9 genotypes, respectively. The intra cluster distance was maximum in cluster IV (35.57) which was closely followed by cluster II (34.07) and cluster III (28.15). The inter cluster distance was maximum between cluster I and IV (2302.00) followed by cluster II and III (1511.20). Findings of this study can be utilized for selection of divergent genotypes for further crossing programme.

Keywords: D^2 analysis, divergence, intra and inter cluster.

Introduction

The cultivated Rice (*Oryza sativa* L.,) species are diploid with 2n=2x=24. Knowledge about deviation of genotypes genetically could be a useful tool in crop improvement strategies. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. Recombinants are generated by utilizing highly divergent parents. The use of advanced biometric techniques such as multivariate analysis based on Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers (Roy and Panwar, 1993). The study was about estimation of magnitude of genetic divergence of 30 Rice genotypes and to identify diverse genotypes for the further utilization in hybridization programme.

Materials and Methods

The experimental material for the present study is laid in Randomized Block Design (RBD) with three replications conducted at experimental farm of plant breeding, Department of Genetics and Plant Breeding, Annamalai University, Tamil Nadu, India. After 25 days of nursery period, seedlings are transplanted to the main field at the rate of one seedling per hill with the spacing of 20 x 30cm. recommended agronomic practices and plant protection measures are taken for the betterment of crop growth. Observations are recorded on five randomly selected plants per replication for days to 50% flowering, plant height (cm), number of tillers/plant, number of productive tillers/plant, length of the panicle, number of filled grains/panicle, 100 grain weight (g), grain length (mm), grain breadth (mm), grain L/B ratio, total grain yield/plant (g) on plot basis. The data was subjected to Mahalanobis D^2 statistics to measure genetic divergence as suggested by Rao (1952).

Result and Discussion

Analysis of variance showed significant differences for all the eleven characters studied, this shows the existence of high genetic variability among the genotypes. The grouping of genotypes in different clusters showed the presence of high degree of diversity in the materials evaluated. Recent workers had also reported the presence of substantial genetic diversity in rice (Toshimenla *et al*., 2016). Both PCV and GCV estimates were highest for number of filled grains/panicle followed by length of the panicle (table.1). Johnson (1955) reported that high heritability should be combined with high genetic advance to arrive at more acceptable conclusion.

Table 1. Magnitude of variability for 11 characters in 36 rice genotypes

S.NO	CHARACTERS	CO-EFFICIENT OF VARIATION	
		PHENOTYPIC	GENOTYPIC
01	Days to 50% flowering	10.15	8.13
02	Plant height(cm)	22.00	19.32
03	Number of tillers/plant	17.31	9.82
04	Number of productive tillers	36.54	26.13
05	Length of the panicle(cm)	31.62	22.46
06	Number of filled grains/panicle	18.50	9.10
07	100 grain weight(g)	15.22	18.06
08	Grain length(mm)	11.38	8.75
09	Grain breadth(mm)	21.50	16.15
10	Grain length/breadth ratio	16.71	20.34
11	Grain Yield/plant(g)	21.18	16.15

Genotypes are grouped into six clusters. Out of the six clusters, cluster I possesses the maximum number of genotypes (i.e.) 13 genotypes, which was closely followed by the cluster II with 9 genotypes (table.2). The other clusters like clusters III, IV, V and VI possesses 2, 4, 1and 1 genotypes respectively.

Intra and inter cluster values of 30 Rice genotypes are also tabulated (table.3). The maximum intra cluster distance existed in cluster IV (35.57), followed by cluster II (34.07) and cluster III (28.15). Similar results were recorded by Kumar *et al.,* 2014. At the same time, the maximum inter cluster was between cluster I and IV (2302.00), next to this was between cluster II and III (1511.20). The pattern of clustering proved to be the existence of significant amount of variability.

Table 2.　Distribution of 36 rice genotypes in different clusters based on d^2 analysis

CLUSTERS	GENOTYPES	NO.OF GENOTYPES
I	ADT 43, ADT 45, CO 49, CO 51, KNM 118, BPT 5204, CO 43, ADT 42, ADT 44, PONNI, TRY 3, MTU 1010, JGL 18047.	13
II	ADT 38, ADT 46, ASD 16, TKM 9, ADT 36, ADT 37, ADT 47, SONA, IR 20.	9
III	ADT 41, MTU 1010.	2
IV	CO 50, IR 8, TKM 13, TKM 14.	4
V	TKM 11.	1
VI	TKM 6.	1

Table 3. Average Inter (d^2) and Intra (D) cluster values for 36 rice genotypes

CLUSTERS	I	II	III	IV	V	VI
I	**22.17**	78.30	270.07	2302.00	1872.52	291.44
II		**34.07**	1511.20	392.09	887.56	356.32
III			**28.15**	208.31	490.38	356.87
IV				**35.57**	718.78	631.11
V					**0.000**	528.62
VI						**0.000**

There exist two mono-clusters (i.e) with single genotype present in clusters V and VI; this indicated that the genotypes are significantly deviated from other genotypes grouped in the clusters I, II, III and IV (table.3). Shanmugam and Rangasamy (1982) reported that grouping of materials of same geographical origin into different clusters was an indication of broad genetic base of genotypes belonging to that origin.

Table 4. Relative contribution of different characters to genetic divergence

S.NO	CHARACTERS	% CONTRIBUTION
01	Days to 50% flowering	7.83
02	Plant height(cm)	7.52
03	Number of tillers/plant	3.61
04	Number of productive tillers/plant	16.60
05	Length of the Panicle(cm)	3.10
06	Numbers of filled grains/panicle	30.82
07	100 grain weight(g)	19.66
08	Grain length(mm)	14.58
09	Grain breadth(mm)	9.53
10	Length/breadth ratio	5.00
11	Grain Yield/plant(g)	7.99

The highest contribution of genetic divergence in this experiment was revealed by number of filled grains/panicle (30.82), 100 grain weight (19.66) and number of productive tillers/plant (16.60) (table.4). Hence, number of filled grains/panicle, 100 grain weight (g) and number of productive tillers/plant be given importance during selection of parents for hybridization and selection in segregating populations.

Reference:

Hossain, S., M.Salim, M.S. Akter, S. Afroz and M.S. Noman. 2015. Genetic diversity of drought tolerant upland rice (*Oryza sativa* L.) genotypes. A scientific J. Krishi Foundation, 13(2): 133-139. http://www.indoastat.com

Kumar, B., Gupta, B.B. and Singh B.2014. genetic diversity for morphological and quality traits in rice(*Oryza sativa* L.). the Bioscan, 9(4): 1759-1762.

Mahalanobis, P.C., 1936. On the generalized distance in statistics. Poc. Nat. Inst. Sci. (India), 2: 49-55.

Mohan, Y.C., S. Thippeswary, K. Bhoomeshwar, B. Madhavilatha and Jameema Samreen. 2015. Diversity analysis for yield and gall midge resistance in rice (*Oryza sativa* L.) in Northern Telangana zone, India. SABRAO J. of Breed. And Genet., 47(2): 160-171.

Nirosha, R., S. Thippeswamy, V. Ravindrababu, V. Ram Reddy and B. Spandana. 2016. Genetic diversity analysis of zinc, iron, grain protein content and yield components in rice. Electronic J. Pl. Breed., 7(2): 371-377.

Samal, K.C., Meti, N., Bastia, D.N., Rout, G.R. 2014. Genetic diversity analysis of traditional aromatic rice using molecular markers. BMR, 1(2): 1-14.

Sandhya, Mukul, Kumari, S. and Babu. G.S. 2015. Estimation of genetic divergence among elite genotypes of rice (*Oryza sativa* L.). the Ecoscan., 9(1&2): 409-411.

Thippeswamy, S., Y.Chandramohan, B. Srinivas and D. Padmaja. 2016. Selection of diverse parental lines for heterotic hybrid development in rice (*Oryza sativa* L.). SABRAO J. of Breed, and Genet., 48(3): 285-294.

Toshimenla, Jogendra Singh and Sapu Changkija. 2016. Genetic divergence studies on upland rice grown in Nagaland, India. Indian J. Agric. Res., 50(6): 555-560.