



GENETIC DIVERSITY ANALYSIS IN RICE (*ORYZA SATIVA* L.) UNDER COASTAL SALINE CONDITION

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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 25 rice genotypes using Mahalanobis D^2 statistics by considering 11 economic characters. In D^2 analysis 25 genotypes were grouped into five clusters with cluster II and I constituted maximum number of genotypes i.e. 11 and 7 genotypes, respectively. The intra cluster distance was maximum in cluster II (33.77) which was closely followed by cluster I (24.27) and cluster III (22.20). The inter cluster distance was maximum between cluster I and V (1872.52) followed by cluster I and IV (1678.94). Findings of this study can be utilized for selection of divergent genotypes for further hybridization programme.

Key words : D^2 analysis, divergence, intra and inter cluster, selection.

Introduction

The cultivated Rice (*Oryza sativa* L.) species are diploid with $2n=2x=24$ whereas the wild species are tetraploid with $2n=4x=48$. Knowledge about deviation of genotypes genetically could be a powerful 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; Ramya and Senthilkumar, 2008). The study was about estimation of magnitude of genetic divergence of 25 Rice genotypes and to identify diverse genotypes for the further utilization in Breeding programme.

Materials and Methods

The experimental material for the present study of Rice 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 seedlings 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 first 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 characters studied, confirms 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 (Kumar *et al.*, 2014; Ahmed *et al.*, 2014;

Sandhya *et al.*, 2015). Both PCV and GCV estimates were highest for productive tillers followed by grain L/B ratio (Table1). 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 first flowering	11.26	9.20
02	Plant height (cm)	24.06	22.83
03	Number of tillers/plant	19.37	7.62
04	Number of productive tillers	35.54	26.96
05	Length of the panicle (cm)	16.62	6.51
06	Number of filled grains/panicle	18.60	10.33
07	100 grain weight (g)	19.72	17.76
08	Grain length (mm)	11.38	8.75
09	Grain breadth (mm)	23.51	15.85
10	Grain length/breadth ratio	26.71	23.34
11	Grain Yield/plant (g)	21.18	14.15

Genotypes are grouped into five clusters. Out of the five clusters, cluster II possesses the maximum number of genotypes (i.e.) 11 genotypes, which was closely followed by the cluster I with 7 genotypes (Table 2). The other clusters like clusters III, IV and V possesses 3, 3, 1 genotypes respectively.

Intra and inter cluster values of 25 Rice genotypes are also tabulated (Table 3). The maximum intra cluster distance existed in cluster II (33.77), followed by cluster I (24.27) and cluster III (22.20). At the same time, the maximum inter cluster was between cluster I and V (1872.52), next to this was between cluster I and IV (1678.94). 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, ADT 47, CO 49, CO 51, SONA, KNM 118.	7
II	BPT 5204, ADT 38, ADT 46, JGL 18047, CO 43, ADT 42, ADT 44, ASD 16, TKM 9, ADT 36, ADT 37.	11
III	PONNI, TRY 3, CO 50.	3
IV	ADT 41, TKM 6, MTU 1010.	3
V	TKM 11.	1

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

CLUSTERS	I	II	III	IV	V
I	24.27	68.30	380.07	1678.94	1872.52
II		33.77	68.73	352.69	567.58
III			22.20	138.31	190.38
IV				20.54	318.78
V					0.000

There exist one mono-cluster i.e with single genotype present in cluster V; 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 first flowering	9.83
02	Plant height(cm)	9.52
03	Number of tillers/plant	2.61
04	Number of productive tillers/plant	4.60
05	Length of the Panicle(cm)	2.10
06	Numbers of filled grains/panicle	17.82
07	100 grain weight(g)	33.66
08	Grain length(mm)	16.58
09	Grain breadth(mm)	7.53
10	Length/breadth ratio	4.00
11	Grain Yield/plant(g)	3.99

The relative contribution of each characters towards D^2 depends on the inter-cluster distance in all combinations. The highest contribution of genetic divergence in this experiment was revealed by 100 grain weight (33.66g), number of filled grains/panicle (17.82) and grain length (16.58mm) (table.4). Hence, 100 grain weight (g), number of filled grains/panicle and grain length (mm) be given importance during selection of parents for hybridization and selection in segregating populations.

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