

Phenotyping of rice genotypes under coastal salinity

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Abstract

Rice (*Oryza sativa* L.) ($2n=2x=24$) is the important cereal crop belonging to the family Poaceae. To identify the saline tolerant genotypes, the current investigation was carried out to analysis the genetic diversity of fifty five rice genotypes using morphological traits. The phenotypic diversity analysis suggested by Mahalanobis's (1936) was followed as a result the genotypes were grouped into five clusters. High intra cluster distance was recorded in cluster III followed by cluster I and the inter cluster distances was found high between cluster IV and V followed by clusters II and V, clusters II and III and cluster III and IV showing divergent. Three major clusters at 0.45 similarity coefficient were obtained. Thus based on the phenotypic and molecular diversity along with *per se* performance, the genotypes namely, ADT 45, Swarna, PMK 2, IR 66, Paiyur 1 and ASD 20 were considered best for hybridization programme.

Keywords: D², genetic diversity, heritability, Phenotyping

Introduction

Rice is a life for thousands of millions of people. In Asia alone, more than 2000 million people obtain 60 to 70 percent of their calories from rice and its products. Hence the slogan "rice for life" would be appropriate. India has the largest acreage under rice at 44135.90 in '000 ha. With annual production of 106645.50 in 000 tonne in the year 2013-14 as per indiastat Report (www.indiastat.com 2013-2014). More than 7.5 millian hectares (IRRI 2004) of the cultivable land is affected by salinity problem. This ultimately reduce the yield as the saline concentration increases. This includes both inland and coastal salinity area. The success of any plant breeding programme largely depends on the diversity exist among the genotypes (Allard, 1960) [1]. Hence it is clear that diverse parents produce better combination in hybridization. Thus it is necessary to assess the genetic diversity. In addition to the phenotypic diversity analysis.

Materials and Methods

The present investigation, which consisted of set of 55 genotypes of Rice was raised at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India during December 2014-March 2015. The genotypes were IR 36, IR 50, IR 66, IR 72, Kerala karna, Swarna, PMK 2, Bhavani, AD 95319, ADT 36, ADT 37, ADT 38, ADT 39, ADT 41, ADT 43, ADT 45, ADT 46, ASD 16, ASD 18, ASD 19, ASD 20, CO 33, CO 43, CO 45, CO 46, CO 47, MDU 3, MDU 4, MDU 5, Padmini, Paiyur 1, Red ponni, TKM 9, TKM 11, TKM 12, White ponni, Ajaya, OM B27-14, Triguna, IR 104-014-44962, IR 1657-5R-B-129, IR 65192-4B-8-1, IR 75000-69-2-1-B, IR 65847-3B-6-2, IR 644-19-3B-31-1, IR 63311-B-3R-B-2-4-3, IR 6199-3B-24-3, IR 58190-40-3-1-2, IR 60823-78-1-2-3-1-2, IR 6192-3B-15-2-2, IR 47547-2B-26-23-1, IR 5931-110-1, CR 1009, PY 3, BPT 5204. Rice is very sensitive to salinity stress and is currently listed as the most salt sensitive cereal crop with a threshold of 3 dS/m for most cultivated varieties (USDA, 2013) [9]. The experiment was conducted at the coastal saline situation with EC of the soil ranging from 3.0 - 4.0 dS/m.

Data recorded for seven quantitative traits *viz.*, Plant height, Number of productive tillers per plant, Boot leaf length, Panicle length, 100 grain weight, Grain yield per panicle, Grain yield per plant from the 55 genotypes were utilized for diversity analysis. Observation were recorded on 10 plants per entry per replication planted at the rate of one seedling per hill with spacing of 30 x 20 cm. Assessment of genetic diversity was carried out using Mahalanobis's (1936) [5] D² statistics. The genotypes were grouped into clusters as per Tocher's method (Rao, 1952).

Results and Discussion

D² Analysis

The divergence of 55 genotypes of rice was assessed for seven economic characters as per Mahalanobis's generalized distance. The analysis of variance for the seven characters showed significant differences among the 55 genotypes (Table 1). These genotypes were grouped into five clusters using clustering technique (Table 2). Cluster I was the largest having maximum of 35 genotypes followed by cluster II and III with 15 and three genotypes respectively. The remaining two clusters had single genotype each. Grouping of genotypes revealed that there was no direct relationship between genetic diversity and geographical diversity since genotypes from different geographical origin were included in same cluster and the genotypes from same origin are genetically dissimilar and fall in different cluster. Thus the geographic and genetic diversity are not necessarily correlated. This lack of correlation was reported by Rather *et al.* (2001) [7], Karthikeyan (2002) [4] and Kandamoorthy and Govindarasu (2005) [3].

The intra cluster D² values are presented (Table 3). The intra cluster distance was found maximum within cluster III (18.15) followed by cluster I (17.91) and minimum intra cluster distance was recorded by cluster II (13.30). Regarding the inter cluster distances, maximum inter cluster distances was found between cluster IV and cluster V (64.90), followed by II and V (58.36), clusters II and III (43.57) and clusters III and IV (42.69). The minimum inter cluster distance was found between cluster I and II (20.01) followed by cluster II and IV (22.64). Higher

the inter cluster indicates the higher genetic divergence. Thus inter cluster distance is the criterion used for selecting the genotypes as parents in hybridization programme (Singh and Narayanan, 2000) [8]. Hence, it would be logical to choose genotypes from these clusters for breeding programme.

The cluster mean values for seven characters were studied and the results are furnished (Table 4). The cluster mean is another criterion to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster mean of cluster IV had the desirable mean for characters such as grain weight per panicle, 100 grain weight and grain yield per plant. Cluster V high mean for boot leaf length and panicle length. Clusters II and III recorded desirable mean for plant height and number of productive tillers per plant respectively. Thus these clusters showed superior desirable mean for various characters could be considered in hybridization programme.

The contribution of each character towards divergence is presented (Table 4). Among the characters, the plant height contributed a maximum of 64.9 per cent followed by boot leaf length (13.8 per cent), number of productive tillers per plant (7.7 per cent) and panicle length (7.0 per cent). The

character 100 grain weight contributed very low 0.7 per cent towards divergence. The relative contribution of each character to the total divergence is another important criterion in the choice of the parents (Singh and Narayanan, 2000) [8]. Hence it is clear that the two characters such as plant height and boot leaf length should be given importance while selecting the genotypes for breeding programme. Venkatesan (2004) [10] concluded that 1000 grain weight and plant height were the main contributors to genetic diversity.

The mean performance of clusters I, III, IV for yield and yield component character are found to be superior. Based on all these criteria, promising genotypes from each clusters were selected based on the *per se* performance for various characters. The genotypes ADT 45 (cluster I), Paiyur 1 (cluster I), PMK 2 (cluster III), Swarna (cluster IV) were considered as potential parents for hybridization.

The present investigation revealed that the genotypes ADT 45, Paiyur 1, PMK 2, and Swarna were found to have greater diversity on morphological traits. It is clear that the phenotypic clustering pattern. Many studies have found less relationships between molecular genotypic analysis and phenotypic diversity Hence these six genotypes recommended for hybridization.

Table 1: Anova for various characters in rice

Source	df	Mean squares						
		Plant height(cm)	Number of productive tillers per plant	Boot leaf length (cm)	Panicle length (cm)	Grain weight per panicle (g)	100 Grain weight (g)	Grain yield per plant (g)
Genotypes	54	1060.34**	73.38**	44.69**	9.79**	0.41**	0.0002**	31.08**
Error	54	2.73	1.72	0.48	0.24	0.03	0.000004	1.70

**Significant at 1 percent.

Table 2: Distribution of 55 genotypes into different clusters based on morphological traits

Cluster no	Number of genotypes	Genotypes	Source
I	35	AD 95319, ADT 38, ADT 39, ADT 43, ADT 45, ADT 46, ASD 18, ASD 19,	Tamil Nadu
		CO 43, CO 45, CO 46, CO 47,	
		Bhavani,	
		CR 1009,	Orissa
		IR 104-014-44962, IR 47547-2B-26-23-1, IR 6192-3B-15-2-2, IR 6199-3B-24-3, IR 63311-B-3R-B-2-4-3, IR 644-19-3B-31-1, IR 65847-3B-6-2, IR 66,IR 72, IR 75000-69-2-1-B, IR 1657-5R-B-129,	Philippines
		MDU 3,MDU 4,MDU 5	Tamil Nadu
		OM B27-14,	Unknown
		Padmini,	Tamil Nadu
		Paiyur 1,	
		Red ponni,	
TKM 11,TKM 12,			
White ponni,	Tamil Nadu		
II	15	ADT 36,ADT 37,ADT 41	Tamil Nadu
		Ajaya,	Unknown
		ASD 16,ASD 20	Tamil Nadu
		BPT 5204,	Andhra Pradesh
		CO 33,	Tamil Nadu
		IR 36, IR 50, IR 5931-110-1, IR 60823-78-1-2-3-1-2,	Philippines
		PY 3,	Pondicherry
		TKM-9,	Tamil Nadu
		Triguna,	Unknown
III	3	PMK 2,	Tamil Nadu
		IR 58190-40-3-1-2, IR 65192-4B-8-1,	Philippines
IV	1	Swarna,	Andhra Pradesh
V	1	Kerala karna,	Kerala

Table 3: Intra cluster distance of various clusters in rice

Clusters	I	II	III	IV	V
I	17.91	20.01	27.61	28.81	41.11
II		13.30	43.57	22.64	58.36
III			18.15	42.69	37.38
IV				0.00	64.90
V					0.00

Table 4: Cluster mean and contribution of various characters towards diversity in rice

Character	Clusters					Contribution towards divergence (%)
	I	II	III	IV	V	
Plant height (cm)	96.5	60.8	125.0	73.0	132.7	64.9
Number of productive tillers per plant	13.0	18.1	30.6	11.3	10.8	7.7
Boot leaf length	28.3	25.7	31.3	18.1	45.2	13.8
Panicle length (cm)	21.9	22.3	22.2	17.2	28.8	7.0
Grain weight per panicle (g)	2.6	2.2	2.9	3.4	2.3	1.1
100 Grain weight (g)	2.3	2.2	2.2	2.3	2.2	0.7
Grain yield per panicle (g)	28.4	25.6	28.3	33.6	22.8	4.9

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