STUDIES ON GENETIC DIVERGENCE AMONG RICE GENOTYPES (*ORYZA SATIVA* L.) UNDER COASTAL SALINE CONDITION

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Abstract

The present investigation was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalainagar during Samba. The experimental field was saline environment with EC of 2.5 ds/m and PH of 7.8. The study was carried out in an effort to assess the extent of genetic divergence, variability and character association in 35 genotypes for 11 character *viz.,* days to first flowering, plant height at maturity, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, 1000 grain weight, grain length, grain breadth, grain L/B ratio and grain yield per plant. Genetic divergence was studied based on Mahalanobis D^2 statistic and grouping of cluster was done following Tocher's method. The analysis of variance for genotypes revealed the presence of significant variability among the genotypes for all the 11 characters studied. Based on D^2 analysis the genotypes were categorized into 10 clusters based on the genetic distance and mean of different characters. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The maximum intra cluster distance was observed in cluster VIII followed by cluster IV. The maximum inter cluster distance was observed between cluster VIII and X followed by cluster VIII and IX. The parents selected from these divergent clusters could produce superior progenies and hybrids. The characters namely grain yield per plant followed by grain length and grain breadth had contributed much towards genetic divergence. The parents from distantly related belonging to clusters X and VIII could be used for combining characters of yield and grain quality components to achieve desirable segregants.

Key words : Genetic divergence, *Oryza sativa*, Saline condition.

Introduction

Rice (*Oryza sativa* L. 2n:2x:24) belonging to the genus *Oryza* includes 24 species, out of which 22 species are wild and only two species *viz., O. sativa* and *O. glaberrima* are cultivated. The genus *Oryza* belongs to the tribe *Oryzeae* in the family Poaceae. Rice is the most important cereal crop cultivated widely in many parts of the world. South and south-east Asia form the primary centre of genetic diversity of the cultivated rice. The genetic diversity of rice available in India is enormous; more than sixty thousand traditional cultivars of rice are grown. Rice thrives over a wide range of climatic conditions extending from 45° N to 40° S and from sea level to 3000 m altitude.

Rice with 1,20,000 varieties, has the richest gene bank in the plant kingdom and feeds more than one half of the world population. Rice fields cover 11 per cent of earth's entire aerable land (IRRI, 2002). Rice provides 21% global human per capita energy and 15% of per capita protein. Asia accounts for 60% of the global population, about 92% of world rice production and 90% of global rice consumption (Agcaoili and Rosegrant, 1994). The greater is the genetic diversity in the germplasm, the more would be the breeding potential and scope for improvement. Crosses between genetically diverse parents are likely to produce high heterotic effects and also produce a wide spectrum of variability in segregating generations. The Mahalanobis D2 statistic is a very useful tool for estimating such genetic divergence.

The best way to achieve net increase in the overall production would be to develop specific genotype for specific environment. The present study therefore, was

conducted to identify suitable genotypes of rice for different economic characters. The genetic divergence study helps to identify parents for hybridization programme. The genetic divergence is dependent on geographical as well as phenotypic components of cultivars and its quantitative assessment could provide a rational basis for selection of parents for breeding programme to obtain high yielding progenies to break the existing yield plateau.

Materials and Methods

The present investigation was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. The experimental material for this genetic divergence study comprised of thirty five rice genotypes collected from various places. Seeds of the thirty five rice genotypes were sown in raised nursery beds during 2015 (January – May). In each genotype, 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 3m long rows. The experiment was carried out in randomized block design (RBD) with three replications. A uniform population of 10 plants in a row was maintained. Recommended agronomic practices and need based plant protection measures were adopted. The study was carried out in an effort to assess the extent of genetic divergence in 35 genotypes for 11 characters *viz.*, days to first flowering, plant height at maturity, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, 1000 grain weight, grain length, grain breadth, grain L/B ratio and grain yield per plant.

Results and Discussion

The analysis of variance revealed significant differences among the accessions for all the characters studied (Table 1). Based on the relative magnitude of D^2 values, 35 rice genotypes were grouped into as many as ten clusters (Table 2). Cluster IV was the largest as it comprised 16 genotypes closely followed by cluster I had five genotypes. The clusters II, III, V, VI, VII and VIII comprised of two genotypes in each whereas cluster 9 and 10 are monogenotypic clusters. This indicated that geographical diversity is not always related to genetic diversity. The genotypes included in cluster I were from different geographical regions indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes (Khan *et al.,* 2007). The distribution of genotypes also indicated that the genotypes from one region were distributed in different clusters. This indicates that there was no parallelism between clustering pattern and geographic distribution of genotypes (Nayak *et al*., 2004). Therefore the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adoption, selection criteria and selection pressure in environmental conditions (Maurya *et al.,* 1997). This further explains that forces other than eco-geographical differentiation such as natural and human selection pressure would exert considerable influence on the genetic divergence. Therefore, selection of cultivars for breeding programme should be based on genetic diversity rather than geographical diversity.

The intra and inter cluster distance among ten clusters were computed and presented in (Table 3). The intra cluster distance ranged from 0.00 to 445.18. The cluster IX and X showed minimum intra cluster distance (0.00). Since each contained single genotype and maximum intra cluster was exhibited by cluster VIII (445.18) followed by cluster IV (377.30). The inter cluster distance varied from 67.55 to 1093.59. Maximum inter cluster distance was observed between clusters VIII and

Table 1: Analysis of variance for eleven characters in 35 rice genotypes.

S.No.	Source	df	Days to first flowering	Plant height at maturity	Number of tillers per plant	Number of panicle per plant	Panicle length per panicle	Number of grains weight	1000 grain	Grain length	Grain breadth	Grain L/B ratio per plant	Grain yield
								Mean Sum of squares					
1	Replication	2	53.2545	8.2098	1.1118	1.7049	0.4125	3.2786	0.8114	0.0000	1.1342	0.0024	8.4750
2	Genotype	34	112.2359**	361.7371**	32.4166**	26.9197**	10.1959**	2195.6423**	18.7147**	0.0265**	0.0037**	0.9412**	281.0343**
3	Error	68	31.7169	4.0729	2.3601	2.3287	1.5502	45.2736	0.6097	0.0001	0.0000	0.0140	8.1808

*Significant at 5 per cent level.

Table 2: Composition of D^2 cluster for 35 rice genotypes.

S. No	Number of genotypes	Name of genotypes
I	5	ADT 36, ADT 37, ADT 39, Anna 4, Shali
II	2	Jaya, Chatoki
III	2	STBN 1, STBN 2
IV	16	ADT 41, ADT42, ADT 43, ADT45, ADT 46, ADT 47, ADT 48, ADT 49, ADT 50, TKM 9, PMK 3, AD 06207, TPS 5, MDU 4, NLR 34449, Bora
V	2	BPT 5204, MTU 1001
VI	2	Porimol, Sampada
VII	2	Gayathri, PY 1
VIII	2	RNR 1446, MTU 1010
IX	1	STBN 3
X	1	Ranjith

Table 3: Average inter and intra cluster D^2 and D values for 35 rice genotypes.

Cluster Number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	308.47 (17.56)	206.903 (14.38)	185.83 (13.63)	501.51 (22.39)	191.74 (13.84)	269.98 (16.43)	316.12 (17.78)	651.03 (25.51)	331.70 (18.21)	637.74 (25.54)
II		17.71 (4.20)	126.01 (11.22)	320.10 (17.89)	67.55 (8.21)	147.73 (12.15)	108.25 (10.40)	649.62 (25.48)	240.39 (15.50)	394.23 (19.85)
III			54.30 (7.36)	380.99 (19.51)	107.65 (10.37)	202.41 (14.22)	282.69 (16.81)	430.05 (20.73)	227.13 (15.07)	586.29 (24.21)
IV				377.30 (19.42)	295.33 (17.18)	415.45 (20.38)	442.23 (21.02)	759.39 (27.55)	551.58 (23.48)	351.47 (18.74)
V					71.377 (8.44)	162.32 (12.74)	207.04 (14.38)	674.17 (25.96)	180.46 (13.43)	367.98 (19.18)
VI						99.85 (9.99)	361.16 (19.00)	684.76 (26.16)	514.49 (22.68)	379.98 (19.48)
VII							132.57 (11.51)	737.42 (27.15)	287.79 (16.96)	590.56 (24.30)
VIII								445.18 (21.09)	915.19 (30.35)	1093.59 (33.06)
IX									0.00 (0.00)	869.14 (29.48)
X										0.00 (0.00)

X (1093.59). This was followed by clusters VIII and IX (915.19) and cluster IX and X (869.14). Whereas lowest inter cluster distance was recorded between cluster II and V (67.55) followed by clusters III and V (107.65) and clusters II and VII (108.25). Thus, the hybridization between genotypes from distant clusters may result in heterotic hybrids and transgressive segregants.

The maximum intra cluster distance was observed in cluster VIII. Hence, genotypes from this cluster could be used as potential line for hybrid to produce superior progenies. The maximum inter cluster distance was observed between cluster VIII and X followed by cluster VIII and IX and cluster IV and VIII. The parents selected from these divergent clusters could produce superior progenies and hybrids. Cluster mean values for yield and its component traits have been presented in Table 4. Cluster X recorded earliness in flowering and may serve as a suitable source for incorporation of earliness in other genotypes. The clusters II, III, V, VI, and VII recorded maximum cluster mean value for grain yield per plant and other yield contributing traits. Cluster II recorded maximum average values for days to first flowering and grain yield per plant followed by cluster X exhibited maximum average values for number of grains per

Table 4: Cluster means of 35 rice genotypes for different traits.

Characters	Clusters										General Mean
	I	II	III	IV	V	VI	VII	VIII	IX	X	
Days to first flowering	59.44	68.65	59.90	63.39	66.04	66.10	65.3	68.17	68.19	55.26	63.52
Plant height at maturity	83.76	80.80	85.59	82.09	76.64	88.02	78.72	110.93	60.75	87.00	83.47
Number of tillers per plant	13.87	18.04	17.54	14.81	15.37	20.20	16.10	17.41	18.46	11.53	15.59
Number of panicles per plant	10.84	14.82	14.93	12.02	12.60	16.10	13.27	13.61	15.40	7.13	12.56
Panicle length	21.40	22.36	22.16	21.92	19.91	19.99	22.53	20.78	20.13	21.79	21.57
Number of. grains per panicle	132.09	142.76	95.66	128.57	126.94	158.60	152.73	78.02	89.78	187.46	128.69
1000 grain weight	18.81	20.52	20.91	17.81	18.98	15.70	20.59	19.04	21.32	17.49	18.55
Grain length	0.74	0.78	0.76	0.88	0.79	0.75	0.80	0.82	0.78	0.90	0.82
Grain breadth	0.25	0.25	0.24	0.24	0.24	0.21	0.30	0.27	0.28	0.20	0.24
Grain L/B ratio	2.92	3.04	3.17	3.63	3.25	3.55	2.61	2.93	2.73	4.40	3.34
Grain yield per plant	25.95	44.14	31.24	26.35	29.96	38.92	43.38	20.71	28.24	23.36	29.13

Table 5: Contribution of different characters to genetic divergence.

S. No.	Characters	Contribution (percent)
1	Days to first flowering	0.00
2	Plant height at maturity	6.21
3	Number of tillers per plant	0.00
4	Number of panicles per plant	0.00
5	Panicle length	0.00
6	Number of grains per panicle	5.71
7	1000 grain weight	3.69
8	Grain length	26.72
9	Grain breadth	20.33
10	Grain L/B ratio	6.36
11	Grain yield per plant	30.92

panicle, grain length and grain L/B ratio whereas cluster VIII recorded maximum for plant height at maturity.

The contribution of different characters towards total divergence has been presented in (Table 5). It revealed that with 30.92 per cent contribution by grain yield per plant with 26.72 per cent contribution by the grain length and 20.33 per cent contribution by grain breadth were the major forces of discrimination among the genotypes tested. Similar findings were made by Arivoli *et al.*, (2009) for number of grains per panicle and grain yield per plant and Senapati and Sarkar (2005) for panicle length. The major traits contributing to total divergence may be utilized as parameters in selecting genetically diverse parents. The major traits contributing to total divergence may be utilized as parameters in selecting

genetically diverse parents. It is necessary to carefully analyse the selection of a particular cluster from which genotypes are to be chosen in crossing programme as well as selection of a particular genotype from a selected cluster. While selecting genotypes from distinct cluster for hybridization programme their *per se* performance of different traits should also be given due importance depending upon the traits to be combined. The parents from distantly related clusters belonging to cluster VIII and IX belonging to cluster VIII and X followed by clusters could be used for combining characters of yield and grain quality components to achieve desirable segregants under coastal saline condition.

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