STUDIES ON GENETIC DIVERGENCE OF SOME IMPROVED RICE GENOTYPES UNDER SALINITY (*ORYZA SATIVA* L.)

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Abstract

An investigation was carried out with fifty rice genotypes to study the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics. Twelve yield and quality traits were recorded on the genotypes raised in RBD design with three replications. The fifty genotypes were grouped into twelve clusters by using hierarchical analysis with cluster IX had maximum of 10 genotypes. Maximum intra cluster distance was observed in cluster XII (24.01) which show the greater genetic divergence between the genotypes belonging to this cluster. Grain yield per plant, days to fifty per cent flowering, hundred grain weight and number of grains per panicle together contributed 76.39 per cent to the total divergence. The maximum inter cluster distance was between clusters VI and XII (40.76) followed by clusters IV and XII, X and XII (37.76) indicating wide genetic diversity and it may be used in rice hybridization programmes for improving grain yield.

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

Introduction

Rice (*Oryza sativa* 2n : 2X = 24) is the most important cereal crop cultivated almost all over the world. Genus *Oryza* belongs to tribe Oryzae of family Poaceae. Out of twenty four species only two species are cultivated are cultivated *i.e.*, *O. sativa* and *O. glaberrima*. It is one of the main sources of carbohydrate for about half of the world population. In 2015, world rice production was about 486.8 metric tons and in India about 44.6 million hectares' area with total production of 90 metric tonnes.

Genetic variability is the important tool in the hands of plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). It is based on multivariate analysis and grouped into various clusters as given by Spark (1973). This is the most effective method for qualifying degree of genetic diversity among the genotypes. The present investigation is about estimation of magnitude of genetic divergence of 50 rice genotypes and to identify diverse genotypes for the future study.

Materials and Methods

Fifty rice genotypes selected from different places were transplanted in RBD design with three replications at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India during year samba 2011 (Aug.-Dec.). In each replication, single seedling per hill was transplanted in main field in 20 rows with 20x15cm spacing. The observations were recorded on single plant basis in five randomly selected plants of genotypes for days to fifty per cent flowering (DFF), plant height (PH), number of tillers per plant (NTPP), number of productive tillers per plant (NPTPP), panicle length (PL), number of grains per panicle (NGPP), grain length (GL), grain breadth (GB), kernel length (KL), kernel breadth (KB), hundred grain weight (HGW) and grain yield per plant (GYPP). The analysis of genetic divergence was done using Mahalanobis (1936) D^2 Statistics. The genotypes are grouped with different clusters, inter and intra cluster distances and mean performances for characters were also computed.

Results and Discussion

The analysis of variance gave significant differences among the genotypes for all the characters and indicated the existence of variability among the genotypes (table 1). The results obtained are in confirmation with the earlier results (Nayak *et al*., 2004; Singh *et al*., 2005; Sabesan,

2005 and Rajasekaran, 2006). Based on D² values, fifty genotypes were grouped into 12 clusters using non-hierarchical cluster analysis as it is a potential tool and emphasized by many workers (Karthikeyan, 2002; Sabesan, 2005) (table 3).

The genotypes in each cluster were closer than the genotypes in different clusters. The clustering pattern of the genotypes indicated that there was no parallelism between genetic and geographical diversity (Nayak *et al*., 2004; Jadhav Pravin *et al*., 2003; Monika *et al*., 2008; Yadav *et al*., 2011).

Cluster IX comprised the largest number with ten genotypes followed by clusters VI & VIII with nine genotypes and eight genotypes respectively. The clusters III and V had four genotypes followed by cluster I with three genotypes the by clusters II, IV, VII, XI and XII with two genotypes each.

Average Inter and Intra Cluster distances have been shown in table 4. The maximum Inter cluster distance existed between clusters VI and XII (40.76) followed by clusters IV and XII, X and XII (37.76) and the minimum Inter cluster distance was between clusters I and VII (5.92) followed by clusters I and X (6.93), respectively.

The Intra cluster distance varies from 2.41 (cluster II) to 24.61 (cluster XII). The genotypes of the clusters VI and XII may be selected as parent for hybridization programme. This is in conformity with the findings of Karthikeyan (2002), Venkatesan (2004), Sabesan (2005), Velmurugan (2006) and Yadav *et al*. (2011).

The Diversity was also supported by the appreciable amount of variations among cluster means for different characters (table 5). The earliness in flowering was observed in cluster IV while late flowering was observed in cluster XII. Cluster III recorded maximum plant height as opposed to cluster VII registered the lowest.

Cluster VIII recorded maximum number tillers per plant whereas cluster V had the least number. Cluster IV and X had long grains while cluster XII had minimum grain length.

Kernel length had maximum in cluster VII and minimum in cluster IV. Cluster VIII had maximum in hundred grain weight while minimum in cluster VII, followed by cluster II.

Among the twelve clusters studied, seven clusters *viz*., II, III, IV, VI, VII, X and XI recorded earliness than the general means. The clusters II, IV, VI and X exhibited higher number of grains per panicle than the general mean. The clusters III, VI, VII, VIII, XI were characterized with high mean value for grain yield per plant than the general mean.

The mean performance of cluster VII had favourable mean than the general mean for ten characters *viz*., plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, grain length, grain breadth, kernel length, hundred grain weight and grain yield per plant and second high yielder cluster III recorded high mean values for eight characters namely days to fifty per cent flowering, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, grain length, kernel length, hundred grain weight and grain yield per plant.

The third high yielder and second largest cluster, cluster VII recorded high mean values the general mean for eight characters including day to fifty per cent flowering, plant height, panicle length, number of grains per panicle, grain breadth, kernel breadth hundred grain weight and grain yield per plant.

Cluster IX the largest cluster had desirable mean than general means for plant height, number of tillers per plant, number of productive tillers per plant, grain length, grain breadth and kernel breadth. Almost the minimum and maximum cluster mean values were distributed in relatively distant clusters.

The contribution of individual trait to the divergence among genotypes is presented in table 6. Grain yield per plant contributed maximum towards divergence (29.14%) followed by days to fifty percent flowering (24.97%), hundred grain weight (12.16%) and number of grains per panicle (10.12%). Remaining traits had very little or no contribution towards the genetic divergence and so they are less important. Since varieties with narrow

Table 1 : Analysis of variance for 12 morphological characters in 50 rice genotypes.

Source	df	MSS											
		DFF	PH	NTPP	NPTPP	PL	NGPP	GL	GB	KL	KB	HGWT	GYPP
Replication	2	25.45	19.63	12.65	6.76	7.34	9.06	0.02	0.002	0.02	0.07	0.03	28.267
Genotypes	49	199.33**	135.59**	32.35**	23.32**	23.32**	1422.87**	0.48**	0.24**	0.27**	0.24**	0.26**	144.67**
Error	98	9.97	6.77	5.06	3.38	3.33	389.27	0.01	0.05	0.05	0.08	0.03	12.29

**Significant at 1% level.

Table 2 : Mean performance of 12 morphological characters in 50 rice genotypes.

Genotypes	DFF	PH	NTPP	NPTPP	PL	NGPP	GL	GB	KL	KB	HGW	GYPP
PS-267	79.50	96.23	20.50	15.83	20.85	105.00	5.55	2.52	5.31	2.32	1.79	29.08
AC-35548	80.82	111.50	27.33**	22.66**	21.41	118.83**	5.58	2.65	5.42	2.44	1.76	46.42**
PS-360	75.00	99.65	19.83	15.66	19.81	92.50	5.87*	2.47	5.69*	2.28	1.95**	28.30
AC-35450	93.83	104.06	22.83	17.66	21.10	100.00	5.70	2.37*	5.57	2.27	1.39	23.64
AC-36110	76.16	90.40	17.33	13.16	20.766	100.83	5.26	2.60	5.16	2.41	1.64	21.58
PS-36	84.66	92.15	20.00	15.66	20.20	94.66	5.40	2.43	5.22	2.25	1.57	23.37
AC-35525	65.50**	89.45	24.00	20.00	21.15	97.16	5.52	2.51	5.33	2.32	1.56	30.16
PS-366	76.56	101.74	23.16	18.00	21.51	129.66**	5.66	2.66	5.47	2.52	1.55	36.20**
JBT-37/85	66.66**	97.63	24.00	19.83	21.13	97.33	5.73	2.46	5.60	2.32	1.80*	34.30
JBT-37/154	72.83*	95.11	24.33	19.83	20.88	112.50**	5.48	2.56	5.39	2.42	1.52	33.50
AC35361	78.16	89.81	19.16	15.50	20.81	89.16	5.59	2.33*	5.45	2.18*	2.13**	29.50
JBT-37/89	76.66	95.43	20.66	16.33	20.43	96.66	5.68	2.65	5.54	2.45	1.54	24.27
PS-367	70.83**	93.70	22.00	17.83	20.70	102.50	5.61	2.52	5.46	2.32	1.47	26.79
PS-259	92.33	98.26	22.33	17.16	22.93**	115.00**	5.40	2.36*	5.28	2.20*	1.65	33.31
PS-91	71.83**	90.10	23.50	19.16	23.73**	107.66*	5.92*	2.70	5.77**	2.53	1.63	33.37
AC-39010	84.33	90.23	23.16	16.83	20.35	101.83	5.46	2.48	5.34	2.31	1.86**	32.09
AC-35170	90.66	87.51*	20.33	15.83	19.65	96.16	5.95**	2.60	5.77**	2.41	1.54	23.80
JBT-38/96	80.50	97.28	22.50	18.16	20.83	98.66	5.90*	2.47	5.68*	2.31	1.68	29.83
PS-325	90.83	95.90	25.33*	20.00	21.21	107.16*	5.57	2.44	5.40	2.30	1.90	40.43**
AC-35135	95.83	95.21	27.00**	22.00*	21.15	96.83	5.60	2.61	5.40	2.49	1.57	34.18*
VANDANA	74.00*	84.73**	23.60	18.83	19.20	77.33	5.60	2.50	5.46	2.27	1.72	25.02
CTH-1	74.16	94.60	20.83	17.00	19.98	90.90	5.57	2.66	5.45	2.49	1.67	25.11
PS-376	80.50	98.66	21.50	17.83	18.18	86.66	5.38	2.27**	5.22	2.11**	1.55	24.47
BPT-5204	74.16	93.83	20.83	17.50	19.30	89.33	5.83*	2.53	5.63	2.39	1.89**	29.83
AC-35187	72.50*	93.38	20.66	17	19.66	85.00	5.82	2.63	5.71*	2.46	1.60	22.92
S-9	85.83	100.53	20.50	16.50	22.00	108.33*	5.37	2.39*	5.25	2.23*	1.74	31.20
DODDABATTA	90.66	103.25	22.66	19.16	19.48	105.33	5.81	2.54	5.61	2.40	1.46	28.67
AC-35066	74.66	91.86	23.00	18.50	20.58	93.83	5.75	2.43	5.63	2.32	1.77*	29.83
JBT-37/164	79.33	93.90	21.16	16.50	21.28	84.50	5.76	2.56	5.59	2.41	1.60	22.66
AC-35298	79.83	91.95	22.00	17.83	21.61	89.00	5.70	2.55	5.53	2.42	1.62	25.33
AC-39020	85.16	89.80	22.66	18.83	20.25	93.00	5.61	2.56	5.38	2.24	1.73	30.09
KRH-2	74.83	91.61	22.00	17.66	22.70*	94.00	5.87*	2.40	5.47	2.14**	1.66	27.45
JBT-36/169	81.16	99.95	23.83	20.16*	20.93	108.83	5.73	2.50	5.59	2.38	1.77*	37.91**
JBT-36/119	74.16	89.03*	19.83	16.16	19.98	97.66	5.67	2.58	5.50	2.43	1.63	25.45
JBT-36/79	81.16	92.66	21.00	16.66	21.01	102.50	5.81	2.36*	5.50	2.24	1.83*	30.85
JBT-37/29	79.16	89.21	23.16	19.50	20.16	102.50	5.64	2.41	5.50	2.28	1.61	30.85
AC-35406	85.16	98.90	22.50	18.83	21.15	99.66	5.78	2.78	5.59	2.61	1.74	32.44
THANU	97.33	99.43	22.16	17.83	20.88	94.16	5.60	2.60	5.45	2.40	1.61	26.96
PS-329	84.00	96.23	21.33	17.00	20.89	83.50	5.31	2.31*	5.56	2.13**	1.58	22.03
AC-35341	71.50**	98.60	19.83	16.50	22.56	81.50	5.59	2.62	5.38	2.43	1.64	21.90
BR-2655	78.00	89.88	20.66	16.00	21.50	101.16	5.51	2.36*	5.30	2.20*	1.78*	28.76
AC-35415	78.66	90.10	24.83*	20.16*	20.76	91.00	5.59	2.36*	5.45	2.20*	1.45	26.89
PS-307	82.00	91.68	26.00	20.50*	21.13	112.00**	5.58	2.45	5.41	2.30	1.77*	40.22**
PS-242	80.00	95.55	21.66	17.33	21.88	98.33	5.87*	2.67	5.70*	2.47	1.56	26.83

Table 2 continued...

Table 2 continued...

JBT-38/116	73.66*	97.48	21.66	17.33	21.28	79.83	5.53	2.58	5.40	2.43	1.57	21.76
JBT-38/114	77.33	92.106	22.16	17.00	22.00	100.33	5.85*	2.62	5.72*	2.48	1.65	27.97
TRY-3	70.83**	99.71	19.50	15.63	21.00	106.00	5.59	2.69	5.44	2.44	1.66	27.08
IR-36	86.16	99.18	22.50	17.50	20.35	91.16	5.33	2.44	5.21	2.22*	1.66	25.88
CSR-27	73.00*	100.65	24.00	18.33	20.33	100.00	5.79	2.41	5.57	2.21*	1.73	31.70
ADT-46	80.16	94.34	22.66	18.0	20.36	82.50	5.70	2.67	5.33	2.51	1.59	26.29
Grand mean	79.65	95.08	22.18	17.82	20.86	97.98	5.65	2.52	5.47	2.35	1.66	28.97
CD (0.05)	5.57	5.99	2.58	2.21	1.47	9.18	0.18	0.13	0.18	0.12	0.11	4.63
CD (0.01)	7.38	7.93	3.41	2.92	1.95	12.15	0.28	0.21	0.28	0.20	0.18	6.13

* Significant at 5% level,   ** Significant at 1% level.

Table 3 : Composition of D^2 clusters for 50 rice genotypes.

Clusters	No. of genotypes	Name of genotypes
I	3	PS-267, CTH1, JBT-36/116
II	2	JBT-37/164, AC-35298
III	4	AC-35548, PS-360, JBT-38/96, PS-242
IV	2	AC-35341, JBT-38/116
V	4	AC-354450, AC-36110, PS-36, IR-36
VI	9	AC-35525, PS-366, JBT-37/85, PS-367, AC-35361, JBT-37/1544, JBT-37/89, JBT-36/79, BR-2655
VII	2	BPT-5206, AC-35066
VIII	8	PS-259, PS-91, AC-39010, AC-35170, PS-325, AC-35135, JBT-36/169, PS-307
IX	10	Vandana, PS-376, AC-35187, S-9, Dodda Batta, AC-39020, JBT-37/29, AC-35406, AC-35415, KRH-2
X	2	JBT-36/114, Trichy-3
XI	2	CSR-27, ADT-46
XII	2	Thanu, PS-329.

Table 4 : Average inter and intra cluster D^2 and D values of 50 rice genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**2.48 (6.19)**	2.81 (7.91)	3.39 (15.44)	2.95 (8.71)	4.25 (18.10)	3.16 (9.99)	2.43 (5.92)	5.19 (29.00)	3.84 (14.76)	2.63 (6.93)	3.35 (11.25)	5.57 (31.02)
II		**1.55 (2.41)**	3.90 (15.22)	2.89 (8.36)	3.78 (14.31)	3.80 (14.46)	2.98 (8.90)	4.40 (19.38)	3.73 (13.96)	3.05 (9.34)	3.35 (11.22)	4.52 (20.44)
III			**4.38 (19.22)**	4.45 (19.83)	4.94 (24.43)	4.40 (19.40)	4.13 (17.10)	4.87 (23.77)	4.53 (20.60)	4.14 (17.21)	4.07 (16.63)	5.50 (30.29)
IV				**1.66 (2.77)**	5.03 (25.35)	3.74 (14.00)	3.15 (9.95)	6.00 (36.01)	4.44 (19.72)	3.18 (10.14)	3.80 (14.43)	6.14 (37.76)
V					**4.13 (17.07)**	5.16 (26.69)	4.90 (24.05)	4.85 (23.56)	4.50 (20.29)	4.87 (23.77)	4.86 (23.64)	4.14 (17.20)
VI						**3.83 (14.72)**	3.23 (10.43)	5.70 (32.58)	4.55 (20.78)	3.33 (11.11)	3.97 (15.78)	6.38 (40.76)
VII							**2.07 (4.32)**	5.45 (29.79)	4.16 (17.36)	2.71 (7.36)	3.72 (13.88)	6.02 (36.27)
VIII								**4.52 (20.43)**	5.17 (26.78)	5.44 (29.65)	5.35 (28.67)	4.77 (22.83)
IX									**4.53 (20.57)**	4.43 (19.63)	4.33 (18.82)	5.16 (26.65)

Table 4 continued...

Table 4 continued...

										X	XI	XII
X										**3.26 (10.66)**	3.72 (13.83)	6.14 (37.76)
XI											**4.07 (16.59)**	5.90 (34.87)
XII												**4.96 (24.01)**

Table 5 : Cluster mean of 50 rice genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	75.94	93.28	20.38	16.33	20.27	97.55	5.60	2.58	5.42	2.41	1.69	26.55
II	79.58	92.92	21.58	17.16	21.45	86.75	5.73	2.55	5.56	2.41	1.63	23.99
III	79.08	100.99	22.83	18.45	20.98	102.08	85.80	2.57	5.62	2.38	1.74	32.84
IV	72.58	98.04	20.16	16.91	21.92	80.66	5.56	2.60	5.39	2.43	1.60	21.83
V	85.20	96.45	20.66	16.00	20.60	96.66	5.42	2.46	5.29	2.28	1.57	23.62
VI	74.03	93.93	22.11	17.77	21.01	103.18	5.62	2.49	5.45	2.33	1.69	30.48
VII	74.41	92.85	21.91	18.00	19.94	91.58	5.79	2.48	5.63	2.35	1.83	29.83
VIII	86.12	93.60	23.93	18.95	21.38	105.68	5.65	2.52	5.49	2.36	1.71	34.41
IX	80.65	94.02	22.41	18.43	20.35	94.28	5.65	2.48	5.46	2.29	1.62	28.00
X	74.08	95.89	20.83	16.41	21.50	103.16	5.72	2.65	5.58	2.51	1.65	27.52
XI	76.58	97.50	23.33	18.16	20.35	96.25	5.75	2.54	5.45	2.36	1.66	28.99
XII	90.66	97.83	21.75	17.41	20.88	88.83	5.60	2.45	5.50	2.26	1.59	24.50
General Mean	79.65	95.08	22.18	17.82	20.86	97.98	5.65	2.52	5.47	2.35	1.66	28.97

Table 6 : Contribution of different characters to genetic divergence.

S. no.	Characters	Contribution of each characters (%)
1.	Days to fifty percent flowering (days)	24.97
2.	Plant height (cm)	1.06
3.	Number of tillers per plant	0.65
4.	Number of productive tillers per plant	2.28
5.	Panicle length (cm)	1.38
6.	Number of grains per panicle	10.12
7.	Grain length (mm)	4.16
8.	Grain breadth (mm)	1.30
9.	Kernel length (mm)	8.70
10.	Kernel breadth (mm)	4.08
11.	100 grain weight (g)	12.16
12.	Grain yield per plant (g)	29.14

genetic base are increasingly vulnerable to biotic and abiotic stress, availability of genetically diverse genotypes for hybridisation programme become more important. Since grain yield per plant contributed maximum towards genetic divergence, we go for direct selection of this trait for the diversity purpose.

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