STUDIES ON NATURE OF GENETIC DIVERGENCE IN RICE
(*Oryza sativa* L.)

N. Chamundeswari
Acharya N.G. Ranga Agricultural University

Abstract: Seventy germplasm lines developed by different Rice Research Centres across the country were evaluated at Rice Research Unit, Bapatla to elicit the information on nature and magnitude of genetic divergence by using Mahalanobis D^2 analysis. The experimental material was divided in to eight clusters based on D^2 values. The clustering pattern showed no relationship between geographic distribution and genotypic diversity. The cluster III was the biggest cluster consisting of 20 genotypes followed by cluster I (19), cluster II (14), cluster IV (8) and Cluster V (6). The clusters VI,VII and VIII are monogenic. The inter cluster distances ranged from 759.25 (cluster V and VIII) to 73.82 (cluster VI and VIII) and the intra cluster distances ranged from 94.90 (cluster IV) to 0.00 (Clusters VI, VII and VIII). Cluster V had highest mean value for grain yield (4.9t/ha), cluster VI had lowest mean value for test weight of (14.8 grams). The characters test weight (29.57%), grain yield (28.51%) and plant height at maturity (19.79%) contributed maximum towards genetic divergence. The genotypes of clusters having high mean value for grain yield and panicle length (cluster V), number of panicles per plant (cluster VII) and slender grains (cluster III) would give high heterotic combinations.
Keywords: Rice, Genetic diversity, Mahalanobis D^2, Germplasm, Clustering.

Introduction

Genetic diversity is one of the key factors in tailoring the effective breeding programme in any crop. Success of hybridization followed by selection depends largely on the selection of parent with high genetic variability for different characters. The genetically diverse parents are likely to produce heterotic effects and desirable seggregants. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murty and Arunachalam (1966); Sinha *et al.* (1991) and Rahman *et al.* (1997), Bose and Pradhan (2005) and Sabesan *et al* (2009)). Therefore, the magnitude of genetic divergence and characters contributing to the genetic divergence were studied among seventy germplasm lines of rice.

Materials and Methods

Seventy germplasm lines developed by different Rice Research Centres across the country were evaluated under All India Coordinated Rice Improvement Project at Rice Research

Unit, Bapatla, Andhra Pradesh, during *Kharif* 2007. The experimental material was planted in RBD design with three replications. Each entry was sown in 10m^{2}plots adopting a spacing of 20x15 cm. All the recommended package of practices was followed and need based plant protection was done. Observations in each replication were recorded on days to 50% flowering, plant height at maturity (cm), number of tillers per plant, number of panicles per plant, panicle length (cm), test weight (g) and grain yield (t/ha). The data generated was utilized to estimate the genetic divergence by using Mahalanobis (1936) D^2 analysis as described by Rao (1952).

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for seven characters, indicating existence of variability among the genotypes for all the characters studied. Based on D^2 values the seventy genotypes were grouped into eight clusters (table1). The clustering pattern showed no relationship between geographic distribution and genotypic diversity as the genotypes from different geographic origins were grouped in the same cluster. This may be due to free exchange of breeding material from one place to another besides unidirectional selection for a particular trait under the respective domestication. Murthy and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater diversity than geographic distances. Earlier reports also indicated that geographic diversity can not always be used as an index of diversity (Ramesh Chandra *et al*., (2007), Bose and Pradhan (2005) and Sabesan *et al* (2009)).

Among the clusters, cluster III was the biggest cluster consisting of 20 genotypes followed by cluster I (19), cluster II (14), cluster IV (8) and Cluster V (6). The clusters VI, VII and VIII are monogenic. The inter cluster and intra cluster D^2 values are presented in table 2. The divergence within the cluster indicates the divergence among the genotypes falling in the same cluster. On the other hand inter cluster distance suggest the divergence between genotypes of different clusters. The data suggested maximum distance between the genotypes falling under cluster IV (94.90) followed by cluster V (85.02) and cluster II (80.64). The clusters VI, VII and VIII are monogenic. The inter cluster distances indicated greater divergence between cluster V and cluster VIII (759.25) followed by clusters V and III (543.04) and minimum inter cluster distance was found in between the clusters VI and VII (73.82) followed by clusters III and VIII (134.92).

The cluster means for different characters were presented in table 3. The cluster VII recorded highest mean value for days to 50% flowering, plant height at maturity (cm) and number of

panicles per plant. Cluster II had highest mean value for panicle length (21.71cm). Mean value for number of panicles per plant was found maximum in cluster VII (10.3) followed by cluster VIII (10.2). The genotypes with slender grain were found in cluster VI (14.8 grams test weight) followed by cluster (15.51 grams) where as highest test weight was recorded in cluster V (25.52) which indicated that bold grain type of these lines. Cluster V had highest mean value for grain yield (4.9t/ha). Short duration genotype was included in cluster VIII with lowest mean value for days to 50% flowering (93.0 days) whereas medium duration genotypes are included in cluster IV and V (102 days). The cluster means indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Hence recombination breeding between genotypes of different clusters may be followed as suggested by Singh *et al* (1996). The relative contribution of characters towards the total genetic divergence is presented in table 4. The character test weight contributed maximum (29.57%) towards genetic divergence followed by grain yield (28.51%), plant height at maturity (19.79%) and days to 50% flowering (10.85%). Iftekharuddaula *et al* (2010) and Vimla Bisht *et al* (2007) also reported the plant height at maturity as one of the potential contributors towards total genetic divergence.

The present study revealed that considerable diversity existed both within and between the clusters. The genotypes from highly divergent clusters may yield the best parents for an effective crossing programme leading to accumulation of favorable genes in to a single genotype. Hence it is suggested that hybridization among the genotypes included in diverse clusters and the clusters having high mean value for grain yield and panicle length (cluster V), number of panicles per plant (cluster VII); slender grains (cluster III) would give high heterotic combinations thus produce large variability and better segregates in the segregating generations.

Literature cited

[1] Bose L.K., and Pradhan S. K. Genetic divergence in deepwater rice genotypes. 2005. J. Cent. Eur. Agric. (2005) 6:4, 635-640.

[2] Deepak Naik, Abhinay Sao, Sarawgi, A.K., and Pushpendra Singh. 2006. Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) Accessions of Central India. Asian J. of Plant Sci., 5(2); 197-200

[3] Iftekharuddaula, K.M., Khaleda Akter, Hassan, M.S., Kaniz Fatema and Adil Badshah.2010. Genetic divergence, character association and selection criteria in irrigated rice. Online J. of Bio. Sci., 2(4); 243-246.

[4] Mahalanobis,P.C. 1936. On generalized distance in statistics. Proc. Natl. Ins. Sci., India, 2, p. 49-55.

[5] Murthy, B.R. and Arunachalam, V. 1966. The nature of divergence in relation to breeding system inn some crop plants. Indian J. Genet. and Plant Breeding. 26 p. 188-198.

[6] Rahman, M., Acharya, B., Sukla, S. N. and Pande K. 1997. Genetic divergence in low land rice genotypes. Oryza, 34: 3, P. 209-212

[7] Ramesh Chandra, Pradhan,S.K., Sanjay Singh, Bose, L.K. and Singh,O.N. 2007. Multivariate Analysis in Upland Rice Genotypes. World J. Agric. Sci. 3(3): 295-300.

[8] Rao, C.R. 1952. Advanced statistical methods in biometrical research. John Wiley & Sons, New York.

[9] Sabesan Thayumanavan, Saravanan Kannapiran and Anandan Annamalai. 2009. genetic divergence analysis for certain yield and quality traits in rice (*Oryza sativa* l.) grown in Irrigated saline low land of Annamalainagar, South India. J. Cent. Eur. Agric. (2009) 10:4, 405-410

[10] Sinha, P.K., Chauhan U.S,K., Prasad, J.S. and Chauhan. 1991. Genetic divergence in indigenous upland rice varieties. Indian J. Genet. 51, P. 47-50

[11] Vimla Bisht, Balbeer Singh, Rao K.S., Maikhuri R.K. and Nautiyal A.R. 2007. Genetic divergence of paddy landraces in Nanakosi micro-watershed of Uttarakhand Himalaya. J. Trop. Agric. 45 (1-2): 48–50.

Table 1. Clustering pattern of genotypes based on D^2 values

Cluster	Number of genotypes	Name of the genotypes
I	19	R1243-1224-575-1, BPT 3291, CN 1265-7-10, US 311, CRAC-2222-545, OR 1631-7, OR 1912-24, CSAR 840, CB 20022, R 1244-1246-1-605-1, HUR SG – 32005, IR 64, JGL 3844, PR106, R 1207-257-5-1, CRAC 2223-767, P 4674-47-1-3 B, RP 4655-3-I 75870-5-5-5-B-2-B-3, P 4075-345-132-27
II	14	CN 1267-5-4, CN 1271-8-6, CR 2340-5, RP 4060-105-6-8-2-5-1-B, MTU HR 2091, WGL 198, BPT 5204, WGL 110, WGL 75, WGL 157, MTU 1088, US 312, MTU 1093, MTU 1094
III	20	OR 2309-19, WGL 190, SKL 53-36-16-55-18, JGL 3828, MTU 1095, CB04-110, SIRI 1253, KJT 15-1-38-8-9, WGL 193, RPHR 1053-6-4, CSAR V 301, AD 1260, PAB 3114, RTN 24, JGL 11470, WGL 167, RD 918, RDKV Shriram, RAU 3036
IV	8	SYE 9-11-16, SYE 18-12-10, RAU 747-12-6, AS 04001, RP 4092-365-117-10, RP 4092-412-120-15, RP 4675-16-2-3-1-4-B, RP 4407-TSH -42-12-1-2-2-1-3
V	6	NDR 9830145, R 1324-1997-1-1, CCRAC 2223-767, ND 9830144, BPT 4358, WGL 44
VI	1	MTU 1092
VII	1	CB 03-045
VIII	1	RP 4334-TSH -41-8-1-1-2-6

Table 2. Intra and inter cluster distances

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**54.95**	151.16	164.72	158.35	272.82	142.94	158.66	270.20
II		**80.64**	206.99	219.17	197.95	149.62	186.67	348.94
III			**70.48**	198.38	543.04	150.97	190.46	134.92
IV				**94.90**	391.23	171.97	324.10	343.32
V					**85.02**	318.85	349.30	759.25
VI						**0.00**	73.82	390.56
VII							**0.00**	369.13
VIII								**0.00**

* Diagonal values are intra cluster distances.

Table 3. Cluster means for the characters under study

Cluster/ Character	Days to 50% flowering	Plant height at maturity (cm)	Number of tillers per plant	Number of panicles per plant	Panicle length (cm)	Test weight (g)	Grain yield (t/ha)
Cluster I	102.61	92.98	9.61	8.63	20.13	23.75	2.82
Cluster II	104.32	102.22	10.50	8.91	21.71	19.00	3.97
Cluster III	102.38	97.10	10.14	9.02	20.00	15.51	2.35
Cluster IV	102.50	77.01	11.37	9.46	17.29	18.04	3.46
Cluster V	108.42	98.19	9.56	8.90	21.46	25.52	4.90
Cluster VI	116.00	89.25	10.50	8.10	18.60	14.80	2.85
Cluster VII	116.00	106.70	10.6	10.30	16.40	18.75	2.5
Cluster VIII	93.00	106.40	14.10	10.20	20.70	18.30	2.12

Table 4: Relative contribution of individual character towards total genetic divergence

S.No	Character	Contribution (%)
1	Days to 50% flowering	10.85
2	Plant height at maturity (cm)	19.799
3	Number of tillers per plant	0.33
4	Number of panicles per plant	0.83
5	Panicle length (cm)	0.12
6	Test weight (g)	29.57
7	Grain yield (t/ha)	28.51