

GENETIC DIVERGENCE IN DEEPWATER RICE GENOTYPES

Lotan Kumar Bose and S. K. Pradhan

Crop Improvement Division, Central Rice Research Institute, Cuttack-753006, Orissa, India, e-mail: lotankbose@yahoo.com

ABSTRACT

The nature and the magnitude of genetic divergence was estimated in 35 deepwater rice genotypes using Mahalonobis's D^2 – statistics. The genotypes were grouped onto 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Cluster IV showed maximum intra cluster divergence while inter cluster divergence was maximum between clusters IX and X. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Traits like plant yield, days to 50% flowering, EBT/m² and plant height were the major contributors to genetic divergence.

KEY WORDS: Deepwater rice, genetic divergence, Yield components

INTRODUCTION

In India around 43 million hectares of total geographical area was cropped with rice but the production is very low due to the low productivity of rice in major rice growing areas of Eastern Indian states. In Eastern India the production of deepwater rice is very low. The major constraint is lack of suitable varieties for this ecosystem. The development of stable rice varieties for this fragile ecosystem should be the major thrust in present situation. The estimate of genetic divergence in the available germplasm is important for the selection of desirable donors for breeding programme. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murty and Arunachalam (3); Sinha et al. (9) and Rahman et al. (5). Therefore, the magnitude of genetic divergence and characters contributing to the genetic divergence were studied for deepwater ecosystem.

MATERIALS AND METHODS

The materials for the present investigation consisted of 35 deepwater rice genotypes collected from different parts of the country. These were grown in randomized complete block design with three replications during wet season 2004 in low land with water depth varying from 50-100 cm during growth period of the crop. Thirty-day-old seedlings were transplanted in six rows/entry, each row having 30 hills with single seedling/hill and 20 x 15 cm spacing. Observations for quantitative traits viz. plant height, panicle length, EBT/m² and seed test weight were recorded on five randomly selected plants excluding the border rows from each entry. Days to 50% flowering was recorded on plot basis. The data was analyzed utilizing Mahalanobis's generalized distance (D²) to measure the genetic divergence among the test varieties and their grouping into different clusters was done by the Tocher's method Rao (7).

RESULTS

The analysis of variance revealed significant differences among the genotypes for all the six characters studied (Table 1). The results indicated high variances for most of the characters, which may favour selection and further utilization in future recombination-breeding programmes.

The thirty-five deepwater rice genotypes were grouped into ten clusters (Fig. 1 and Table 2). Cluster I is the largest cluster comprising of eleven genotypes followed by Cluster IV containing eight genotypes. Six genotypes were grouped in Cluster II; four in Cluster VII and one

genotype each in Cluster IV, V, VI, VIII, IX and X. It is interesting to observe that most of the genotypes of one cluster were adapted to only one region. The clustering pattern reflects the closeness between the clusters and the geographical adaptation of the genotypes. In cluster IV, all the genotypes are adapted to Orissa and cluster I mostly for West Bengal.

The intra and inter cluster distance is presented in Table 3. The intra cluster distance analysis revealed that the maximum divergence was observed in cluster IV. It is reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance. The other clusters showing high intra cluster values were cluster VII, II and I. The minimum or nil intra cluster values were exhibited by cluster III, V, VI, VIII, IX and X. This indicated negligible genetic diversity among the genotypes for each character.

The maximum inter cluster divergence was observed between cluster IX and X (67.45) followed by cluster VI and X and V and IX. Highly divergent genotypes would produce a broad spectrum of variability in the subsequent generation enabling further selection and improvement. Thus hybrids developed from the cross of CR 661-236 with NDRSB 96009, CR 662-2211 with NDRSB 96009 and CR 665-64 with CR 661-236 may produce high magnitude of heterosis or desirable transgressive segregants, which would facilitate successful breeding of deepwater rice.

The cluster mean for the characters studied are presented in Table 4. High grain yield, high-test weight and moderate plant height were recorded from cluster VI. Better grain yield, good seed weight, more EBT/m² and moderate plant height were observed in cluster IX. However cluster III gave high panicle length, more test weight and moderate plant height with very late maturity duration. These observations suggested that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Also, almost all the minimum and maximum cluster mean values were distributed in relatively distant clusters. The hybridisation between genotypes of different clusters is necessary for the development of desirable genotypes.

The data in Table 5 indicated that plant yield, days to 50% flowering, EBT/m² and plant height were the major contributors to the genetic divergence among the genotypes. These traits can be utilized as parameters in selecting genetically diverse parents.

DISCUSSION

The results of analysis of variance indicated high

Table 1. Analysis of variance for six characters of 35 deepwater rice genotypes (Mean sum of square)

Characters	Sources of variation		
	Replication (2)	Genotypes (34)	Error (68)
Days to 50% flowering	0.924	375.477**	1.139
Plant height	82.638**	996.360**	6.158
Panicle length	0.41	6.813**	0.625
EBT/m ²	0.867	1511.575**	9.298
Seed test weight	0.106	8.982**	0.136
Yield	0.003	2.949**	0.006

** Significant at 1% level probability

Table 2. Clustering pattern of 35 deepwater rice genotypes

Cluster No.	No. of Genotypes	Name of genotypes
I	11	CR 661-246, Golak, Dalbao, Amulya, Purnendu, Sabita, Matangini, Saraswati, Niraja, Sudhir, CR 2023-3
II	6	LPR 91, LPR 106-25, CN 1038, NDR 9730023, CR 665-64, RAU 1326-94-69
III	1	OR 1207-17-3
IV	8	OR 877-ST-4-2, Sarala, OR 1358-RGA-4, CR 778-95, Durga, OR 1359-RGA-10-4, CR 2006-10, CR 2003-13
V	1	CR 665-64
VI	1	CR 662-2211
VII	4	JM 50, NDR 40053-5-8, OR 1550-23, NPT 8
VIII	1	RAU 500-860-4
IX	1	CR 661-236
X	1	NDRSB 96009

Table 3. Average intra (bold) and inter cluster D² values

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	15.11	23.78	19.89	28.87	21.64	43.81	24.81	34.06	50.92	37.13
II		15.53	28.86	32.94	31.99	49.84	25.23	23.35	51.17	31.52
III			0.00	25.75	33.34	39.97	20.54	42.53	50.64	43.45
IV				17.88	40.52	25.59	33.47	45.42	32.27	52.04
V					0.00	54.62	32.59	35.03	60.56	32.83
VI						0.00	48.02	58.75	18.54	66.49
VII							17.13	32.02	54.11	29.83
VIII								0.00	56.54	18.90
IX									0.00	67.45
X										0.00

Table 4. Cluster means of characters in D2 analysis

Cluster	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	EBT/m ²	Test weight (g)	Yield kg/ha
I	154.97	139.39	24.85	119.09	24.41	840
II	139.83	129.61	24.94	155.61	24.06	840
III	164.67	112.67	28.33	135.33	25.43	680
IV	159.00	121.00	26.38	152.75	24.25	2200
V	151.33	149.00	22.67	84.67	20.40	610
VI	163.00	114.00	24.00	136.67	27.53	3560
VII	150.33	93.75	25.50	136.58	23.19	520
VIII	121.33	119.00	24.33	124.33	24.13	1060
IX	146.33	112.67	25.00	152.00	16.70	4330
X	126.67	96.33	24.33	106.33	20.47	230

Table 5. Character contribution to the genetic divergence

Character	% Contribution to divergence	
Days to 50% flowering	161	27.06
Plant height (cm)	80	13.45
Panicle length (cm)	1	0.17
EBT/m ²	88	14.79
Test weight (g)	21	3.53
Yield (kg/ha)	242	41.01

variances for most of the characters, which may favour selection and further utilization in future recombination-breeding programmes.

It is observed that most of the genotypes of one cluster were adapted to only one region. The clustering pattern reflects the closeness between the clusters and the geographical adaptation of the genotypes. The clusters containing solitary genotype were not in the clusters for the specific region might be due to the parentage of the genotype. For example CR 661-236 (CR 563-1014/BG 90-2//IR 42) present in cluster IV may be due to the diverse origin of the parents (India, Srilanka and Philippines). Earlier similar results have been reported by Ram and Panwar (6) and Mahajon et al. (1). However, majority of the results suggest no good correspondence between genetic divergence and geographical origin of varieties.

The maximum divergence was observed in cluster IV. It is reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance. Therefore due emphasis should be given on the members of cluster IV for selection of parents for hybridization programme. The other clusters showing high intra cluster values were cluster VII, II and I. the minimum or nil intra cluster values were exhibited by cluster III, V, VI,

VIII, IX and X. this indicated negligible genetic diversity among the genotypes for each character.

The maximum inter cluster divergence was observed between cluster IX and X (67.45) followed by cluster VI and X and V and IX. Highly divergent genotypes would produce a broad spectrum of variability in the subsequent generation enabling further selection and improvement. Thus hybrids developed from the cross of CR 661-236 with NDRSB 96009, CR 662-2211 with NDRSB 96009 and CR 665-64 with CR 661-236 may produce high magnitude of heterosis or desirable transgressive segregants, which would facilitate successful breeding of deepwater rice. Pradhan and Ray (4) and Rahman et al. (5) have also reported that selection of parents for hybridisation should be from two clusters having wider inter cluster distance to get maximum variability in the segregating generations. Pradhan and Ray (4) and Rahman et al. (5) have also reported that selection of parents for hybridisation should be from two clusters having wider inter cluster distance to get maximum variability in the segregating generations.

Observations from cluster mean suggested that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Interestingly, most of the minimum and maximum cluster means were distributed in relatively distant clusters. The

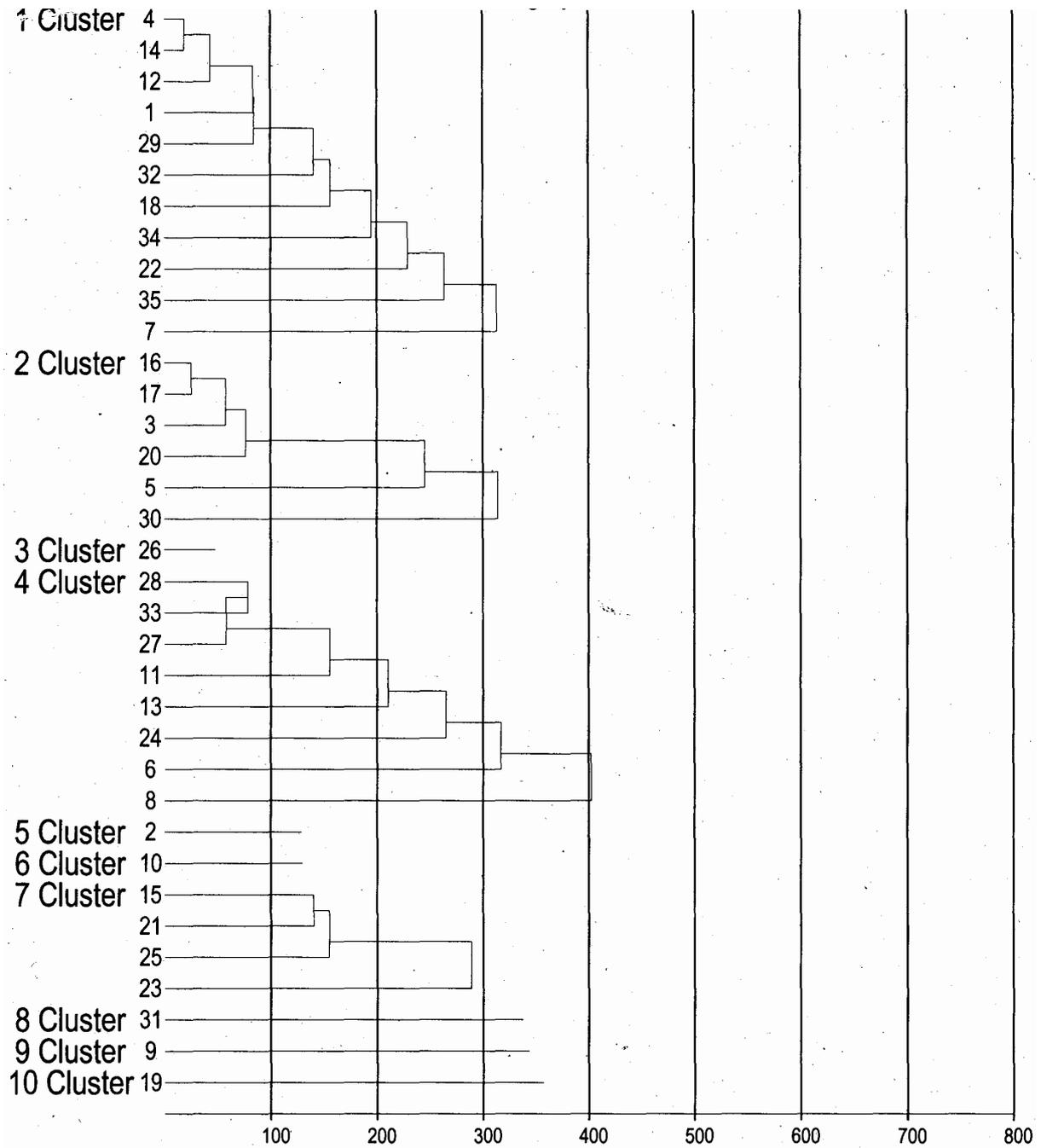


Fig.1. Clustering of genotypes by Tocher Method

hybridisation between genotypes of different clusters is necessary for the development of desirable genotypes. Recombination breeding between genotypes of different clusters have also been suggested by Sinha et al. (9) and Singh et al. (8).

Plant yield, days to 50% flowering, EBT/m² and plant height were observed to be the major contributors to the genetic divergence. These traits may be useful for selection of more diverse parents. Similar observations were also reported by Murty and Arunachalam (3) that greatest contributor to the genetic diversity in grain crops were flowering time, plant height and tiller number/plant.

In the present investigation, it is suggested that hybridisation programme within the divergent cluster IV and between CR 661-236 with NDRSB 96009, CR 662-2211 with NDRSB 96009 and CR 665-64 with CR 661-236 are expected to give promising and desirable recombinants in the segregating generations. Also, traits contributing maximum to genetic divergence viz. yield, days to 50% flowering, EBT/m² and plant height may be utilized in selecting genetically diverse parents.

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