

GENETIC DIVERSITY IN SALT TOLERANT RICE (*Oryza sativa* L.)

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ABSTRACT

Genetic diversity of 36 genotypes of salt tolerant coastal rice collected from IRRI (Philippines), BRRI (Bangladesh), China and Sri Lanka were studied through Mahalanobis  $D^2$  statistics to identify the most genetically distant parental genotypes for improving salt tolerant rice varieties. The genotypes were grouped into five clusters. The cluster II and cluster V contained the highest and the lowest number of genotypes, respectively. The highest intra-cluster distance was noticed for the cluster I and the lowest for the cluster V. The highest inter cluster distance was observed between cluster I and cluster V followed by cluster III from cluster I, cluster V from cluster II, III and IV. The second highest cluster mean for yield and the highest for other two yield contributing characters and the lowest for % sterility are obtained from cluster III, the highest mean values for tiller per plant and panicle per plant and the second highest for days to flowering and lowest for flag leaf angle, panicle length, grain per panicle and yield are found in Cluster I. The cluster mean of V ranked first for yield and second for tiller per plant, panicle per plant and panicle length and lowest for days to flowering and second lowest for duration. Therefore, more emphasis should be given on cluster I for selecting genotypes as parents for crossing with the genotypes of cluster III and cluster V, which may produce new recombinants with desired traits for yield and yield components.

**Key word:** Genetic divergence, salinity tolerance, rice

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important economic activity on earth as it is the second largest single use of the land for food production and also consumed by the half of the world's population. It occupies about 153 m ha of the world's area and is the staple food for about 90 percent population of South and Southeast Asia. About 0.83 million hectares of land affected by salt in the coastal region of Bangladesh (Karim *et al.*, 1990). In rainy season (Transplant Aman) farmers cultivated some traditional and a few modern high yielding rice varieties. Due to high rainfall the soil salinity was remain less than 4 dS / m electrical conductivity (EC) in *Transplant Aman* season. But in the *boro* season most of the lands were kept fallow due to lack of suitable salt tolerant rice varieties, because the soil salinity becomes higher at that time. This higher salinity rate ( $> 4 \text{ dS m}^{-1} \text{ EC}$ ) affected rice production in different growth stages. So it is needed to develop suitable salt tolerant rice varieties for *boro* season in coastal region.

Genetic divergence is a very useful tool for an efficient choice of parents for hybridization to develop high yield potential cultivars (Bhaumik *et al.*, 1971; Vairavan *et al.*, 1973; Parsons *et al.*, 1997; Sun *et al.*, 2003). Such a study also permits to select the genetically divergent parents to create a broad spectrum of genetic variation in segregating populations to obtain the desirable recombinants. The understanding of association of characters is prime important in developing an efficient breeding program. With the development of advanced biometrical techniques such as multivariate analysis based on Mahalanobis (1936) Statistics, quantification of degree of divergence among the biological population and assessing of relative contribution of different components to the total divergence at intra and inter cluster levels have now become possible (Vairavan *et al.*, 1973). Inclusion of more diverse parents (within a limit) in crossing is believed to increase the chance of obtaining stronger heterosis and gives broad spectrum of variability in segregating generations (Joshi and Dhawan, 1966; Anand and Murty, 1968). An attempt was made in the present study to analyze the genetic divergence of 36 coastal rice genotypes for identifying parental genotypes for further improvement of salinity tolerant rice varieties.

## MATERIALS AND METHODS

Twenty nine salt tolerant rice genotypes from International Rice Research Institute (IRRI), Philippines; four salt tolerant lines and one popular cultivars as check from Bangladesh Rice Research Institute (BRRI), and one of each from China and Sri Lanka were grown in the field of BRRI Regional Station Satkhira in *boro* season, 2002-2003. All of the IRRI and BRRI developed salt tolerant lines have ability to tolerate salinity at 6-12 dSm<sup>-1</sup> EC level. The trial was laid out in a Randomized Complete Block (RCB) Design with three replications. Forty five day old seedlings were transplanted in a 5 sq. meter plot following 25 cm and 15 cm spacing between rows and plants, respectively. Single seedling was used per hill for transplanting. Fertilizers were applied @ 100:60:40:12:3.5 kg N, P, K, S and Zn per hectare. All the recommended fertilizers except N were applied at final land preparation. Nitrogen (N) was applied in three equal splits at 15, 35 and 55 DAT (days after transplanting). Intercultural operations and pest control measures were done as and when necessary. Ten plants from each entry were randomly selected for recording data. Data were collected on plant height (cm), days to flowering, days to maturity, tiller plant<sup>-1</sup>, panicle plant<sup>-1</sup>, flag leaf angle, panicle length (cm), grain panicle<sup>-1</sup>, % sterility and yield (t/ha). Genetic diversity studied following Mahalanobis (1936) generalized distance (D<sup>2</sup>) was extended by Rao (1952). Based on the D<sup>2</sup> values, the varieties/ lines were grouped into clusters following the methods suggested by Tocher (Rao, 1952). Intra and inter cluster distances were calculated by the methods of Singh and Chowdhury (1985). Statistical analyses were carried out using IBM computer at BRRI, following Genstat 5 program.

## RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the 36 rice genotypes for all the ten characters under study indicating the presence of notable genetic variability among the genotypes. It was observed that in the principal component analysis, the first three components accounted for 92.97 % of total variation. Based on the degree of divergence 36 genotypes were grouped into five clusters on the basis of cluster analysis (Table 1).

Maximum 13 entries were grouped into the cluster II followed by 10, 9, 3 and 1 in clusters IV, I, III and V, respectively.

**Table 1. Rice genotypes in different clusters**

Cluster	Numbers of line/ variety	Numbers of population	Genotypes
I	4, 5, 7, 12, 13, 17, 27, 28, 30	9	IR61228-3B-10-3-1, IR61919-3B-24-3, IR72048-B-R-11-1-1, IR71990-3R-2-2-2, IR65185-3B-8-3-2, IR65192-4B-14-1, IR72046-B-R-15-3-1, IR72046-B-R-15-2-1, IR72046-B-R-7-1-1
II	1, 2, 3, 6, 15, 16, 19, 21, 22, 25, 32, 33, 36	13	IR64419-3B-12-2, IR45427-2B-2-2B-1-1, IR51941-AC10, IR64196-3B-14-3, IR63307-4B-4-3, IR64419-3B-4-3, IR10206-29-2-1, IR63275-B-1-1-3-3-2, IR72046-B-R-10-1-1, IR72046-B-R-6-2-2, IR60483-2B-17-2-1-2, IR64426-4B-17-2, BRRI DHAN28
III	11, 23, 31	3	BR5333-34-4-6, IR65196-3B-13-3-2, IR66401-2B-14-1-1
IV	8, 9, 10, 14, 18, 20, 24, 26, 29, 35	10	IR72046-B-R-1-1-1, IR72046-B-R-3-2-1, IR70031-4B-R-9-2-1, BR5778-156-1-3-HR1, AT309-1-GAZ, BR5777-11-2-4-1-HR2, IR72046-B-R-1-3-1, IR72046-B-R-6-3-1, PURBACIII, IR61247-3B-8-2-1
V	34	1	BR5777-4-2-4-2-HR2

Estimates of intra and inter cluster distances are presented in Table 2. The inter cluster distances in all the cases was larger than the intra cluster distances. It was indicated that wider diversity was present among genotypes of distant groups. The intra cluster distance was maximum in cluster I followed by II, III, IV and V indicating that the cluster I was the most heterogeneous. The intra cluster distance was 0.00 in cluster V indicating there was no heterogeneity, this result was found due to only one entry was there. The similar results were reported by Rahman *et al* (1998) in wheat and Islam *et al* (2004) in rice. Regarding inter cluster distance cluster V showed maximum genetic distance (14.4) from cluster I followed by cluster III (13.1) from cluster I, cluster V (12.3), (12.1) and (12.0) from cluster II, III and IV, respectively. This was suggested that wide genetic diversity remained among them. -A moderate or intermediate cluster distance was observed between cluster III and II (9.1) followed by cluster IV and I (6.7) and cluster IV and III (6.3). It was suggested that the genotypes of these clusters were genetically moderately distant. The minimum inter cluster divergence was observed between cluster IV and cluster II (2.8) and cluster II and cluster I (3.9) indicated that the genotypes of these clusters were genetically closed.

**Table 2. Intra (bold) and inter cluster distances ( $D^2$ ) of 36 rice genotype**

Cluster	I	II	III	IV	V
I	<b>1.0</b>	3.9	13.1	6.7	14.4
II		<b>0.8</b>	9.1	2.8	12.3
III			<b>0.7</b>	6.3	12.1
IV				<b>0.6</b>	12.0
V					<b>0.0</b>

Cluster I had the highest mean values for tiller per plant and panicle per plant and second highest for days to flowering and the lowest for flag leaf angle, panicle length, grain per panicle and grain yield (Table 3). Such results indicated that the genotypes of this cluster were good as parental selection for further improvement for yield and its components. The mean values for cluster II ranked the first for days to flowering, duration and % sterility which have the negative role to yield and the lowest for yield. Thus the genotypes of this cluster may not be good as parents for improving yield and yield components. The mean values for cluster III ranked the first for plant height, panicle length, grain per panicle and second highest for duration, flag leaf angle and yield and lowest for panicle per plant and % sterility which have the positive role to increase the yield. From this result it was suggested the genotypes of this cluster were suitable for selecting as parents for improving yields and its components. The cluster IV had the second highest cluster mean value for grain per panicle and the third highest yield and the lowest for duration, which is encouraging for developing short duration variety. The cluster mean of V ranked the first for yield and the second for tiller per plant, panicle per plant and panicle length and the lowest for days to flowering and the second lowest for duration which is expectable for improving yield and yield contributing traits.

**Table 3. Cluster mean for 10 characters of 36 rice genotypes**

Characters	I	II	III	IV	V
1. Days to flowering	125.67	126.69	126.67	123.30	121.00
2. Days to maturity	147.11	150.15	149.33	145.50	146.00
3. Plant height (cm)	84.36	93.11	101.77	91.41	93.00
4. Tiller/plant	15.89	13.23	11.00	12.50	15.00
5. Panicle/plant	14.67	12.38	10.33	11.90	14.00
6. Flag leaf angle	16.10	17.85	26.90	17.45	84.70
7. Panicle length (cm)	22.46	23.27	25.37	22.54	23.50
8. Grain/panicle	103.89	130.15	195.00	153.70	138.00
9. % sterility	13.46	17.30	8.17	12.52	12.50
10. Yield (t/ha)	4.36	4.36	5.20	4.51	5.50

A two dimensional scatter diagram was constructed using component I as X axis and component II as Y axis, reflecting the relative position (Fig. 1). As per scatter diagram, the genotypes were apparently distributed into five clusters. Only one genotype was in the cluster V. It was also revealed that the genotypes of cluster I was more diverse from the genotypes of cluster V and cluster III.

Contributions of the characters towards divergence are presented in the Table 4. The canonical variate analysis revealed that the vectors (Vector I and II) for days to maturity, plant height, tiller per plant, flag leaf angle, % sterility and yield were positive. Such result indicated that these six characters contributed maximum towards divergence. Similar result was also observed by Kadir *et al.* (1997) in wheat and Islam *et al.* (2003) in rice. It is interesting that the greater divergence in the present materials due to these six characters may offer a good scope for improvement of yield through rational selection of parents for producing heterotic rice hybrids.

**Table 4. Relative contribution of the ten characters to the total divergence**

Characters	Vector I	Vector II	Characters	Vector I	Vector II
1. Days to flowering	-0.0355	-0.2017	6. Flag leaf angle	0.0742	0.1455
2. Days to maturity	0.0207	0.0024	7. Panicle length(cm)	-0.0061	0.0367
3. Plant height (cm)	0.0408	0.0329	8. Grain/panicle	0.1216	-0.0250
4. Tiller/plant	0.1488	0.8399	9. Sterility %	0.0289	0.1069
5. Panicle/plant	-0.2231	-0.7518	10. Grain yield (t/ha)	0.3598	0.2137

It is assumed that, maximum amount of heterosis might be manifested in cross combination involving the parents belonging two most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production and reducing the life duration. In the present study, the maximum distances existed between cluster I and cluster V, but considering other yield component characters like panicle length, grain per panicle, % sterility and also yield, crosses involving parents from cluster I and cluster III may exhibit high heterosis for yield. Here it may be mentioned that cluster V consisted of only one variety/ line, that may be a problem for taking it in crossing program for improvement of coastal rice. Mian and Bahl (1989) reported that parents separated by  $D^2$  values of medium magnitude generally showed higher heterosis. Keeping this in view, it appears that the crosses between the genotypes/ parents belonging in cluster I with that of cluster III and cluster I and cluster V would exhibit high heterosis as well as earliness and higher level of production. So based on the results, the genotypes under cluster I and cluster III and cluster I and cluster V have been selected for future breeding program.

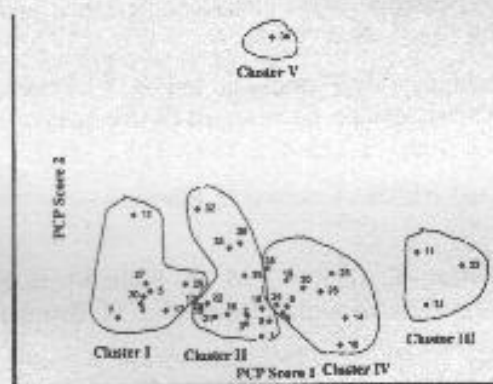


Fig 1. Scatter diagram for 36 rice genotypes

The genotypes under study were grouped into five clusters. The cluster II and cluster V contained the highest and lowest number of genotypes, respectively. The most heterogeneous cluster was identified as cluster I. The most genetically distant genotypes were found between clusters I and V followed by clusters III and I, clusters V and II, clusters III and IV. Therefore, more emphasis should be given on genotypes of cluster I viz. IR61228-3B-10-3-1, IR61919-3B-24-3, IR72048-B-R-11-1-1, IR71990-3R-2-2-2, IR65185-3B-8-3-2, IR65192-4B-14-1, IR72046-B-R-15-3-1, IR72046-B-R-15-2-1 and IR72046-B-R-7-1-1 for selecting as parents for crossing with the genotypes of cluster III and V viz. BR5333-34-4-6, IR65196-3B-13-3-2, IR66401-2B-14-1-1 and BR5777-4-2-4-2-HR2, which may produce new recombinants with desired traits for yield and yield components.

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