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Genetic Diversity in Irrigated Rice

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Abstract: Genetic diversity of 62 genotypes of irrigated rice originating from BRRI, IRRI and China were studied through Mahalanobis D^2 statistic. The genotypes were grouped into five clusters. The cluster II and IV contained the highest number of genotypes (16) and the cluster I contained the lowest (7). The highest intra cluster distance was noticed for the cluster I and the lowest for cluster III. The highest inter cluster distance was observed between cluster I and cluster IV followed by cluster I and cluster V, cluster I and cluster III, cluster III and cluster IV and lowest between cluster IV and cluster V. The highest cluster means for yield and other three yield contributing characters are obtained from cluster I, six highest and two second highest means for yield contributing characters are found in cluster III but the lowest cluster mean for yield. Therefore more emphasis should be given on cluster I for selecting genotypes as parents for crossing with the genotypes of cluster III, which may produce new recombinants with desired traits.

Key words: Rice, genetic diversity

INTRODUCTION

Rice is the main cereal crop of Bangladesh. Among other ecosystem, irrigated (boro) is one of the suitable for growing rice in Bangladesh context. Area under boro is the second largest comparing to others. Genetic divergence is an useful tool for an efficient choice of parents for hybridization to develop high yield potential cultivars. Such a study also permits to select the genetically divergent parents to obtain the desirable recombinants in the segregating generations. The understanding of association of characters is of prime importance in developing an efficient breeding program. With the development of advanced biometrics techniques such as multivariate analysis based on Mahalanobis^[1] Statistic, quantification of degree of divergence among the biological population and assessing of relative contribution of different components to the total divergence intra and inter cluster levels have now become possible. Inclusion of more diverse parents (within a limit) is believed to increase the chances of obtaining stronger heterosis and gives broad spectrum of variability in segregating generations^[2,3]. An attempt was made in the present study to analyze the genetic divergence of 62 irrigated (boro) rice genotypes.

MATERIALS AND METHODS

Sixty two rice genotypes from International Rice Research Institute (IRRI) (58), Bangladesh Rice Research

Institute (BRRI) (3) and China (1) sources were grown in the research field at Satkhira site in boro season, 2001-2002. All of the IRRI lines were salinity tolerance in the range of 6-10 dS m^{-1} EC level. The trial was conducted in Randomized Complete Block (RCB) design with three replications under PETTRA (Poverty Elimination Trough Rice Research Assistance) project. Forty five day old seedlings were transplanted in a 5 sq.m plot following 25X15 cm spacing between rows and plants respectively. Single seedling was used for per hill. 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 was applied in three equal splits at 15, 35 and 55 DAT. Intercultural operations and pest control measures were done as and when necessary. The experiment was conducted on irrigated situation. Ten plants from each entry were randomly selected for recording data. Data were collected on plant height (cm), days to flowering, duration (days), number of tiller per plant, number of panicle per plant, flag leaf angle, panicle length (cm), spikelets per panicle, % sterility and yield ($t ha^{-1}$).

Genetic diversity studied following Mahalanobis^[1] generalized distance (D^2) extended by Rao^[4]. Based on the D^2 values, the varieties were grouped into clusters following the method suggested by Tocher^[4]. Intra and inter cluster distances were calculated by the methods of Singh and Chaudhury^[5]. Statistical analyses were carried using IBM computer at BRRI, following Genstat 5 program.

RESULTS AND DISCUSSION

Analysis of variance showed the differences among the 62 rice genotypes were significant for all the ten characters under study indicating the presence of notable genetic variability among the genotypes. The principal component analysis showed that the first two components accounted for 89.75% of the total variation.

Based on the degree of divergence sixty two genotypes were grouped into five clusters on the basis of cluster analysis (Table 1). Maximum 16 entries were grouped into the cluster II and IV, followed by 12 and 11 in clusters V and III, respectively. Seven entries were grouped into cluster I.

Intra and inter cluster distance were presented in Table 2. The inter cluster distances in all of the cases was larger than the intra cluster distance indicating that wider diversity was present among genotypes of distance groups. The intra cluster distance was maximum in cluster I followed by V, II, IV and III indicating that the entries in cluster I was most heterogenous. This result was supported by the findings of Rahman *et al.*^[6] in wheat. Regarding inter cluster distance cluster IV showed maximum genetic distance (12.43) from cluster I followed by cluster V (10.68), cluster III (8.61) from cluster I and cluster IV (8.39) from cluster III suggesting wide diversity between them. Moderate or intermediate inter cluster distance was observed between cluster V and cluster III (7.31) followed by cluster II and cluster I (7.27), cluster III and cluster II (5.65) and cluster IV and cluster II (5.16).

The minimum inter cluster divergence was observed between cluster IV and cluster V (1.75) and cluster II and cluster V (3.42) indicating that the genotypes of these clusters were genetically closed.

The mean values of cluster I ranked first for panicle per plant, panicle length, spikelets per panicle and yield and second for plant height, days to flowering, duration and flag leaf angle (Table 3). Cluster II had the second highest cluster mean value for % sterility which have the negative role in yield and ranked third for plant height, days to flowering, duration, panicle length, spikelets per panicle and flag leaf angle on the other hand cluster mean for panicle per plant was the lowest. Cluster III ranked highest for plant height, days to flowering, duration, tiller per plant, flag leaf angle and % sterility and lowest for yield. This result indicated, although other yield contributing characters were highest but due to highest % sterility the yield become lowest. The cluster IV had the second highest cluster mean values for tiller per plant and panicle per plant and lowest for plant height, days to flowering, duration, flag leaf angle, panicle length, spikelets per panicle and % sterility. The cluster mean of V ranked second for yield and lowest for tiller per plant.

A two dimension 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. It was also revealed that the genotypes of cluster I was more diverse from the genotypes of cluster IV.

Table 1: Rice genotypes in different clusters

Cluster #	Line/ variety no's	No of popn.	Genotypes
I	2, 3, 4, 10, 22, 23, 25	7	IR65851-4B-7-1-3, Purbachi, IR66065-3B-6-1-2, IR61919-3B-24-3, IR71829-3R-10-3, IR71829-3R-12-2, IR71829-3R-41-1
II	5, 6, 7, 16, 18, 19, 20, 21, 24, 26, 27, 31, 32, 41, 49, 53	16	IR45427-2B-2-2B-1-1, IR51491-AC10, BRRI dhan28, IR72046-B-R-1-1-1, IR72046-B-R-6-1-1, IR0031-4B-R-9-2-1, IR0031-4B-R-14-3-1, IR0031-4B-R-21-3-1, IR71829-3R-33-3, IR71829-3R-73-1, IR71829-3R-82-1, IR71991-3R-2-1, BR5333-34-4-6, IR72593-B-8-3-3-1, IR71866-3R-1-2-1, IR72583-B-2R-2-2-2
III	12, 13, 54, 55, 56, 57, 58, 59, 60, 61, 62	11	IR72048-B-R-4-2-1, IR72048-B-R-4-3-1, BRRI dhan29, IR43976-24-3-1-2, IR44035-367-3-1-1-22, IR47393-301-1, IR48299-238-3-3-1-1-2-2, IR48303-37-3-3-2-1-2, IR60431-B-60-3, IR62653-28-12-1-2-1, IR64588-47-2-2B-12-1-2-3
IV	8, 30, 33, 35, 36, 37, 38, 39, 40, 43, 45, 46, 48, 50, 51, 52	16	IR61228-3B-1-3-2, IR71912-3R-1-1, IR72593-B-3-2-1-2, IR72593-B-3-2-3-3, IR72593-B-5-2-2-1, IR72593-B-5-2-2-2, IR72593-B-6-1-3-2, IR72593-B-6-2-2-1, IR72593-B-8-1-1-2, IR72593-B-13-1-3-1, IR72593-B-13-3-3-1, IR72593-B-18-2-2-2, IR71830-3R-2-2-3, IR71893-3R-1-2-2, IR71899-3R-2-1-1, IR71990-3R-2-2-2
V	1, 9, 11, 14, 15, 17, 28, 29, 34, 42, 44, 47	12	IR64419-3B-12-1, IR61247-3B-8-2-1, IR64196-3B-14-3, IR72048-B-R-11-1-1, IR72048-B-R-16-2-1, IR72046-B-R-3-2-1, IR71895-3R-17-1, IR71866-3R-3-1, IR72593-B-3-2-2, IR72593-B-11-1-2-1, IR72593-B-13-3-2-1, IR72593-B-19-2-3-1

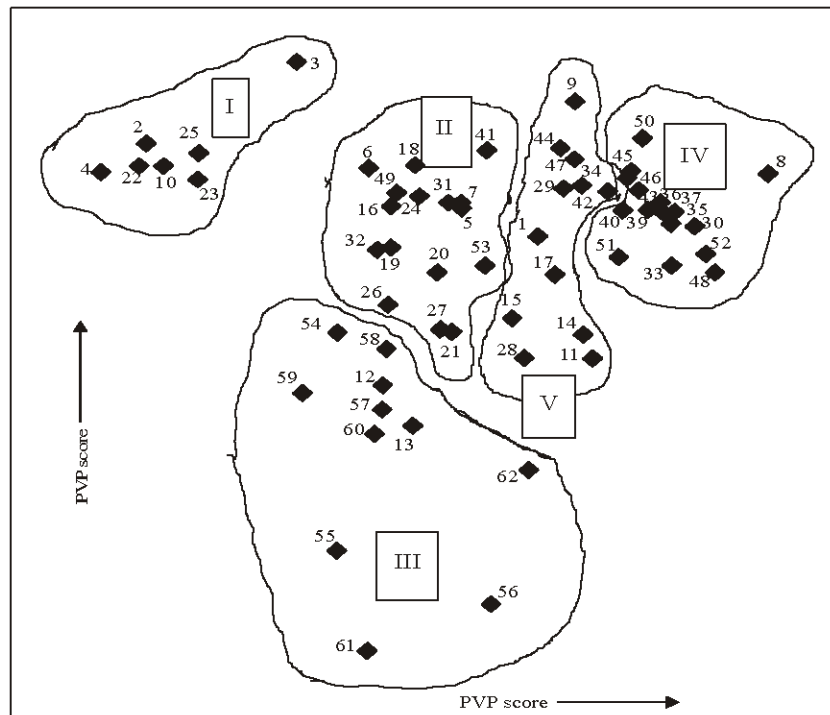


Fig. 1: Scatter diagram of 62 rice genotypes

Table 2: Intra (bold) and inter cluster distances (D^2) of 62 rice genotypes

Clusters	I	II	III	IV	V
I	1.06	7.2	8.6	12.4	10.6
II		0.7	5.6	5.1	3.4
III			0.5	8.3	7.3
IV				0.7	1.7
V					0.8

Table 3: Cluster means for ten characters in rice

Characters	I	II	III	IV	V
Plant height (cm)	94.41	91.59	108.15	79.31	87.95
Days to flowering	131.21	130.57	144.65	125.24	126.64
Duration (days)	153.91	153.00	170.39	148.94	150.18
Tiller/ plant	14.49	12.88	16.06	15.44	12.64
Panicle/ plant	21.46	11.73	14.57	14.81	11.92
Flag leaf angle	22.96	21.62	23.72	19.71	20.52
Panicle length	26.79	25.29	26.39	21.24	22.72
Spikelets/ panicle	201.37	140.39	140.82	93.87	112.95
% Sterility	11.41	11.76	13.38	8.27	11.77
Yield (t ha ⁻¹)	6.36	5.93	3.85	5.41	5.95

Table 4: Relative contribution of the ten characters to the total divergence of the rice

Characters	Vector I	Vector II
Plant height (cm)	-0.0078	-0.0182
Days to flowering	-0.1086	0.0667
Duration (days)	0.0202	-0.3015
Tiller/ plant	-0.1958	-0.0553
Panicle/ plant	0.0107	0.0248
Flag leaf angle	-0.0225	-0.0521
Panicle length	0.0653	0.1681
Spikelets/ panicle	0.1128	0.0252
% Sterility	0.0077	-0.0074
Yield (t ha ⁻¹)	0.0636	0.3087

Contributions of the characters towards divergence are presented in Table 4. The canonical variate analysis revealed that the vectors (Vector I and II) for panicle per plant, panicle length, spikelets per panicle and yield were positive. Such results indicated that these four characters contributed maximum towards divergence. The similar result was observed by Kadir *et al.*^[7] in wheat. It is interesting that the greater divergence in the present materials due to these four characters will offer a good scope for improvement of yield thorough rational selection of parents for producing heterotic rice hybrids. It is assumed that, maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to 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 clusters I and cluster IV. But considering the yield and duration, crosses involving cluster I and cluster III may exhibit high heterosis for yield. Mian and Bahl^[8] reported that the 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 the cluster I with that of cluster III and cluster I and cluster IV would exhibit high heterosis as

well as earliness and higher level of production. So based on this result, the genotypes under cluster I and cluster III and cluster I and cluster IV have been selected for future breeding program.

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