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Original Research Article

Genetic Divergence in Indigenous and Exotic Rice (*Oryza sativa* L.) under Saline-Alkali Condition

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A B S T R A C T

Genetic divergence of 41 indigenous and exotic rice varieties of which five procured from India, one from Sri Lanka and 35 from IRRI, Philippines was investigated using Mahalanobis, D^2 statistic. Based on thirteen agromorphological characters, the forty one germplasm both indigenous and exotic were grouped into seven clusters based on the relative magnitudes of D^2 values following Tocher's method of cluster formation. Cluster II is the largest cluster consisting of 12 genotypes while Cluster I was the smallest with only a single genotype. The maximum intra cluster distance (D = 133.58) was found in cluster III consisting of 5 varieties. In the present study, maximum inter cluster distance was estimated between cluster III and VII ($\sqrt{D^2}$ = 913.36) which was followed by clusters II and VI ($\sqrt{D^2}$ = 755.83). Based on the rank totals, the characters which contributed maximum towards genetic divergence in the present studies were spikelets per panicle (30.24%) followed by days to 50% flowering (16.59%), flag leaf area (16.34%), plant height (14.39%), biological yield per plant (9.15%), spikelet fertility (5.12%), length/breadth ratio (3.41%), 1000 grain weight (3.17%), harvest index (1.46%) and panicle length (0.12%). Hence these traits could be focused for selection while improving quantitative traits. On the basis of their greater inter cluster distance, high value of cluster mean and performance of the individual germplasms for the character, the germplasm could be used in hybridization programme for improvement of different plant characters of the rice.

Keywords

Exotic Rice (*Oryza sativa* L.) under Saline-Alkali Condition

Introduction

Rice, being the staple food for more than 70 per cent of our national population and source of livelihood for 120 to 150 million rural households, is backbone of the Indian Agriculture. Salt affected areas have increased day by day because of excessive use of irrigation water with improper drainage coupled with the poor quality irrigation water. Development of varieties for underutilized soil is the only option to increase the production. Thus, adoption of high yielding rice varieties to various stress environment and underutilized land such as saline-alkalinity affected soil would be an important strategy to meet this challenge. The scarcity of productive agricultural land

may force us to grow agricultural crops in harsher environments. The salt tolerant rice varieties are sparse and the success of any breeding programme mainly depends on presence of genetic variability in the germplasm.

It is extremely important to study the genetic composition of the germplasms of existing modern day cultivars in comparison with their ancestors and related species. this will not only provide information on their phylogenetic relationship but also will indicate a chance of finding new and useful genes, as the accessions with most distinct DNA profiles are likely to contain a greater number of novel alleles. The use of Mahalanobis D^2 statistics for estimating genetic divergence had been emphasized by many workers (Murty and Arunachalan, 1966; Singh and Gupta, 1968) because it permitted precise comparison among all possible pairs of population in any group before affecting actual crosses.

In addition to aiding in the selection of divergent parents for hybridization, D^2 statistics measures the degree of diversification and determines the relative contribution of each component character to the total divergence (Singh, 1990).

The utility of multivariate analysis in quantifying the degree of divergence between populations to understand the trend of evolutionary pattern, to assess the relative contribution of different components to the total divergence and to determine the nature of forces operating on inter- and intra-cluster levels has greatly been emphasized (Micherer and Sokal, 1957; Murty and Quadri, 1966). Further, such studies have also permitted the choice of genetically divergent parents to obtain desirable recombinants in segregating generations Ram and Panwar (1970).

Materials and Methods

The materials for the present experiment consisted of 41 rice genotypes along with one standard (check) variety viz., Narendra Usar Dhan 3 received from the genetic resource pool and different part of the World through Rice Improvement Project of the university. The details of genotype are given in Table 1.

These germplasms were grown in the experimental farm of Genetics and Plant Breeding at N.D. University of Agriculture and Technology, Kumarganj, Faizabad (UP), India during *Kharif* season of 2014. The experiment was laid out in the Randomized Block Design with three replications. The inter and intra row spacing were maintained at 20×15cm. The recommended plant protection measures and agronomical practices were followed. The experimental data on various quantitative characters were recorded as per criteria laid down in the standard Evaluation System for rice IRTP and "Descriptors for Rice" published jointly by International Rice Research Institute and International Board for Plant Genetic Resources (IBPGR and IRRI, 1980). Five plants from middle three rows of each plot were randomly sampled and the quantitative characters were recorded following actual measurement on each of the sampled plants and then averaged it out. The variables measured for quantitative characters were days to 50 per cent flowering, plant height (cm), panicle bearing tillers per plant, panicle length (cm), flag leaf area (cm^2), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g), kernel length (mm), kernel breadth (mm), L: B ratio, biological yield per plant (g), harvest-index (%), grain yield per plant (g). Mahalanobis (1936) D^2 statistics was used to estimate genetic divergence among the 41 germplasms. The

germplasms were grouped into clusters according to Tocher's methods by Rao (1952).

Results and Discussion

The Forty one rice germplasms both indigenous and exotic were grouped into 7 different non-overlapping clusters based on the relative magnitude of D^2 values following the Tocher's method of cluster formation (Rao, 1952) with the criterion that the intra cluster average D^2 values should be less than the inter cluster D^2 values. Clustering of 41 germplasms with 12 germplasms into cluster II, 10 germplasms in clusterV II, 7 germplasms in cluster IV, 5 germplasm in cluster III, 4 germplasm in cluster VI, 2 germplasm in cluster V and one germplasms in cluster I indicated presence of genetic diversity among the germplasms (Table 2).

The random clustering pattern of germplasms from different origins indicated that the genetic diversity of the germplasms is not necessarily related with the distribution of germplasms in different country. The genetic diversity among the germplasms in the present study may be resulted from genetic drift and selection that cause greater diversity than geographical distribution of countries as suggested by Murty and Arunachalan (1966). Pokkali maintained their separate identities by making monogenetic groups, that is, clusters while forming clusters. It might be due to its different genetic makeup from that of the other germplasms.

The maximum inter-cluster distance was observed between cluster III and VII (913.36), followed by cluster II and VII (755.83), cluster I and VII (585.05), cluster III and V (428.41). The minimum estimate for inter-cluster distance was recorded between cluster I and IV (87.25) followed by cluster I and II (108.91), cluster IV and V (118.60), and between cluster II and III(143.21) (Table 3). Average inter- and intra-cluster distances are presented in cluster diagram (Figure 1) and are also presented as a supplement of the table using $D = D^2$ values of average inter- and intra-cluster. This depicted the genetic diversity in an easily understandable manner and provided information about relationships of different clusters. But the diagram presented was not exactly to the scale. The value of intra cluster distance ranged from 0.00 (cluster VI, V VI and VII) to 133.58 (cluster III). It could be indicated that clusters I, II and III were highly divergent from clusters IV, V, VI and VII.

Moreover, cluster IV appeared less divergent from cluster II and cluster V to cluster III based on the values of intra cluster distances. The average inter cluster distance varied from 87.25 (cluster I and IV clusters) to 913.36 (cluster III and VII). From the inter cluster distances, it could be inferred that the cultivars belonging to clusters III and II (913.36) and cluster II and VII (755.83) were more divergent and had a wide genetic variation than the others.

Maximum inter cluster distance suggested wider diversity between the groups; while minimum inter cluster distance indicated closer relationship by Singh *et al.*, (1987). Higher intra-cluster distance also indicated greater heterogeneity of the cultivars by Pattnaik (1992). Genotypes belonging to different clusters separated by high estimated statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants (DeReddy *et al.,* 1992). Further, the magnitude of heterosis largely depends upon the degree of genetic diversity in the parental lines Roy and Panwar (1993).

Table.1 Details of genotypes included in experiment

S. No.	Name of Genotype	Parentage	Source
1.	IR 12T 193	IR 61920-3B-22-2-1(NSIC RC 106/SAMBHA MAHSURI)	IRRI
2.	IR 13T 135	IR 72046-B-R-3-2-2-1-2/IR00A110	IRRI
3.	IR 12T 127	IRRI 126/AS 996//IR 65195-3B-13-2-3(PSB RC 86)/IR 77778-B-8-1-2	IRRI
4.	IR12T 153	CHERIVIRUPPU/IR05F101//IR05F102/IR66946-3R-178-1-1	IRRI
5.	IR12T 133	IR 84087-19/IR00A110//IR00A110	IRRI
6.	IR12T 198	IR 84089- 35/IR 72875-94-3-3-2//IR 72875-94-3-3-2	IRRI
7.	IR12T 146	IR07F101/IRRI126	IRRI
8.	IR12T 171	IRRI 149/IR 65185-3B-8-3-2(PSB RC 84)	IRRI
9.	IR12T 172	IRRI 149/IRRI126	IRRI
10.	IR12T 173	IRRI 149/IRRI126	IRRI
11.	IR12T 174	IRRI 149/IRRI126	IRRI
12.	IR12T 175	IRRI 149/IRRI126	IRRI
13.	IR12T 147	IRRI 149/IRRI126	IRRI
14.	IR12T 177	IRRI 149/IRRI126	IRRI
15.	IR12T 154	IRRI 149/IRRI126	IRRI
16.	IR12T 156	IRRI 149/IRRI126	IRRI
17.	IR12T 157	IRRI 149/IRRI126	IRRI
18.	IR12T 198	IRRI 149/IR 61920-3B-22-2-1 (NSIC RC 106)	IRRI
19.	IR12T 220	IRRI 149/IR 61920-3B-22-2-1 (NSIC RC 106)	IRRI
20	IR12T 224	IRRI 149/IR 61920-3B-22-2-1 (NSIC RC 106)	IRRI
21.	IR12T 266	A 69-1/IR 73718-23-2-1-3	IRRI
22.	IR12T 246	IR 4630-22-2-5-1-3/IR 72046-B-R-8-3-1-3	IRRI
23.	IR89609-8-2-B	IR 61920-3B-22-2-1(NSIC RC 106/IR05N173)	IRRI
24.	IR13T143	IR 61920-3B-22-2-1(NSIC RC 106/IR05N173)	IRRI
25.	IR13T146	IR 03A477*4/CHERIVIRUPPU	IRRI
26.	A69-1	BG 94-1/POKKALI	SRI LANKA
27.	CSR28	IR 42/IR 4630-22-2-5-1-3	INDIA
28.	CSR 90 IR2	IR 10206-29-2-1/SUAKOKO(SEL)	INDIA
29.	IR 28	IR 833-6-2-1-1//IR 1561-149-1/IR 1737	IRRI
30.	IR455427-2B-2-2-B-1-1	CHERIVIRUPPU/IR 10205-37-1-3	IRRI
31.	IR55179-3B-11-3	IR 4630-22-2-5-1-3/NONA BOKRA	IRRI
32.	IR58443-6B-10-3	AT 401/IR 31868-64-2-3-3-3	IRRI
33.	IRRI147 (IR633O7-7B-4-3)	IR 51511-B-B-34-B/TCCP 266-2-49-B-B-3	IRRI
34.	IR6694 6-3R-178-1-1(FL 478)	IR 29/POKKALI B	IRRI
35.	IRRI 165(IR71896-3R-8-3-13)	IR 55182-3B-14-3-2/IR 65195-3B-13-2-3 (PSB RC 86)	IRRI
36.	Nona bokra	Land race	INDIA
37.	IRRI 154	IR 73012-137-2-2-2/PSB RC 10(IR 50404-57-2-2-3)	IRRI
38.	Pokkali	Land race	INDIA
39.	IRRI 123 (IR 64683-87-2-2-3-3 PSB RC 82)	IR 47761-27-1-3-6/PSB RC 28 (IR 56381-139-2-2)	IRRI
40.	Swarna sub 1	IR 82809:227/SWARNA	IRRI
41.	Narendra Usar Dhan 3	Leaungya 1148 x IR 9129-20g-2-2-2-1 x IR 18272 -27-3-1	INDIA

Table.2 Clustering pattern of 41 rice genotype on the basis on D2 analysis for 13 characters under saline-alkali condition

Cluster no	No of genotype	Genotype
I	1	Pokkali
II	12	IR12T 153,IR12T 146,IR12T 173, IR12T 172, IR12T 171, IR12T 157, IR12T 266, IR13T146, CSR28, IRRI147(IR633O7-7B-4-3), IRRI 154, Narendra Usar Dhan 3
III	5	IR 12T 193, IR 13T 135, IR 12T 127, IR12T 174, IRRI 123 (IR 64683-87-2)
IV	7	IR12T 133, IR12T 198, IR12T 147, IR12T 154, IR12T 198, IR12T 224, IR12T 220
V	2	NONA BOKRA, SWARNA SUB 1
VI	4	IR12T 156, IR12T 177, IR 28, IR455427-2B-2-2-B-1-1
VII	10	IR12T 175, IR12T 246, IR89609-8-2-B, IR13T143, A69-1, CSR 90 IR2, IR55179-3B-11-3, IR58443-6B-10-3, IR6694 6-3R-178-1-1(FL 478), IRRI 165(IR71896-3R-8-3-13)

Table.3 Estimates of average intra and inter-cluster distances (Tocher Method) for 7 clusters in rice (*Oryza sativa* L.)

Cluster No.	I	II	III	IV	V	VI	VII
1. Cluster	**49.136 (7.01)**	108.91 (10.44)	195.26 (13.97)	87.25 (9.34)	145.83 (12.08)	281.20 (16.77)	585.05 (24.19)
2. Cluster		**92.46 (9.62)**	143.21 (11.97)	201.26 (14.19)	290.09 (17.03)	303.91 (17.43)	755.83 (27.49)
3. Cluster			**133.58 (11.56)**	321.68 (17.94)	428.41 (20.70)	407.76 (20.19)	913.36 (30.22)
4. Cluster				**0.00**	118.60 (10.89)	178.62 (13.36)	401.09 (20.02)
5. Cluster					**0.00**	342.88 (18.52)	401.71 (20.04)
6. Cluster						**0.00**	346.65 (18.62)
7. Cluster							**0.00**

Bold figures represent intra-cluster distance.

Table.4 Diversity in 13 agronomic characters of 41 rice germplasms

S.N.	Characters	Minimum	Maximum
1.	Days to 50% flowering	76.0 (IR12T220)	116.33 (Nona Bokra)
2.	Plant height (cm)	82.66 (IR66946-3R-178-1-1)	173.10 (Pokkali
3.	Panicle bearing tillers per plant	5.2 (IR12T146)	11.6 (Swarna Sub 1)
4.	Panicle length (cm)	20.65 (IR12T127)	29.05 (IR13T135)
5.	Spikelets per panicle	73.8 (IR12T177)	162.8 (IR12T127)
6.	Grains per panicle	61.26 (IR28)	149.4 (IR12T127)
7.	Spikelet fertility (%)	80.56 (IR12T177)	92.33 (IR12T224)
8.	1000 seed weight (g)	18.43 (IRRI 154)	28.21 (IR12T173)
9.	L:B ratio	2.22 (IR55179-38-11-3)	3.81 (Narendra Usar Dhan 3)
10.	Flag leaf area (cm^2)	14.32 (IR55179-38-11-3)	49.22 (IR12T156)
11.	Biological yield (g)	31.66 (IR12T153)	70.08 (IRRI 165)
12.	Harvest index (%)	26.24 (IR112T147)	46.98 (IR12T171)
13.	Grain yield per plant (g)	10.59 (IR12T173)	27.60 (Nona Bokra)

Table.5 Relative contributions of individual character towards divergence

S.N.	Characters	Rank total	Percentage to rank total
1.	Days to 50% flowering	136	16.59
2.	Plant height (cm)	118	14.39
3.	Panicle bearing tillers per plant	0	0.00
4.	Panicle length (cm)	1	0.12
5.	Spikelets per panicle	248	30.24
6.	Grains per panicle	0	0.00
7.	Spikelet fertility (%)	42	5.12
8.	1000 seed weight (g)	26	3.17
9.	L:B ratio	28	3.41
10.	Flag leaf area (cm^2)	134	16.34
11.	Biological yield (g)	75	9.15
12.	Harvest index (%)	12	1.46
13.	Grain yield per plant (g)	0	0.00

Table.6 Best performance for hybridization

S. N.	Characters	Germplasms
1.	Days to 50% flowering	76.0 (IR12T220)
2.	Plant height (cm)	82.66 (IR66946-3R-178-1-1)
3.	Panicle bearing tillers per plant	11.6 (Swarna Sub 1)
4.	Panicle length (cm)	29.05 (IR13T135)
5.	Spikelets per panicle	162.8 (IR12T127)
6.	Grains per panicle	149.4 (IR12T127)
7.	Spikelet fertility (%)	92.33 (IR12T224)
8.	1000 seed weight (g)	28.21 (IR12T173)
9.	L:B ratio	3.81 (Narendra Usar Dhan 3)
10.	Flag leaf area (cm^2)	49.22 (IR12T156)
11.	Biological yield (g)	70.08 (IRRI 165)
12.	Harvest index (%)	46.98 (IR12T171)
13.	Grain yield per plant (g)	27.60 (Nona Bokra)

In the present study, maximum inter cluster distance was estimated between cluster III and VII ($\sqrt{D^2}$ = 30.22), which was closely followed by cluster II and VII (D^2 = 27.49) and cluster I and VII (D^2 =24.19). It is suggested that the crossing between the selected germplasms from clusters III and VII or clusters II and VII or cluster I and VII will give rise to high heterotic crosses and a wide spectrum of variation among the segregants. Since cluster II consisted of 12 germplasms with appreciably high value of intra cluster distances, presence of high heterogeneity among the germplasms is expected. Hence, subclustering of cluster II is an approach towards the effective selection of desired parents for hybridisation programme within the cluster.

Diversity in 13 agronomic characters of rice germplasms was shown in Table 4. Considerable genetic diversity is observed in almost all the characters of the cultivars under study.

The salient findings obtained from the present studies and their possible implications in the genetic improvement of indigenous and exotic germplasms are summarised here under. In the studies for genetic divergence of 41 rice germplasms, significance of D^2 values revealed the presence of considerable divergence among the genotypes.

Based on the rank totals, the characters which contributed maximum towards genetic divergence in the present studies were spikelets per panicle, days to 50% flowering, flag leaf area (cm^2), plant height (cm), and biological yield (g) (Table 5). Clusters with the highest mean values of agronomic characters and best-performing germplasms within the cluster were identified. Best performers for hybridisation were shown in Table 6.

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