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GENETIC DIVERGENCE IN RICE

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ABSTRACT

Seventy five strains comprising indica (Assam Rice Collection, or ARC, and non-ARC), japonica, ponlai and javanica rice were grouped into 13 clusters using D^2 statistic. The association of ARC strains with javanica in the same group has great significance. Sixty seven ARC strains revealed high order of genetic diversity, indicating the importance of the northeastern region of India as a rich source of diverse rice germplasm and in tracing the centre of origin of cultivated rice. The possibility of existence of intergrades between various subspecies in this region cannot be ignored. Genetic drift and selection pressure were inferred to have played a great role in bringing about genetic divergence among the strains. The ARC strains also generated noteworthy variability among themselves with regard to intraand intercluster distances. Two characters, viz., 100-grain weight and number of grains per panicle, were the highest contributors to D^2 values. Six clusters consisting of 14 strains (10 in ARC, 2 in javanica, and 2 in ponlai) have been judged as important for use as base material (from this study) for varietal improvement programme on the basis of their greater intercluster distances and higher cluster mean values for the aforementioned two characters.

Key words: Genetic divergence, rice subspecies, D² statistic.

Rice germplasm collected from the northeastern region of India, known as Assam Rice Collection (ARC), is considered to be a rich source of germplasm [1-4] due to existence of a high degree of phenotypic divergence. Geographic and phenotypic diversity serve as inferential criteria and it is not practicable for quantifying or genetically discriminating among populations. Precise information about the extent of genetic divergence and on characters used for discrimination among populations is crucial in any crop improvement programme, because selection of parents based on genetic divergence has become successful in several crops [5-10]. The literature available on this aspect is limited for ARC. Therefore, the nature and magnitude of genetic divergence and the characters contributing to genetic diversity were studied in the ARC collection.

MATERIALS AND METHODS

Sixty seven strains randomly sampled from the Assam Rice Collection (ARC) and 8 strains, two each from the four geographical subgroups (also referred to as

subspecies) of Oryza sativa, i.e., indica, japonica, javanica and ponlai, were grown at the Central Rice Research Institute, Cuttack, in randomised block design with three replications, with the net plot size of 0.60 m^2 at $20 \times 20 \text{ cm}$ spacing. Observations were recorded on 10 randomly selected competitive plants from two middle rows (out of four rows) for 10 quantitative characters. The data were subjected to Mahalanobis' D² statistic to measure genetic divergence as suggested by Rao [11]. The relative contributions of different characters towards genetic divergence were also worked out.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the strains for all characters. All the 75 strains were grouped into 13 clusters (Table 1), using the clustering technique. Out of 75 strains, 67 ARC strains collected from the northeastern region of India were distributed in ten clusters, indicating the existence of considerable genetic diversity among the ARC strains. This confirms the earlier reports [1, 2, 12-15]. The composition of the individual cluster with regard to number of strains also varied.

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Cluster No.	Strains in each cluster
Α	ARC 13294, ARC 13303, ARC 15601, ARC 18057, ARC 14446, ARC 13297 ARC 11346, ARC 13632, ARC 13299, ARC 18281, ARC 11210, ARC 13286
В	ARC 15917, ARC 15781, ARC 15750, ARC 13769, ARC 13566, ARC 15899 ARC 13300, ARC 14906, ARC 13565, ARC 15913, ARC 15061, ARC 15574 ARC 15916, ARC 13528, ARC 13715, ARC 11321
С	ARC 15054, ARC 13539, ARC 18345, ARC 18268
D	ARC 15047, ARC 15716, ARC 14684, ARC 14455, ARC 14367, ARC 11345 ARC 18265, ARC 14433, ARC 13301, ARC 13151, ARC 18122, ARC 13287 ARC 11149
E	ARC 15306, ARC 15645
F	Ginbozu, Asahi (j) N 22, SLO 16 (i)
G	ARC 14365, ARC 18443, ARC 13284, ARC 18231, ARC 14861
Н	ARC 15647, ARC 13517, ARC 13496, ARC 15072, ARC 14911, ARC 18286
I	Taichung-65 Tainan-3] (P)
J	ARC 15819, ARC 15164, Sigadis (java)
K	ARC 15184, ARC 15229, ARC 13576, ARC 13540, ARC 11100, ARC 14523
L	ARC 15669
м	Mas (java)

Table 1. Clustering pattern among 75 rice_collections

ARC-Assam Rice Collection, j-japonica, p-ponlai, java-javanica, and i-non-ARC indica.

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Clusters K and E showed the maximum and minimum intracluster distances, respectively, and both groups comprised, solely, ARC strains (Table 2). Besides, some of the ARC strains also showed a tendency towards grouping in the same cluster along with strains from other distinct subgroups. For example, one javanica strain (Sigadis) was included with two ARC strains in the same cluster J; another javanica strain (Mas) constituted a separate group (cluster M) including only one strain. The existence of a separate statistical group (M) for javanica is of considerable phylogenetic interest and could be of practical value in rice breeding. The fact that javanica rice has clustered with ARC indica rice is significant, which confirms the existence of considerable diversity in the material from the northeastern region of India.' The result indicates the possibility of javanica strains being a synthetic genetic assemblage of *indica* and *japonica* genotypes, as was indicated by earlier workers [16-18]. From the standpoint of origin of cultivated rice, this study has produced evidence in favour of the conclusion that the northeastern region of India occupies an important position, thereby substantiating the earlier evidence provided by the studies of Ramiah and Ghosh [19] and Chatteriee [20].

						2.								
	A	В	C	D	F	F	G	Ħ	I	J	K	L	М	
A	10.46	19.79	18.22	20.53	43.20	211.71	32.45	34.00	206.11	196.52	37.49	38.41	213.95	
В		17.80	26.71	29.02	38.96	213.44	35.93	35.99	206.70	195.53	36.94	34.17	204.85	
С			9.53	26.76	37.27	217.88	27.16	25.08	212.46	203.68	38.87	40.13	221.67	
D				19.16	53.16	203.09	31.60	45.22	198:05	189.33	38.00	52.79	207.23	
E					7.06	242.20	46.98	24.69	234.80	223.22	54.16	25.42	238.79	
F						11.59	210.98	234.02	24.59	53.97	203.11	236.86	62.65	
G							14.67	36.88	205.20	196.60	37.16	56.61	214.10	
H.								22.15	227.94	218.25	50.16	34.90	235.16	
ľ.									13.36	33.53	196.07	229.07	45.11	
Je i L										18.20	185.09	217.15	33.60	
ĸ	6 · ·										35.28	54.36	201.74	
Ĺ.													232.61	
М	· · · ·	÷		÷	•									

Table 2. Intra- and intercluster average D values of 13 clusters (A-M)

Two *indica* (non-ARC) and two *japonica* strains formed one cluster (F). The coexistence of *japonica* and *indica* rices in one cluster lends credence to an earlier proposition [21] that the origin of the *japonica* types now grown in the temperate zone may be traced back to *aus* rice of Tropical Asia. Sharma et al. [2] also reported the presence of *japonica* plant type in the eastern region of India. The two *ponlai* strains collected from Taiwan formed a separate cluster (I) between clusters F (*indica* and *japonica*) and J (*javonica* and *indica*). Huang et al. [22] had mentioned that the term *ponlai* rice refers to the Japanese varieties grown in Taiwan since the early part of the 20th century.

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The genetic affinity or similarity between the strains of these subspecies, in the present study, is due to the application of directional selection pressure for realising high yield. Genetic drift and selection in different environments have caused greater genetic diversity than the geographical distance, as suggested by earlier workers [23-25].

Statistical distances represent the index of genetic diversity amongst clusters. As regards intercluster distance, cluster E showed maximum genetic distance from cluster F. This suggests a possibility of obtaining greater variation among segregants by crossing between ARC and non-ARC *indica* strains. Clusters F, I, J and M are mostly distantly related not only with cluster E but also with the other nine clusters, each of them having ARC strains only. Genotypes belonging to the clusters separated by high estimated statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. It is also evident from the estimates of intercluster distances that a number of strains have crossed their respective subspecies limits and have clustered with strains belonging to other subspecies as in clusters J and F.

	Character	Contribution (%)
	Heading date	4.05
1	Plant height	6.55
	Total tillers	16.86
	Ear bearing tillers	3.01
	Panicle length	1.39
	Grains/panicle	20.57
	Sterile spikelets/panicle	6.0 .14 .
	100-grain weight	22.64
	Grain yield/plant	9.83
	Length/breadth ratio of grain	14.93

Table 3. Relative contribution of different characters to D² values

The characters contributing maximum to the D^2 values are given greater emphasis for deciding on the clusters for the purpose of further selection and choice of parents for hybridization. The highest contributor in this regard was 100-grain weight. The other characters deserving consideration are: grains per panicle, total tillers, length/breadth ratio of grains, and grain yield per plant (Table 3).

On considering cluster means (Table 4) in respect of the above mentioned characters (high contribution to D^2 values), the importance of cluster L for 100-grain weight, cluster I for tillers (both total and ear bearing), cluster G for grains per panicle, cluster E for length/breadth ratio of grains, and clusters M and J for yield becomes obvious.

In terms of intercluster distance and characters with higher contribution to D^2 values, there is scope for varietal improvement through hybridization programme between the two ARC strains of cluster J and ARC strains from L, G or E clusters.

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Clus- ter	Heading date (days)	Plant height (cm)	Total tillers	Ear bearing tillers	Panicle length (cm)	Grains . per panicle	Sterile spikelets per panicle	100- grain weight (g)	Grain yield per plant (g)	Length/ breadth ratio of grain
A	102.2	124.7	7.52	6.60	22.5	66.9	18.1	2.53	10.35	2.51
В	113.3	128.3	6.98	6.18	24.7	73.1	28.3	2,40	11.03	2.56
С	97.7	144.4	7.57	6.32	22.3	52.3	33.6	2.45	8.39	3.03
D	96.7	112.8	8.00	7.22	21.4	62.2	25.3	2.14	9,49	2.49
E	121.5	139.5	5.18	4.51	22.7	82.7	26.7	2.71	11.45	3.67
F	76.2	108.2	11.94	10.95	19.6	68.6	26.4	1.84	9.95	2.97
G	9.5	122.4	10.39	9.66	21.6	119.9	26.3	1.57	14.51	3.57
Н	106.0	133.8	6.42	5.47	22.7	72.7	31.9	2.61	9.47	3.55
1	92.7	83.5	14.63	13.53	17.8	80.5	10.7	2.60	16.98	2.06
J	115.2	148.8	10.18	9.34	23.8	83.3	27.0	2.69	25.89	2.86
K	112.4	134.3	8.53	7.42	25.6	92.2	27.2	1,70	10.38	2.67
L	123.9	138.6	4.83	3.86	22.2	86.3	36.9	3.38	13.43	2.63
Μ	128.9	148.5	12.93	11.83	23.7	99.4	30.6	2.73	27.26	3.63

Table 4. Cluster means for different characters

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