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GENETIC DIVERSITY OF SALT-TOLERANT INDIGENOUS RICE GERMPLASM OF WEST BENGAL

R. K. CHAUDHURI, ANUP DAS AND ILA CHAUDHURI, Molecular Biology Laboratory, Botany Department, Calcutta University, Calcutta (West Bengal)

Genetic diversity of indigenous West Bengal salt-tolerant rices was made on yield and seven other yield attributes. Eighteen rice varieties, selected on salinity tolerance character, could be grouped into four clusters. The observations show that two Chinsura-Boro rice varieties may be of distant origin or have diverged at two rice research stations of W. Bengal. Two Patnai rice varieties. P 23 and P298, collected from CRRS, are distantly placed.

Key words: Rice, *Oryza sativa*, clustering, genetic diversity, salt tolerance

The final goal of rice breeding programme is to develop hybrids having stress tolerance and out-yielding the existing yield potential (hybrid vigour). To harness better recombinants, breeders choose genetically diverse parents. The variability and reliability of divergence, therefore, lies in the parents showing heterotic relationship with degree of divergence. Statistical distance of the parents represents the index of genetic diversity. Members grouped in a cluster would be least diverse and they could be utilized to develop a population. In general, indigenous rice germplasm possess high adaptability, because they were built up on agro ecological niches. Intermating of these varieties would give desirable recombinants with mixed characters. An attempt was, therefore, made to study the genetic diversity of indigenous rice germplasm, using multivariate statistical technique based on yield and seven yield-attributes.

The aim of the study is to note clustering, and probable inter-mixing, of these rice varieties, at two research station fields, namely Chinsura Rice Research Station (CRRS), Chinsura and Central Soil Salinity Research Institute (CSSRI), Canning Centre, West Bengal. Clustering of indigenous rice, which would be obtained from this analysis, based on genetic divergence, may provide a basis for selecting parents for heterotic combination. To our knowledge, in last few decades, no such report was published on these germplasm.

MATERIALS AND METHODS

Eighteen genotypes of rice were collected from the CSSRI at Canning and from the CRRS at Chinsura. The genotypes were planted in a randomized block design with two replications. Thirty days old seedlings were used for transplantation in the month of July, at 5m × 3m plot for each cultivar, and normal cultural practices were followed. The experiments were conducted for two consecutive years. The following observations were recorded for ten randomly

Corresponding author

selected plants in each replication, except for the border plants.

Table 1. Rice cultivars with their accessions

Rice cultivars	Accession No.	Rice cultivars	Accession No.
Nigra	C05	FR13A	IR-FR13
Patnai23	C07	Rupsail	CAC 56
Patnai298	C09	Latisail	CAC174
CBII	C11	Kalma 222	CAC243
Tilakachari	C31	Damodar	CAC334
NC1281	C49	CBI	CAC396
OC1393	C51	Pokkali	CAC652
Hamilton	C52	Bhasamanik	CAC667
Matla	C55	SR26B	CAC676

IR-FR means International Rice Research Institute's (Philippines) accession,

CAC means Central Soil Salinity Research Institute's (Canning, W. Bengal) accession;

C means Chinsura Rice Research Station's (Hoogly, W. Bengal) accession.

RESULTS AND DISCUSSION

The agro-morphological characters used for this study are: plant height (cm), number of panicle per plant, thousand seed weight (g), yield (tons/ha), grains per panicle, 50% flowering or heading date (D) and duration (D). Canonial analyses were done according to the method of Anderson (1958) (Table 3). Study of analysis of variance (ANOVA) shows distances in indigenous rice genotypes for 8 characters. Mean characters were found to be significant and represented by double asterix in the table. The ANOVA calculation was made on the following model: $Y_{ij} = m + g_i + r_j + e_{ij}$, where Y_{ij} = phenotypic observation in i^{th} genotype and j^{th} replication; m = general mean; g_i = effect of i^{th} genotype; r_j = effect of j^{th} replication; e_{ij} = random error associated with i^{th} genotype and j^{th} replication. Differences between genotypes for different

Table 2. Values of physiological characters of indigenous salt-tolerant rice varieties of West Bengal

Var. Acs.	50% Fl Period (D)	Duration (D)	Panicle no.	Inflores. length (cm)	Height (cm)	Grains/1000 seeds wt(g)	Yield (q/ha)	
CAC396	100	143	21	19	83	103	21	26
C11	100	143	17	19	83	95	25	24
CAC667	98	128	14	22	124	126	19.4	30
CAC174	94	125	12	25	117	103	26	28
CAC243	98	128	7	26	122	97	28	28
C07	98	128	8	26	139	117	32	31
CAC676	83	101	8	26	124	87	26	34.9
C09	82	128	8	26	139	117	32	31
C31	112	157	7	26	137	119	20	25
IR-FR13	103	143	8	23	126	152	25	24
CAC56	100	130	11	27	142	163	17	25
C49	112	148	10	28	147	230	23.6	38
C51	112	148	13	31	165	137	29	35
C05	118	168	12	31	146	134	27	34.6
CAC652	82	100	8	29	159	102	25	16.6
CAC334	82	100	9	30	113	73	22	17
C 52	88	104	10	30	110	80	31	21.1
C 55	88	104	10	30	120	85	23	21

characters were tested for significance using ANOVA. It is shown here that eight physiological characters are significant according to the variance ratio value.

Table 3. Analysis of Variance of 18 indigenous rice genotypes

Physiol Characters	Source of variation	Total sum of squares (TSS)	Mean sum of squares (MSS)	Variance ratio (F)
Fl. Period	Replication	266.78	33.39	162.612**
	Variety	6720.833	95.343	481.953**
	Error	27.89	0.8203	
Duration	Replication	130.26	65.13	42.799**
	Variety	21873.70	1286.699	845.524**
	Error	51.74	1.5218	
Panicle no.	Replication	13.48	6.741	193.373**
	Variety	698.535	41.090	1064.850**
	Error	1.185	0.03486	
Infl. Length (cm)	Replication	26.926	13.463	190.171*
	Variety	678.815	39.930	564.034**
	Error	2.407	0.0708	
Height (cm)	Replication	26.93	13.495	190.754**
	Variety	25221.70	1483.63	21018.102**
	Error	2.40	0.0706	
Grains/ panicle	Replication	69.59	34.795	24.104**
	Variety	69382.81	4081.342	2827.335**
	Error	49.08	1.4435	
Thousand Grains weight (g)	Replication	29.16	14.58	246.627**
	Variety	940.695	55.335	936.016**
	Error	2.01	0.0591	
Yield (q/ha)	Replication	0.096089	0.048	33.860**
	Variety	19.654	1.156	814.785**
	Error	0.0482	0.0014	

**Means characters are significant; Degree of Freedom (DF) for replication, variety and error are 2,17,34 respectively.

The genetic divergence of 18 rice cultivars was studied by means of Mahalanobis D^2 technique (1936). Uncorrelated functions of the original values were obtained by transforming the original correlated non-standardized character-mean by the pivotal condensation method described by Rao (1952). The differences between the varieties for physiological character set, taken together, were tested by Wilk's criteria (1932). After testing the feasibility of characters, a computer-assisted D^2 statistic was used for assessing the genetic divergence between populations. One thousand divergence values were computed for 18 rice local genotypes and their D^2 statistic are shown in table 4.

Possible physiological character values, of 18 indigenous rice cultivars, were calculated utilising uncorrelated varietal means, with respect to yield and its seven attributes, namely, 50% flowering period, duration, panicle number, inflorescence length, height, grains/panicle, 1000 grains weight, yield in q/ha (Rao, 1952). The rice germplasm selected for this study are salinity tolerant, though their tolerance levels are not the same. For example, cv. Pokkali, SR26B, Matla, Hamilton, Damodar could tolerate high level of salinity; Patnai 23, Patnai 298, Latisail, Rupsail, CBI, CBII, Bhasamanik, Tilakachari could tolerate medium level of salinity, and, remaining five rice cultivars can withstand salinity for a short duration or mild salinity. The clustering analysis could substantiate their adaptability to saline soil (vide table 5).

Based on these calculations, a clustering analysis was done for these rice germplasm (Table 5). It shows four groups. This clustering agrees to a large extent to the clustering made by molecular (DNA) and protein markers (data not shown here) (Das, 1997; Prasad, 1998). The salt-tolerant rice cultivars could be grouped into

Table 4. Genetic divergence (D^2) values for 18 rice genotypes

	GENOTYPES																	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0	1.3	56.3	36.7	46.7	100.2	57.3	98.4	88.9	52107	120	232	124.4	206.1	31.6	26.2	46.1	
2		0	62	39.5	47.5	104.4	60.3	103	91.8	55	118	130	243	131.5	213.8	2.6	26.8	49.0
3			0	3.9	5.7	8.9	5.1	8.5	9.2	3.3	10.0	19.2	64.4	17.8	50.6	11.5	14.7	4.8
4				0	1.6	16.0	4.2	15.6	14.9	4.0	23.9	35.0	14.9	29.8	71.4	3.2	3.8	1.7
5					0	12.4	3.7	12.9	10.6	4.2	23.9	37.3	83.5	26.7	64.1	4.4	5.8	2.3
6						0	10.7	0.7	5.7	11.4	6.8	16.9	33.4	5.8	23.1	26.8	30.9	13.9
7							0	9.7	15.9	7.6	20.4	29.0	77.1	27.0	59.3	9.2	10.9	4.8
8								0	8.5	10.7	6.5	14.0	36.6	8.4	25.6	26.7	29.8	14.2
9									0	10.3	10.6	29.2	43.6	7.9	30.2	21.9	28.4	12.1
10										0	14.6	22.2	76.4	24.1	58.9	10.3	12.3	6.1
11											0	7.4	30.3	7.9	21.3	36.2	42.9	21.0
12												0	43.3	21.7	39.6	53.4	56.5	36.6
13													0	17.8	6.3	110.6	19.8	80.9
14														0	15.4	43.2	48.7	25.9
15															0	85.3	96.3	60.7
16																0	1.6	2.4
17																	0	4.9
18																		0

The number designates the rice accessions in the following manner :
1 = CAC396; 2= C11; 3 = CAC667; 4 = CAC 174; 5 = CAC243; 6 = C07; 7 = CAC676; 8 = C09; 9 = C31; 10 = IR-FR; 11 = CAC56; 12 = C49; 13 = C51; 14 = C05; 15 = CAC652; 16 = CAC334; 17 = C52; 18 = C55

4 inter-variety clusters, when clusters, computed in relation to Matla, a CSSRI rice accession (Table 5).

Table 5. Group clustering of 18 indigenous rice cultivars with respect to cultivar Matla

Group I	Group II	Group III	Group IV
C55,CAC174	C52,IR-FR13	C05,C07	C11,C49
CAC243,CAC334	CAC667	C09,C31	C51,CAC652
CAC576		CAC56	CAC396

This grouping shows interesting observations, *viz.*, new and old Chinsura collections, mentioned herein as NC1281 and OC1393, form a cluster with Pokkali, Chinsura Boro (CB) I and II. Similarly, Tilakachari could be grouped with Rupsail, Nigra, Patnai 23 and Patnai 298, and Bhasamanik, another Chinsura collection was grouped with FR13A and CSSRI Hamilton. On the other hand, cv Matla was grouped with indigenous non-familiar cultivars like Kalma, Damodar and the popular rice SR26B. However, these associations became insignificant when ten traits of 18 rice cultivars were analyzed statistically. The following observations were noticed: Chinsura Boro rices (CBI and CBII) are not very close (D value 9.5); they are almost equidistant with SR26B (D value 10.7). It is possible that two CB rice varieties had diverged during years of maintenance at two rice-research stations at W. Bengal. Our molecular biology studies (Prasad 1998) also

supported this observation in that these two West Bengal rice accessions have distinct DNA patterns. From D2 analysis CBII is very close to the FR13A (D value 0.7), and this divergence value is lowest in our analysis (table 4). (ii) Similarly, other two Chinsura collections, Patnai rice (P23 and P298), were found to have distant genotypes (D value 85.3). Here also, P298 is more close to latisail (D value 1.6), Rupsail (D value 2.4) and NC1281 (D value 3.2). Close relative of P23 is Hamilton (D value 6.3) and most distant relatives of this rice variety are Bhasamanik (D value 206) and Matla (D value 213), These values are the maximum D2 values observed for indigenous rice varieties (iii) close relative of NC1281 is not OC1393 (D value 3.9) but is Rupsail (D value 1.7) and, as mentioned above P. 298 (iv) close relatives of cv. Tilakachari are NC1281 (D value 1.6) and Rupsail (D value 2.3). From table 4 many such conclusions could be made which were supported by our molecular biology studies (Das 1997; Prasad, 1998).

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