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Genetic divergence in rice germplasm collected from North east India

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ABSTRACT : The nature and the magnitude of genetic divergence were estimated in 54 rice genotypes collected from Arunachal Pradesh and upper parts of Assam state using Mahalonobis's D² statistics. The analysis of variance revealed significant differences among the genotypes for nine quantitative characters studied. The genotypes were grouped into 18 clusters showing fair degree of relationship between geographic distribution and genetic divergence. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Maximum numbers of genotypes were included in cluster I which has 26 genotypes. Traits contributing maximum to genetic divergence viz., plant height, days to 50% flowering, 100 grain weight and leaf width may be utilized in selecting genetically diverse parents.

KEY WORDS : *Oryza sativa*, Rice, Germplasm, Variability, Yield components

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Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world and is main source of carbohydrate for nearly half of the world population. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using D² statistics developed by Mahalonobis (1936). It is based on multivariate analysis and grouped into various cluster and also it quantifies the genetic distance among the selected genotypes and reflects the relative genetic contribution of specific traits towards the total divergence (Iftekharruddala *et al.*, 2002 and Manonmani and Fazlullah Khan, 2003). Grouping of the genotypes into different clusters was done by Tocher's method as suggested by Rao (1952). The present investigation was aimed to estimate the magnitude of genetic divergence present in the 54 rice genotypes collected from north east India along with 4 popular check

varieties and to identify the diverse genotypes for further breeding programme.

RESEARCH PROCEDURE

The materials for the present investigation consisted of 54 land races collected in 2010 from different parts of Arunachal Pradesh and parts of upper Assam which is the eastern stretch of the Himalayas (Table A). The collected samples along with four popular checks were grown in Randomized Complete Block Design with three replications during wet season 2011 in irrigated land. Thirty-day-old seedlings were transplanted in six rows/entry, each row having 30 hills with single seedling/hill and 20 x 15 cm spacing. Observations for quantitative traits viz., plant height, leaf length and width, panicle length, ear bearing tiller/ plant, seed test weight (100), single plant yield and grain length-breadth ratio were

Table A : List of genotypes with their place of collection

Sr. No.	Genotypes	District	State
1.	Kala joha	Sonitpur	Assam
2.	Tenglai	Sonitpur	Assam
3.	Bora	Sonitpur	Assam
4.	Mota Dhan	Sonitpur	Assam
5.	Kala Bora-1	Sonitpur	Assam
6.	Sri Lanka	Sonitpur	Assam
7.	Halli Dhan-1	Sonitpur	Assam
8.	Khesra	Sonitpur	Assam
9.	Ranjit	Sonitpur	Assam
10.	Kumari	Sonitpur	Assam
11.	Kati khalli	Sonitpur	Assam
12.	Lal Aijung	Sonitpur	Assam
13.	Laxman	Sonitpur	Assam
14.	Shanti joha	Sonitpur	Assam
15.	Nashket Bora	Sonitpur	Assam
16.	Kunkuni joha	Sonitpur	Assam
17.	Koli joha	Sonitpur	Assam
18.	Joha Bora	Dhemaji	Assam
19.	Ranga Bora	Dhemaji	Assam
20.	Bor-janghia	Dhemaji	Assam
21.	Basumati	East Siang	Arunachal Pradesh
22.	Shillong Andeng	East Siang	Arunachal Pradesh
23.	Amro(Dalmang)	East Siang	Arunachal Pradesh
24.	Umkel	East Siang	Arunachal Pradesh
25.	Shillong	East Siang	Arunachal Pradesh
26.	Miching	East Siang	Arunachal Pradesh
27.	Amdeng	East Siang	Arunachal Pradesh
28.	Tagur	Pasighat	Arunachal Pradesh
29.	Itanagar	Pasighat	Arunachal Pradesh
30.	Kala Bora-2	Pasighat	Arunachal Pradesh
31.	Beckjer	Dhemaji	Assam
32.	Geko	Dhemaji	Assam
33.	Darim	Dhemaji	Assam
34.	Chhota jangia	Dhemaji	Assam
35.	Kokua	Dhemaji	Assam
36.	Chokua	Dhemaji	Assam
37.	Bada jangia	Dhemaji	Assam
38.	Alpana	Dhemaji	Assam
39.	Gamiri	Dhemaji	Assam
40.	Ampi	Dhemaji	Assam
41.	Joha	Dhemaji	Assam
42.	Effcey	Dhemaji	Assam
43.	Bogadhan	Dhemaji	Assam
44.	Lahi joha	Itanagar	Arunachal Pradesh
45.	Airi	Itanagar	Arunachal Pradesh
46.	Ampaki	Itanagar	Arunachal Pradesh
47.	Jangia	Papum Pare	Arunachal Pradesh
48.	Boradhan	Papum Pare	Arunachal Pradesh
49.	Hallidhan-2	Papum Pare	Arunachal Pradesh
50.	Gadra	Papum Pare	Arunachal Pradesh
51.	Nania	Papum Pare	Arunachal Pradesh
52.	Aijung	Sonitpur	Assam
53.	Birohi	Sonitpur	Assam
54.	Nagahalli	Sonitpur	Assam
55.	Jaya	HYV- as Check variety	
56.	Pusa Basmati	HYV-as Check variety	
57.	IR 64	HYV-as Check variety	
58.	Swarna	HYV- as Check variety	

recorded on five randomly selected plants excluding the border rows from each entry. Days to 50% flowering was recorded on plot basis. The data were analyzed utilizing Mahalanobis's generalized distance (D^2) to measure the genetic divergence among the test varieties.

RESEARCH ANALYSIS AND REASONING

The analysis of variance revealed significant differences among the genotypes for all the nine characters studied (Table 1). The results indicated high variances for most of the characters, which may favor selection and further utilization in future recombination-breeding programmes.

The 58 genotypes were grouped into 18 clusters (Fig. 1 and Table 2). Cluster I is the largest cluster comprising of 26 genotypes followed by Cluster II containing eight genotypes. Five genotypes were grouped in Cluster III and V and one genotype each in remaining 13 clusters. It is interesting to observe that most of the genotypes of one cluster were adapted to only one region. The clustering pattern reflects the closeness between the clusters and the geographical adaptation of the genotypes. The intra and inter cluster distance is presented in Table 3. The intra cluster distance analysis revealed that the maximum divergence was observed in cluster IV. It is reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding

Table 1 : Analysis of variance for nine characters of 58 genotypes

Sr. No.	Characters	Sources of variation		
		Replication (2)	Genotype (57)	Error (114)
1.	Days to50% flowering	0.120690	452.541641 **	0.483263
2.	100 grain weight	0.009117	25.432784 **	0.126216
3.	Leaf length	1.463908	8336.171954 **	63.169425
4.	Leaf width	0.008576	7.005233 **	0.049224
5.	Plant height	0.154943	84625.563736 **	91.425057
6.	Panicle length	0.422414	1399.088276 **	18.357586
7.	Grain yield /Plant	19.376790	2969.909966 **	38.526539
8.	Tillers/Plant	0.019023	6.830797 **	0.092064
9.	Grain length/Breadth	0.008040	0.881195 **	0.007402

Table 2 : Clustering pattern of 58 genotypes

Cluster No.	No. of genotypes	Name of genotypes
I	26	Beckjer, Bada jangia, Kala Bora-1, Tagur, Kala Bora-2, Bora, Miching, Halli dhan-1, Chhota jangia, Mota Dhan, Bor-janghia, Joha Bora, Tenglai, Jangia, Umkel, Halli Dhan-2, Ampa, Darim Gamiri, Ranga Bora, Chokua, Gadra, Joha, Kati khalli, Nashket Bora, Birohi, Ampaki
II	8	Efucey, Bogadhan, Swarna, Basumati, Shillong Andeng, Itanagar, Geko
III	5	Laxman, Naga halli, Khesra, Lal Aijung, Kumari
IV	1	Airi
V	5	Lahi joha, IR-64, Jaya, Ranjit, Pusa Basmati
VI	1	Koli joha
VII	1	Shanti joha
VIII	1	Alpana
IX	1	Kokua
X	1	Amdeng
XI	1	Sri Lanka
XII	1	Aijung
XIII	1	Amro (Dalmang)
XIV	1	Boradhan
XV	1	Kala joha
XVI	1	Nania
XVII	1	Shillong

materials for achieving maximum genetic advance. The other clusters showing high intra cluster values were cluster II and I. The minimum or nil intra cluster values were exhibited by cluster III, V, VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII. This indicated negligible genetic diversity among the genotypes for each

character. The maximum inter cluster divergence was observed between cluster IV and XVI (70.25) followed by cluster IV and XIV; IV and VI; IV and VIII; IV and XVIII; IV and VII. Highly divergent genotypes would produce a broad spectrum of variability in the subsequent generations enabling further selection and improvement.

Table 3 : Average intra cluster and inter cluster D² values for 58 genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	17.42	26.97	38.04	43.48	21.62	25.24	23.24	29.39	29.9	29.07	22.62	32.1	28.62	29.41	29.05	37.92	29.55	34.58
II		19.51	23.85	29.55	27.58	37.94	35.95	38.89	24.23	27.79	30.2	29.47	30.07	40.29	30.46	49.77	29.38	41.34
III			0.00	32.07	39.81	43.91	44.73	44.82	26.04	39.53	37.44	40.26	32.16	48.59	44.6	53.73	34.14	50.28
IV				21.86	40.97	58.51	55.4	58.3	39.4	31.16	48.17	32.53	45.74	60.12	36.08	70.25	42.21	56.79
V					0.00	27.71	27.94	28.16	28.84	31.77	17.64	33.17	27.72	26.38	16.74	40.58	27.01	21.47
VI						0.00	17.56	16.79	30.98	46.82	15.89	48.11	25.14	16.52	42.6	17.45	34.2	28.35
VII							0.00	13.81	32.17	44.93	22.08	49.16	26.1	21.53	40.03	23.79	35.7	30.94
VIII								0.0	32.97	51.24	19.41	54.09	26.46	18.74	42.35	22.38	36.17	23.36
IX									0.00	40.42	23.51	40.71	18.99	33.25	39.09	39.13	32.15	37.15
X										0.00	38.96	14.87	45.26	48.84	26.27	59.87	31.64	51.38
XI											0.00	41.01	22.41	19.04	33.25	27.57	25.06	23.45
XII												0.00	45.19	51.17	28.19	63.37	39.43	50.36
XIII													0.00	33.37	40.74	34.07	38.84	32.98
XIV														0.00	39.81	21.68	31.49	23.63
XV															0.00	55.52	32.38	33.97
XVI																0.00	41.56	38.52
XVII																	0.00	40.38
XVIII																		0.00

Table 4 : Cluster means of characters in D² analysis 58 genotypes

Cluster	50% DF (Days)	100 GW (g)	Leaf length (cm)	Leaf width (cm)	Plant height (cm)	Panicle length (cm)	GY/Plant (g)	Tillers/Plant	Grain L/B
I	128.77	2.47	47.12	1.03	134.83	25.71	11.69	5.67	2.48
II	110.43	2.26	39.49	1.14	121.4	24.11	12.52	6.49	2.9
III	91.33	2.57	37.5	1.43	127.4	24.53	7.93	4.67	3.25
IV	100.61	1.97	37.19	0.96	91.21	24.24	8.97	7.05	7.05
V	129.33	1.56	49.4	0.90	132.5	25.6	8.88	5.6	3.6
VI	129.33	2.46	56.03	1.27	166.5	26.5	11.22	4.77	2.92
VII	129.67	2.46	45.67	0.98	159.77	31.77	17.11	8.00	2.96
VIII	126.67	2.01	44.63	1.06	169.19	31.5	11.31	8.4	3.1
IX	105.33	2.13	54.3	1.34	142.17	23.9	22.11	8.77	2.79
X	129.33	2.49	43.73	1.14	94.9	22.77	7.88	4.6	2.7
XI	126.67	1.94	56.7	1.32	149.33	27.5	9.39	6.83	2.85
XII	124.33	2.31	44.73	1.04	97.6	17.3	5.69	3.27	1.88
XIII	105.00	2.25	58.17	0.96	153.9	29.73	13.24	5.9	2.96
XIV	137.33	1.85	48.47	1.36	164.4	25.73	19.41	5.27	3.42
XV	132.33	1.42	40.27	0.68	110.6	22.53	8.06	5.67	4.14
XVI	131.33	2.63	62.23	1.48	183.27	30.73	18.94	5.77	3.7
XVII	128.67	2.16	45.17	1.66	125.67	26.4	10.22	4.77	4.45
XVIII	130.67	0.94	44.87	0.89	158.83	26.9	8.26	6.0	2.94

Thus hybrids developed utilizing Airi, Koli joha, Shanti joha, Alpana, Kokua, Amdeng, Sri Lanka, Aijung, Amro, Bora dhan, Kala joha, Nania and Shillong may produce high magnitude of heterosis or desirable transgressive segregants, which would facilitate successful breeding of rice. Pradhan and Ray (1990) and Rahman *et al.* (1997) have also reported that selection of parents for hybridisation should be from two clusters having wider inter cluster distance to get maximum variability in the segregating generations. The cluster mean for the

characters studied are presented in Table 4. High grain yield per plant with more number of tillers per plant were recorded from cluster IX. Large panicle was recorded in cluster VII. Better grain weight (100), tall plant, moderate leaf length and width, panicle length, grain. The data in Table 5 indicated that plant height, days to 50% flowering and 100 grain weight were the major contributors to the genetic divergence among the genotypes. These traits can be utilized as parameters in selecting genetically diverse parents. The results of analysis of variance indicated high variances for most of the characters, which may favor selection and further utilization in future recombination-breeding programmes. The clustering pattern reflects the closeness between the clusters. The maximum divergence was observed between cluster IV and XVI. It is reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance. Therefore, due emphasis should be given on the members of cluster IV and XVI for selection of parents for hybridization programme. The other clusters showing high intra cluster values were cluster I, II and IV. The minimum or nil intra cluster values were exhibited by cluster III, V, VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII. This indicated negligible genetic diversity among the genotypes for each character. Observations from cluster mean suggested that none of the clusters contained genotypes with all the desirable traits, which could directly be selected and utilized. Interestingly, most of the minimum and maximum cluster means were distributed in relatively distant clusters. Mahajan *et al.* (1981) also reported that during hybridisation selection from two clusters having wider inter cluster distance ensures to get maximum variability. The genotype Nania with better grain 100 grain weight, tall plant, moderate leaf length and width, panicle length,

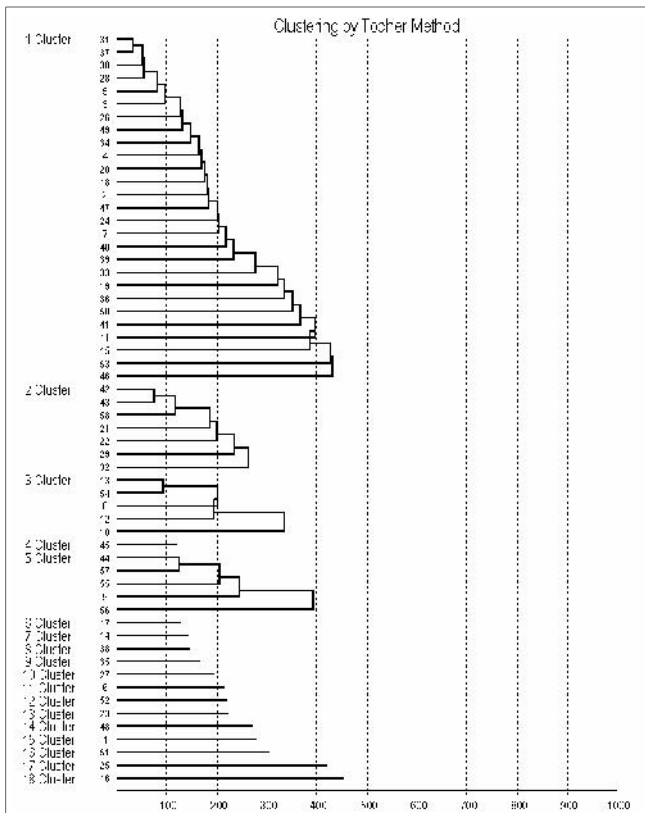


Fig. 1 : Clustering of genotypes by Tocher Method

Table 5 : Character contribution to the genetic divergence

Sr. No.	Characters	Contribution (%)	
1.	Days to50% flowering	372	22.5
2.	100 grain weight	193	11.7
3.	Leaf length	59	3.6
4.	Leaf width	106	6.4
5.	Plant height	810	49.0
6.	Panicle length	20	1.2
7.	Grain yield /Plant	40	2.4
8.	Tillers/Plant	21	1.3
9.	Grain length/Breadth	32	1.9

grain yield/plant more EBT/plant may be utilised as one of the diverse parent in hybridisation programme. Recombination breeding between genotypes of different clusters has also been suggested by Sinha *et al.* (1991) and Singh *et al.* (1996). Plant height, days to 50% flowering and 100 grain weight were observed to be the major contributors to the genetic divergence. These traits may be useful for selection of more diverse parents. The present study also revealed that the greatest contributor to the genetic diversity in field grain crops were flowering time, plant height and 100 grain weight (Murty and Arunachalam, 1966). In the present investigation, it is suggested that hybridisation programme within the divergent cluster IV and between Airi, Koli joha, Shanti joha, Alpana, Kokua, Amdeng, Sri Lanka, Aijung, Amro, Bora dhan, Kala joha, Nania and Shillong are expected to give promising and desirable recombinants in the segregating generations. Also, traits contributing maximum to genetic divergence *viz.*, plant height, days to 50% flowering and 100 grain weight may be utilized in selecting genetically diverse parents.

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