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Divergent gene pools in rice improvement

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Summary. The objective of the present study was to investigate the genetic architecture of yield in diverse populations of rice. Multivariate analysis by Mahalanobis's D^2 statistic and canonical (vector) analysis revealed that panicle weight, days to maturity, plant height and seed size were the important forces contributing towards divergence. One hundred rice strains were grouped into nine clusters with the help of D^2 and canonical analysis. The grouping pattern of the varieties were quite at random indicating that the geographical and genetic diversity were not related.

Key words: Rice – Genetic divergence – Gene pools

Introduction

Genetic uniformity has set the stage for crop destructive insect and disease epidemics in the past (Nat. Acad. Sci 1972). The diffusion of narrow genetic bases, such as 'Dee-Gee-Woo-Gen' and 'I-Geo-Tse', as the dwarfing genes, have increased the vulnerability of present day high yielding rice varieties. Thus, scientists engaged in rice improvement have an interest in the genetic diversity of improved rice varieties. This calls for strong and autonomous breeding programmes using genetically divergent gene pools and for identification of the alternative sources of dwarfism (Vairavan et al. 1973, Hargrove 1979; Hargrove et al. 1979; Murty 1979; Singh et al. 1979).

In our endeavour to diversify the genomes of rice we have collected local germplasm from U.P. (India) and parts of Nepal which appear to be phenotypically diverse. However, genetic diversity may not always be synonymous with geographical and phenotypical diversity (Murty 1979). Thus, measurements such as distance, canonical and cluster analysis based on genetic criteria quantifying diversity have been carried in an effort to locate divergent gene pools for recombination breeding.

Materials and methods

The experimental material comprised of 100 rice strains which included: (i) 74 indigenous collections having about 10 dwarfs and semi dwarfs, (ii) improved plant types from IRRI, CRRI, and AICRIP and (iii) commercially grown cultivars endemic to the area. The material was grown in a replicated trial at the Institute of Agricultural Sciences, B.H.U., Varanasi during 1979. Random and competitive five plants were tagged in each replication during emergence in order to record biometrical observations. Characters of fitness and physiological efficiency were scored at the appropriate developmental stages of plant growth. These included: (1) days to emergence, (2) days to maturity, (3) effective tillers per plant, (4) height of the plant at maturity, (5) panicle length, (6) panicle weight, (7) numbers of grains per panicle, (8) length of grain, (9) breadth of grain, (10) L/B ratio, (11) test weight and (12) seed yield per plant.

A 12×12 dispersion matrix was used for the simultaneous test of significance of difference in the mean values of 12 variables based on Wilk's criterion (Rao 1952). Mahalanobis's D^2 statistic was used for assessing the genetic divergence between the populations. Simple criteria, suggested by Tocher (Rao 1952), for determining the group constellations was used. The canonical analysis was carried out by the method described by Arunachalam (1967). All these statistics have been established to be sensitive tools for the determination of genetic affinities.

Results

The populations differed significantly with regard to the characters studied individually (Table 1) and had a marked divergence when subjected to Wilk's criterion

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Table 1. Analysis of variance and estimates of parameters of variation in rice (*Oryza sativa* L.)

Sources of variation	df	Mean squares											
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
Replication	1	–	11.00	0.52	216.90	–	12.00	807.50	0.0037	–	0.058	2.02	11.25
Treatment	99	444.60*	390.19*	11.57*	1724.07*	11.78*	2.29*	4891.57*	0.0223*	0.002257*	0.37*	42.45*	35.25*
Error	99	5.33	5.59	2.91	55.61	1.24	0.18	422.85	0.0009	0.000115	0.21	0.52	13.02
Grand mean		99.53	133.37	8.88	115.94	23.33	3.53	153.28	0.71	0.27	2.60	20.26	16.43
SE (d)		±2.30	±2.36	±1.71	±7.46	±1.11	±0.43	±20.56	±0.03	±0.01	±0.14	±0.71	±3.61
C.V. (g)		14.97	10.40	23.42	24.91	9.84	29.05	30.84	14.54	11.92	16.09	22.59	20.29
C.V. (p)		15.15	10.55	30.29	25.73	10.94	31.53	33.63	15.15	12.54	17.02	22.86	29.91
C.V. (e)		2.32	1.77	19.20	6.43	4.78	12.25	13.41	4.25	3.90	5.56	3.54	21.96
h^2 (Broad sense)		0.98	0.97	0.60	0.94	0.81	0.85	0.85	0.92	0.90	0.89	0.97	0.46
G.A.		30.34	28.16	3.32	57.61	4.25	1.95	89.29	0.20	0.06	0.82	9.32	4.46
Genetic advance over discriminant function coefficient = 6.11													
Expected gain (%) = 543.74													

* Significant at 1% level of probability

X_1 = Days to flowering
X_2 = Days to maturity
X_3 = Effective tillers per plant
X_4 = Height of the plant at maturity
X_5 = Panicle length
X_6 = Panicle weight
X_7 = Grains per panicle
X_8 = Length of grain
X_9 = Breadth of grain
X_{10} = L/B ratio
X_{11} = Seed index
X_{12} = Seed yield per plant

Table 2. Distribution of 100 strains of rice in different clusters

Cluster	Strains included	N	Mode of origin
I	Muturi (7), Nagina-32 (58), IET-2683 (89), Bala (93), Jakkoku × Serapheehil-214-55-102 (97) and CRM-13-3241 (100)	6	Nepal, U.P., CRRI, IRRI and A.P.
II	Parwanipur (48), IR 4412-207-2-3 (78), IR 2307-217-2-3 (79), Dhaneshwar (88) and Jaya (91)	5	Nepal, U.P., CRRI and IRRI
III	Kachani (3), Ramachur (8), Saro (35), Sonkharcha (43), N_{22} (50), Ch_4 (51), Duddhee (53), Silhat (54), Japanee (57), Kabiraj (65), IR 3941-25-1 (81), Rasi (84), IR 36 (86), IR 30 (87), Ratna (90), Sherammi × Serocepheehil-215-54-1A (98) and Sherammi × Eyoinchich-219-61-8 (99)	17	U.P., CRRI and IRRI
IV	Samsafiroj (2), Bachee (26), Parhanee (38), Baburam (49), Ramjiyawan (68) and Badshaw Pasand (69)	6	U.P.
V	MPR-7 (6), Singar (20), T 39 (22), Sadhuya (24), Lezura (27), Bhanslote (47), Safari (56), Ghoghar (66) and Bansee (74)	9	M.P., U.P. and Nepal
VI	Mahishra (1), Sathari (9), Anandi-II (11), Mansara-I (17), Dedaie (23), Zelona (25), Sarju-49 (28), Mansora II (30), Bakail (31), Badali (32), Sudas (33), Kalakant (42), Amawadhawad (44), Zhanghir (45), Madrasi (52), Motichur (59), Chanaw (62), Palamu (67), Rajal (70), Ahraura (71), Oorairoot (73), IR 4417-179-1-5-2 (75), IR 5853-118-5 (76), IR 2863-38-1-2 (77), IR-2863-35-3-3 (80), IR 2070-414-3-9 (83), IET 5656 (85), IR 34 (95) and IR 46 (96)	29	U.P., A.P. and IRRI
VII	Amzhos (18), Zhingee (60) and IR 3880-10 (82)	3	U.P. and IRRI
VIII	Lawangchur (4), Anandi-I (5), Sathari (10), Bajar Bhang (14), Bhajarbong (15), Latera (16), Basmati (19), Gauriya I (21), Kapoorsal (29), Nazir (34), Tulsi Ram (37), Ram Bhoj (39), Barhany (40), Morangee (46), Udraj (72), Mahsuri (92) and IR 42 (94)	17	U.P. and Nepal
IX	Bahraini (12), Adamchini (13), Gauriya II (36), Kanakzeera (41), Brahma (55), Zeera (61), Sonabhusi (63) and Manbhog (64)	8	U.P.

when all 12 variables were taken together. The value of the V-statistic was 4,076.47 at 1,188 degrees of freedom.

The range of D^2 was from 5.98 between a local collection 'Anandi' from Mirzapur and another having the same local name collected from Nepal, to 2,149.33 between a local collection named 'Sonabhusi' – a small seeded tall and late maturing strain collected from Mirzapur and 'Dhaneshwar' – a high yielding early variety of medium height with bold seeds. The wide range of distance in the populations confirmed the divergence arrived at by the V-Statistic. One hundred populations were grouped into nine clusters and their placement in the respective cluster is given in Table 2.

The intra- and inter-cluster distance in terms of average D values are presented in Table 3 and Fig. 1. The greatest intercluster distance was between cluster I and IX (D = 34.95) and the lowest between cluster VIII and IX (D = 15.13). The minimum divergence was found in cluster IX (D = 7.11) and a maximum D value of 14.19 was observed in cluster II.

Based on 12 characters, canonical analysis confirmed the clustering pattern obtained by the D^2 statistic. The composition of the clusters and their relative disposition remained almost the same. The first canonical root accounted for 54.48% of the total variability and the first two canonical roots together shared 80% of the variation. This indicated that a two dimensional representation could give a fairly accurate picture of the configuration of the groups in the 12 dimensional space. The two dimensional representation with the canonical variates as the coordinate axis is given in Fig. 2.

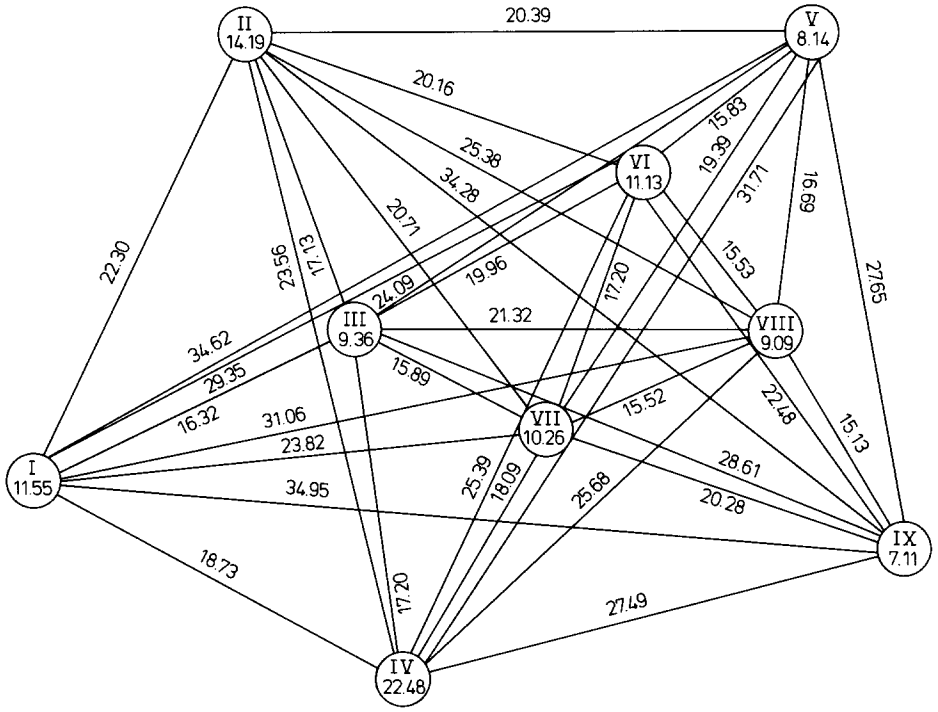

Fig. 1. Mutual relationships among clusters based on statistical distance ($\sqrt{D^2}$)

Table 3. Intra- and Inter-cluster average D^2 in 100 strains of rice. Underlined diagonals denote intra-cluster D^2 values whereas off-diagonals are inter-cluster values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	11.55	22.30	11.62	18.73	34.62	29.35	22.82	31.06	34.95
II		14.19	17.13	23.54	20.39	20.16	20.71	25.38	34.28
III			9.38	17.20	24.09	19.96	15.89	21.32	28.61
IV				12.48	31.71	25.39	18.09	25.68	27.49
V					8.14	15.83	19.39	16.69	27.65
VI						11.13	17.20	15.53	22.48
VII							10.26	15.52	20.28
VIII								9.09	15.13
IX									7.11

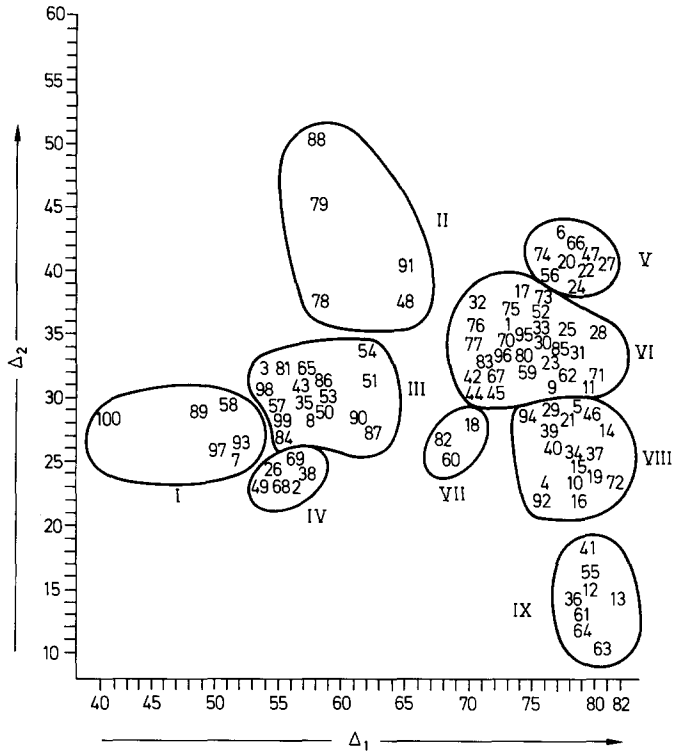

Fig. 2. Group constellations of 100 populations of rice (*Oryza sativa* L.) in Δ_1 and Δ_2 chart

Discussion

The sensitiveness and the utility of Mahalanobis's D^2 technique in identifying genetically diverse parents for obtaining success in recombination breeding by arriving at the gene constellations of divergent origins have been emphasized by several workers (Dhawan and Singh 1961; Matzinger et al. 1962, Chandersekhariah et al. 1969; Sethi et al. 1978).

Earlier workers assumed that geographical diversity reflected genetic diversity. However, Moll et al. 1962, Timothy 1963, Murty and Arunachalam 1966, Arunachalam and Ram 1967 and Narsinghani et al. 1978 could not find any direct relationship between the two. The clustering pattern in the present case also supports the above view as the genotypes from different origins cluster together in 6 out of 9 cases.

A crossing of genotypes belonging to the same cluster would not be expected to yield desirable segregates. Consequently, a crossing programme involving genetically diverse parents belonging to different topologically distinct clusters would provide an opportunity for bringing together gene constellations of divergent origins as isolation in time and space results in the locking up the genes in different constellations.

The statistical distance (D) given in Table 3 represents the index of the genetic diversity among the clusters. In the present study the maximum distance of D = 34.95 exists between cluster I and IX. The second largest distance of D = 34.28 appears between cluster II and IX. The 36 possible combinations of 9 clusters may be arranged in a descending order of magnitude of distance. The mean statistical distance (D = 21.75) may be considered as a guideline and crosses belonging to different clusters showing an inter-cluster distance of 21.75 or more should be attempted. However, other practical considerations e.g. disease reaction, lodging index and maturity etc., should also be taken into account when choosing between genotypes from a cluster.

The relative contribution of each character to the total divergence shows that yield per se had a low contribution (7.4%). Therefore, the parental material, chosen on the basis of a single complex character, i.e. yield, may not necessarily throw transgressive segregates for yield potential. However, relatively simply inherited characters, such as panicle weight, contributed maximally towards total divergence (52.9%). Therefore, it is possible that a crossing programme involving parental material selected on the basis of total divergence for the character studied might lead to an overall improvement in yield through considerable improvement in panicle weight, which is an important component of rice plant.

The idea put forth for choosing the parents on the basis of total divergence is based on the assumption

that genetic drift and selection in different environments could cause greater diversity than geographical distance.

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