Multivariate Analysis in Tropical Japonica "New Plant Type" Rice (*Oryza sativa* L.)

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Genetic diversity among fifty two "new plant type" lines including four improved cultivars was studied using Mahalanobis D^2 statistic under shallow lowland ecosystem. The genotypes were grouped into 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Cluster I with 33 genotypes was the largest, while cluster III, IV, V, VII, VIII, IX, X were monogenotypic. Genotypes in cluster VI had highest intra-cluster divergence followed by cluster II and I while highest inter-cluster divergence was between cluster VI and IX followed by VII and X. Maturity duration contributed the maximum to the total divergence. Other traits with appreciable contribution to total divergence were spikelets per panicle, grain filling (%), panicle number/m^2, panicle length (cm) and harvest index (%). All the minimum and maximum cluster mean values were distributed in relatively distant clusters. The member of the clusters VII, X, VI and I may be further evaluated as these clusters were observed to possess high cluster mean for grain yield. Further, it is suggested that cross combination of IR73964-120-5-3-2 x IR72164-110-1-2, IR73964-120-5-3-2 x IR72967-12-2-3, Naveen x IR71701-28-1-4-3, IR75268-45-2-5-3 x IR71676-106-10-3, Naveen x IR72967-12-2-3, IR73964-120-5-3-2 x IR71701-28-1-1 showing high D^2 matrix value are expected to produce superior progenies.

Key Words: Genetic diversity, New plant type, Rice, Yield component

Introduction

A quantitative assessment of genetic diversity present among selected genotypes serves as a valuable tool to exploit the genetic variability for the rapid progress in breeding programmes. The more diverse the plants, the greater chances of obtaining heterotic F_1's and broad spectrum of variability in the segregating generations (Chen *et al.*, 2002). Therefore, parental diversity plays a vital role in the success of any hybridization programme. In the present study, genetic diversity among tropical *Japonica* "New Plant Type" (NPT) lines was investigated using this technique for further choice of donors in the hybridization programme.

Materials and Methods

The experimental material comprised of 48 NPT lines and 4 check varieties (IR64, PR106, Lalat and Neveen). These lines were received from International Rice Research Institute (IRRI), Los Baños, the Philippines and evaluated at Central Rice Research Institute, Cuttack, Orissa, India. The experiment was laid out in a complete randomized block design with three replications during wet season 2005 and 2006. Twenty one days old seedlings were transplanted in field. Each plot had five rows of two meter length with an inter and intra-row spacing of 20 cm x 15 cm, respectively. The normal cultural practices (120 N: 60 P: 40 K kg/ha) and need based crop protection practices were followed to raise healthy crop. The observations on total biomass production (t/ha), harvest index (%), number of panicle/m^2, spikelet number per panicles, panicle length (cm), grain filling (%), 1000-grain weight (g), and grain yield (t/ha) were recorded on ten randomly selected plants. The mean values were subjected to analysis of variance and then to multivariate analysis using Mahalanobis D^2 analysis to measure genetic distance as suggested by Rao (1952). The genotypes were grouped into clusters following Tocher's method. The criterion used in clustering was that any two genotypes belonging to the same cluster at least on an average, show a smaller intra-cluster distance than the inter-cluster distance. The relative contributions of different characters towards genetic divergence were also worked out as the percentage contribution in which the characters were ranked first using Tocher's method.

Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the characters. The results indicated high variances for most of the characters under study.

The forty-eight NPT lines including checks were grouped into ten clusters (Table 1). Cluster I was the largest comprising of 33 genotypes followed by Cluster II having seven genotypes. Five genotypes were clubbed in Cluster VI and Cluster III, IV, V, VII, VIII, IX and X had one genotype each. All the genotypes each belonging

Table 1. Clustering pattern of 52 genotypes on basis of D^2 values

Cluster No.	No. of Genotypes	Genotypes
I.	33	IR72158-116-6, IR73707-45-3-2-3, IR75279-43-2-1-3, IR73896-51-2-1-3, IR77186-34-2-3-3, IR73930-41-5-3-1, IR72158-10-2-1-3, IR71780-1-1-3-2, IR72969-143-5-3-6-2, IR739333-8-2-2-3, IR72158-16-3-3, IR72967-94-3-1-1, IR75268-45-2-5-3, IR73944-143-3-2-3-2, IR72158-11-5-2-3, IR75279-43-2-1-3, IR72967-12-2-3, IR73971-87-1-1-1-1, IR73931-40-1-2-3-2, IR71701-28-1-4, IR74714-141-3-3-2-3, IR72158-62-6-3, IR73439-11-1-3-1, IR71676-106-10-3, IR73898-71-2-6-3, IR72176-140-1-2-2-3, IR72158-16-3-3-1, IR73895-33-1-3-2, IR74295-2-2-2-3, IR72985-65-3-1, IR71676-90-2-2, IR72981-92-1-1-2-2, IR71693-111-6-2-2
II.	7	PR106, IR 64, IR73930-313-2-2, IR72176-307-4-2-2-3, IR73963-86-1-5-2-2, IR71698-193-3-2, IR77186-122-2-2-3
III.	1	IR72164-348-6-2-2-2
IV.	1	IR72196-143-5-3-6-2
V.	1	IR74963-262-5-1-3-3
VI.	5	IR72164-110-1-2, IR73973-27-1-1-1-2, IR72967-12-2-3, IR72164-352-2-5-5, IR71701-28-1-4-3
VII.	1	IR73907-75-3-2-3
VIII.	1	IR75282-58-1-2-3
IX.	1	Neveen
X.	1	Lalat

to this cluster were developed at IRRI, the Philippines. D^2 values of the cluster ranged from 0.00 to 68.72 indicting that the material was quite diverse. Sister lines selected from the same cross were found to be grouped in different clusters. The average intra-cluster distance ranged from 0.0 (cluster III, IV, V, VII to X) to 10.18 (cluster VI). Cluster III, IV, V, VII to X were having minimum or no-cluster distance as these were monogenotypic clusters and possessing negligible genetic diversity among the genotypes for each character. Maximum intra-cluster distance was observed in cluster VI (10.18) followed by cluster II (8.82). Therefore, care should be taken to select the member of these two clusters as these may give superior progenies in combination with other members of the cluster. Genotypes in cluster VI and IX had the maximum inter-cluster divergence (D^2=68.72), while the closest proximity was observed between clusters I and V (Table 2). Taking multivariate analysis into account and the D^2 matrix value of the pairs of the genotypes, combinations, like IR73946-120-5-3-2 x IR72164-110-1-2, IR73964-120-5-3-2 x IR72967-12-2-3, IR75282-58-1-2-3 x IR71701-28-1-4-3, IR75268-45-2-5-3 x IR71676-106-10-3, IR75282-58-1-2-3 x IR72967-12-2-3 and IR73964-120-5-3-2 x IR71701-28-1-4 were predicted to give good spectrum of variability in F_2 generation. The results suggested a possibility for obtaining greater variation in the segregating generations derived from hybridization between genotypes of cluster VI and IX, VIII and X and IX and X (Table 3). The relative contributions of different characters towards total divergence (D^2) indicated that maturity duration had the maximum contribution (45.25%) and this together with panicle number (10.41%), panicle length (5.88%), spikelet/panicle (19.83%), grain filling (12.97%) and harvest index (3.93%) accounted for 95 % of total divergence. Similar findings were also reported by Shukla *et al.* (2006) and Ahmad and Baroh (1999). The present study suggested that spiklets per panicle, grain filling (%), panicle number/m^2, panicle length (cm) and harvest index (%) deserved consideration besides maturity duration while choosing parents.

Table 2. Average intra (diagonal) and inter-cluster D^2 values and distances (in parentheses) for ten clusters of fifty two genotypes of *Oryza sativa* (L.)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	6.81	19.98	12.04	11.42	1.76	18.67	12.39	12.61	36.60	27.24
II		**8.82**	17.72	16.32	16.32	30.25	20.25	18.23	23.72	25.20
III			0.00	23.72	26.21	36.97	9.24	10.96	17.56	38.94
IV				0.0	3.00	6.0	21.25	39.56	49.84	12.82
V					0.00	8.94	24.90	35.28	54.76	18.40
VI						1018	28.62	57.15	68.72	18.66
VII							0.00	26.21	21.16	23.72
VIII								0.00	16.40	58.52
IX									0.00	57.84
X										0.00

Table 3. Cluster mean values for nine agro-morphologic characters

Characters	Duration (No.)	Panicle number per plant	Panicle length (cm)	Spiklets per panicle (No.)	Grain filling (%)	1000-grain weight (No.)	Total biomass production (g)	Harvest index (%) (t/ha)	Grain yield (t/ha)
I	129.45	395.77	24.39	97.20	74.74	23.75	14.42	42.64	6.17
I	121.95	358.10	22.10	74.20	70.55	23.76	12.74	41.71	5.13
III	135.00	367.00	25.33	84.17	70.33	22.57	11.90	48.67	5.77
IV	117.67	379.33	24.33	92.73	70.90	23.97	12.40	43.13	5.36\
V	118.83	396.00	20.67	93.33	70.80	22.47	14.53	41.83	5.89
VI	117.40	397.20	24.40	100.94	71.83	24.06	14.73	42.38	6.28
VII	133.00	355.67	21.67	94.30	79.60	22.63	15.93	44.20	6.73
VIII	136.00	369.33	23.97	98.77	84.97	23.07	12.27	39.80	4.89
IX	135.67	346.33	27.67	82.40	83.70	23.43	13.77	41.47	5.00
X	115.33	375.00	20.00	100.53	81.87	25.37	16.93	41.00	6.61

The cluster means for different traits varied considerably. Breeding lines of duration (115-118 days) were grouped in cluster IV, V, VI and X. Cluster X and VIII had the genotypes with proper grain filling. Long panicle length was observed in the members of cluster IX. All the cluster possessed high number of panicles/m^2. Maturity of the clusters possessed good number of spikelets per panicle. High biomass was observed in cluster X and VII, while high harvest index was observed in cluster II, High grain yield was observed from cluster VII, X, VI and I.

Considering the importance of genetic distance, relative contributions of characters towards total divergence and yield potential of genotypes, the present investigation suggested that hybridization between cluster IX (for panicle length and grain filling), cluster VI (for 1000-grain weight, panicle number per plant and spikelets per panicle), cluster VII (for harvest index and total biomass production) would produce heterotic F_1 combinations. Total duration, spikelets per panicle, total panicle number grain filling and panicle length were major contributors to the genetic divergence among the genotypes. These traits can be utilized as parameters in selecting genetically diverse parents. Further, the members of the cluster VII, X, VI and I showed high grain yield and may be evaluated for grain yield and desirable traits for identification of the superior genotypes.

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