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Genetic divergence among some maintainer and restorer lines in relation to hybrid breeding in rice (*Oryza sativa* L.) *

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Summary. A representative group of 100 elite lines, 67 of which are restorers and 33 maintainers, from 68 crosses made at IRRI and 18 improved varieties from five countries were studied, using Mahalonobis' D^2-statistic and canonical analysis, to understand the nature and magnitude of divergence and to assess the importance of a set of quantitative characters related to yield in genetic differentiation. The 100 genotypes were grouped into 13 clusters. There were three single variety clusters and the number of lines in the remaining clusters ranged from 2–36. Canonical vector values indicated the importance of yield followed by 1,000-grain weight, days to maturity and plant height in primary as well as in secondary differentiation. Results showed that yield, number of tillers per plant, days to maturity and 1,000-grain weight contributed largely to the divergence. There were no indications of a relationship between geographical diversity and genetic diversity in the present study. Disposition of IRRI developed maintainers and restorers into various clusters indicated the presence of large amounts of diversity within the IRRI elite lines which suggested that these materials could be used in crossing programs to produce heterotic F_1 hybrids. Crossing of maintainers and restorers among the highly diverse groups was suggested as it may produce F_1s that will give higher magnitudes of heterosis.

Key words: Genetic diversity – D^2-analysis – Heterosis – Canonical analysis

Introduction

The successful development and adoption of seed production techniques using male sterility and fertility restoration systems in China (Lin and Yuan 1980) encouraged the IRRI to explore the potentials and problems of hybrid breeding approaches in increasing the yield potential of rice varieties in the tropics (IRRI 1980). The F_1 rice hybrids and their parents developed in China are not adapted to the tropics on account of their susceptibility to major diseases and insects (Virmani et al. 1981). Therefore, a hybrid breeding program at the IRRI has been identifying effective maintainer and restorer lines for the 'WA' cms system used extensively in China.

One of the challenges in hybrid breeding is the selection of suitable parental (cms/maintainer and restorer) lines with which to develop heterotic combinations. This, however, may be facilitated by determining genetic divergence among them. Inclusion of more diverse parents (within a limit) in hybridization is believed to increase the chances of obtaining stronger heterosis in hybrids (Joshi and Dhawan 1966; Anand and Murty 1968). The extent of heterosis has been found to be proportional to the genetic diversity between the parents (Kwangsi Rice Utilization Co-operative Team 1977; Jinfei and Luin 1983). Very limited work has been done on the genetic divergence in rice in relation to hybrid breeding.

The present studies were undertaken to i) ascertain the magnitude of genetic diversity among a number of elite maintainer and restorer lines which could be used to develop F_1 rice hybrids for the tropics, ii) classify the elite lines into clusters and iii) assess the importance of a set of quantitative characters related to yield in genetic differentiation.

Materials and methods

We selected 100 elite lines, 67 of which were restorers and 33 maintainers for 'WA' type cytosterile lines: Zhen Shan 97A

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*** Associate Professor, Department of Agronomy, University of the Philippines at Los Baños, College, Laguna, 3720, Philippines and V20A (Virmani, unpublished). These lines represented 68 crosses made at IRRI and 18 improved varieties from five countries.

The experiment was conducted using a lattice design with two replications at the IRRI experimental farm under uniform levels of fertilizer and other cultural practices. Each entry was grown in five rows with a spacing of 20 cm between rows and 20 cm between plants, with a single seedling per hill. The two peripheral rows were discarded to avoid border effects. Ten plants were selected at random from the middle three rows and their identities were maintained throughout the study by marking them. Data were recorded on the selected plants from each plot on nine characters, namely, plant height at 40 days after transplanting, plant height at maturity, days to maturity, number of tillers per plant, number of panicles per plant, number of spikelets per panicle, number of fertile spikelets per panicle, 1,000-grain weight, and yield.

Analyses of variance were done based on plot means. Based on the procedure described by Rao (1952), Mahalonobis' distance (D^2) values between all possible pairs were calculated using transformed uncorrelated means of the nine variables. Following Tocher's method as also given in Rao (1952), clusters were made and confirmed by canonical analysis as described by Singh and Chaudhary (1977).

Results

Analyses of variance based on individual plot means showed highly significant differences among entries for all characters, indicating the existence of considerable genetic variation among the materials. Therefore, it was considered worthwhile to classify the 100 maintainer and restorer lines on the basis of these characters.

Nature and magnitude of diversity

Clustering done by Tocher's method (Rao 1952). On the basis of D^2-values, the 100 maintainer and restorer lines formed 13 clusters (Table 1). There were three single variety clusters (XI, XII and XIII) and the number of lines included in the remaining clusters varied from 2–36.

Thirty-six genotypes were included in cluster I of which seven were maintainers. The maintainer BG 379 from Sri Lanka and the restorer Milyang 46 from Korea were included in this cluster along with other IRRI developed elite lines. IR19672-140-2-3-2 (a maintainer) and IR19672-195-2-2 (a restorer) were derived from the same cross and were included in this cluster. Similarly, two restorers: IR9761-19-1 and IR9761-45-1-3 (also from the same cross) were included in cluster I. The maintainers IR19657-34-2-2-3-3 and IR19657-87-3-3 of the same cross were included in cluster X. Likewise, the two restorers IR13149-149-3-2-2 and IR13149-23-2 were included in cluster IV, indicating close affinity between the advanced lines of the same crosses. The two maintainer lines IET 3257 and MR 365 from India were included in clusters II and VII, respectively, indicating no relationship between genetic diversity and geographical distribution of the varieties.

The restorer IR11248-148-3-2-3-3 and the maintainer IR11248-242-3-2 derived from the same cross were included in clusters I and II, respectively. Likewise, restorers IR13149-113-1 and IR13149-3-2-2 were included in clusters I and IV; restorer IR13429-150-3-2-1-2 and maintainer IR13429-196-1 were in II and III; restorer IR19660-187-2-2-3-2 and maintainer IR19660-109-3-2-3-2 in clusters IV and I, respectively. Furthermore, it can be noted that the maintainer IR19661-3-2-2-3-1, restorer IR19661-63-1-3 and maintainer IR19661-156-1-2-3-2 being of the same cross were included in clusters VIII, IX and VI, respectively. This indicated the presence of variation among the elite lines derived from the same cross.

The average D^2-values and D-values within and between clusters (Table 2) showed that the intra cluster divergence was maximum for cluster VII ($D = 33.61$) and minimum for cluster V ($D = 20.80$). The D-values in any inter cluster level ranged from 32.73–75.97. Considering the range of D-values, three distinct classes were made, namely, low divergence ($D = 32–45$), intermediate divergence ($D = 46–60$), and high divergence ($D = 61$ and above).

The low diverse clusters are III, IV, VI and VIII from clusters I and II; clusters I, II and IV from cluster VI; clusters I, II, IV and VI from VIII; cluster XIII from I, IV, VI, VIII and X; and cluster IX from I, II, III, IV, V, VI and VII. The intermediate diverse clusters are V, VII and X from clusters I and II; cluster VIII from III, V and IX; cluster XIII from II, III, V and IX; clusters IV and VI from V and X; and cluster VII from I, II and III. The most diverse clusters were IV, VI, VIII and XIII from cluster VII; clusters XI and XII from I, IV, VI, VIII and X; and V from X.

Canonical analysis. In the present study it would appear from the canonical analysis that the two canonical roots accounted for most of the variability (Table 3). Therefore, a two dimensional representation of relative positions of the varieties in the Z_1-Z_2 graph was found adequate (Fig. 1). It is interesting to note that the clusters were distinctly delineated to their respective positions similar to their positions in D^2-analysis except for cluster XI, containing maintainer IR10154-23-3-3, and cluster XII, containing restorer IR11297-49-1-3. Although these two clusters were closer in the Z_1-Z_2 graph, the D^2-value between them was very high ($D^2 = 5{,}233.1$) and the two could not be grouped together. The higher D^2-value between them may be due to the fact that these are single lines clusters. Examination of the number of parents involved in these two lines revealed that IR11297-49-1-3 had only three parents in its parentage out of which

Table 1. Grouping of 100 rice varieties into clusters

Cluster no.	Entry no.	Variety/line	
I	2[b]	BG 379 (Sri Lanka)[c]	
	6[a]	IR10781-143-2-3	(IRRI)
	7[a]	IR11248-148-3-2-3-3	(IRRI)
	13[a]	IR13149-71-3-2-3	(IRRI)
	15[a]	IR13240-108-2-2-3	(IRRI)
	16[a]	IR13292-5-3-1	(IRRI)
	17[a]	IR13419-113-1	(IRRI)
	22[a]	IR13525-2-3-3-2-1	(IRRI)
	23[a]	IR13538-6-2-2-3-2	(IRRI)
	24[a]	IR13539-41-22-2-3-2	(IRRI)
	25[a]	IR15314-43-2-3-3	(IRRI)
	27[b]	IR15429-268-1-2-1	(IRRI)
	28[a]	IR15795-232-3-3-3-2	(IRRI)
	29[a]	IR15797-74-1-3-2	(IRRI)
	31[b]	IR17429-18-10-2-2-2	(IRRI)
	32[b]	IR17492-18-10-2-2-2	(IRRI)
	33[a]	IR17494-32-2	(IRRI)
	37[a]	IR18349-22-1-2	(IRRI)
	39[a]	IR18599-68-1	(IRRI)
	40[a]	IR19058-107-1	(IRRI)
	45[a]	IR19577-80-3-1	(IRRI)
	46[a]	IR19588-166-3-1	(IRRI)
	50[b]	IR19660-109-3-2-3-2	(IRRI)
	55[b]	IR19672-140-2-3-2	(IRRI)
	56[a]	IR19672-195-2-2	(IRRI)
	64[a]	IR20154-180-3-3	(IRRI)
	66[a]	IR21178-26-1	(IRRI)
	68[a]	IR21734-70-3-2	(IRRI)
III	19[b]	IR13429-196-1	(IRRI)
	21[a]	IR13524-21-2-3-3-2-2	(IRRI)
	26[a]	IR15324-12-2-3-3-2	(IRRI)
	44[a]	IR19575-85-2-2-3	(IRRI)
	58[b]	IR19746-27-3-3-1-3	(IRRI)
	77[a]	IR286-39-2-8	(IRRI)
	78[a]	IR32 (Philippines)	
	80[a]	IR36 (Philippines)	
	86[a]	IR54 (Philippines)	
IV	11[a]	IR13149-3-2-2	(IRRI)
	12[a]	IR13149-23-2	(IRRI)
	34[a]	IR17521-27-2-2-2-2	(IRRI)
	41[a]	IR19083-22-2-2	(IRRI)
	49[b]	IR19657-90-3-3-2	(IRRI)
	51[a]	IR19660-187-2-2-3-2	(IRRI)
	70[b]	IR21845-90-3	(IRRI)
	72[a]	IR21912-9-2	(IRRI)
V	60[b]	IR19799-17-3-1-1	(IRRI)
	75[a]	IR24 (Philippines)	
	83[a]	IR4763-73-1-11	(IRRI)
	85[a]	IR52 (Philippines)	
	88[b]	IR747B2-6-3-1	(IRRI)
I	69[a]	IR21734-88-3-1	(IRRI)
	73[a]	IR2307-247-2-2-3	(IRRI)
	81[a]	IR42 (Philippines)	
	87[a]	IR56 (Philippines)	
	93[b]	IR9708-51-1-2	(IRRI)
	94[a]	IR9761-19-1	(IRRI)
	95[a]	IR9761-45-1-3	(IRRI)
	99[a]	Milyang 46 (Korea)	
II	4[b]	IET 3257 (India)	
	8[b]	IR11248-242-3-2	(IRRI)
	18[b]	IR13429-150-3-2-1-2	(IRRI)
	30[a]	IR15847-215-2-1	(IRRI)
	35[b]	IR17525-278-1-1-2	(IRRI)
	36[a]	IR18342-4-3	(IRRI)
	57[b]	IR19722-9-1-3-2-1	(IRRI)
	59[b]	IR19792-15-2-3-3	(IRRI)
	61[b]	IR19805-12-1-3-1-2	(IRRI)
	62[b]	IR19819-31-2-3-1-1	(IRRI)
	63[a]	IR20985-93-5-2	(IRRI)
	65[a]	IR2035-182-3-2	(IRRI)
	67[a]	IR21526-4-3-3	(IRRI)
	79[b]	IR34 (Philippines)	
	89[a]	IR7963-30-4-3	(IRRI)
	92[a]	IR9217-6-2-2-2-3	(IRRI)
	96[a]	IR9802-50-1-2-2	(IRRI)
	98[a]	IR9828-41-2-1	(IRRI)
III	1[a]	B441b-126-3-2-1	(IRRI)
	14[b]	IR13240-6-3-MR-8	(IRRI)
V	90[a]	IR8073-43-3-2	(IRRI)
	98[b]	Jikkoku Seranai (India)	
VI	20[b]	IR13458-52-1-1-3	(IRRI)
	38[a]	IR18349-65-1-3	(IRRI)
	54[b]	IR19661-150-1-2-3-2	(IRRI)
	71[b]	IR21845-90-3-1	(IRRI)
VII	75[a]	IR26 (Philippines)	
	84[a]	IR50 (Philippines)	
	91[b]	IR9215-69-1-2	(IRRI)
	100[b]	MR 365 (India)	
VIII	10[a]	IR13146-243-2-3	(IRRI)
	43[a]	IR19431-72-2	(IRRI)
	52[b]	IR19661-3-2-2-3-1	(IRRI)
	76[a]	IR2797-105-2-2-3	(IRRI)
IX	3[a]	BPI-RI-4 (Philippines)	
	42[a]	IR19090-224-3-2	(IRRI)
	53[a]	IR19661-63-1-2-3	(IRRI)
X	47[b]	IR19657-34-2-2-3-3	(IRRI)
	48[b]	IR19657-87-3-3	(IRRI)
XI	5[b]	IR10154-23-3-3	(IRRI)
XII	9[a]	IR11297-49-1-3	(IRRI)
XIII	82[a]	IR46 (Philippines)	

[a] Restorer

[b] Maintainer

[c] Within parentheses is the country of origin

Table 2. Intra- and inter-cluster average D² values of 13 clusters formed by Tocher's method. Values in parentheses are the D values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	1,058.88 (32.54)	1,103.12 (33.21)	1.223.48 (34.98)	1,196.03 (34.98)	2,766.48 (52.60)	1,476.09 (38.42)	3,548.64 (59.57)	1,796.63 (42.39)	1,462.76 (37.98)	2,494.32 (49.94)	4,163.65 (64.53)	3,952.27 (62.87)	2,058.92 (45.39)
II		725.08 (26.93)	1,180.84 (34.36)	1,337.03 (36.57)	2,231.61 (47.24)	1,528.97 (39.10)	3,164.05 (56.25)	1,870.45 (43.25)	1,331.82 (36.49)	2,952.38 (54.34)	3,587.79 (59.90)	3,331.27 (57.72)	2,628.25 (51.27)
III			933.45 (30.55)	1,562.26 (39.53	2,074.09 (45.42)	2,007.19 (44.80)	2,904.40 (53.89)	2,606.41 (51.05)	1,099.42 (33.16)	3,583.21 (59.86)	2,978.88 (54.58)	3,164.96 (56.26)	3,030.16 (55.05)
IV				789.71 (28.10)	3,332.87 (57.73)	1,242.95 (35.26)	4,054.67 (63.68)	1,780.54 (42.20)	1,708.53 (41.33)	2,475.20 (49.75)	4,791.88 (69.22)	4,430.05 (66.56)	1,888.30 (43.45)
V					432.42 (20.80)	3,379.40 (58.13)	1,071.45 (32.73)	3,561.04 (59.67)	1,166.36 (34.15)	4,178.30 (64.64)	1,803.51 (42.47)	1,766.08 (42.02)	3,077.27 (55.47)
VI						1,053.30 (32.45)	4,780.77 (69.14)	1,365.53 (36.95)	2,144.24 (45.98)	2,388.92 (48.88)	4,800.22 (69.28)	4,991.70 (70.65)	1,771.25 (42.09)
VII							1,129.70 (33.61)	4,844.85 (69.60)	1,805.03 (42.49)	5,491.21 (74.10)	1,331.07 (36.48)	1,264.96 (35.57)	5,015.98 (70.82)
VIII								735.70 (27.12)	3,455.26 (58.78)	1,966.51 (44.35)	5,405.74 (73.52)	5,226.69 (72.30)	1,566.39 (39.58)
IX									758.78 (27.55)	3,893.96 (62.40)	2,104.80 (45.88)	2,357.03 (48.55)	3,638.74 (60.32)
X										881.94 (29.69)	5,771.56 (75.97)	5,561.49 (74.58)	1,675.89 (40.94)
XI											00.00	5,233.10 (72.34)	5,515.98 (74.27)
XII												00.00	5,432.40 (73.70)
XIII													00.00

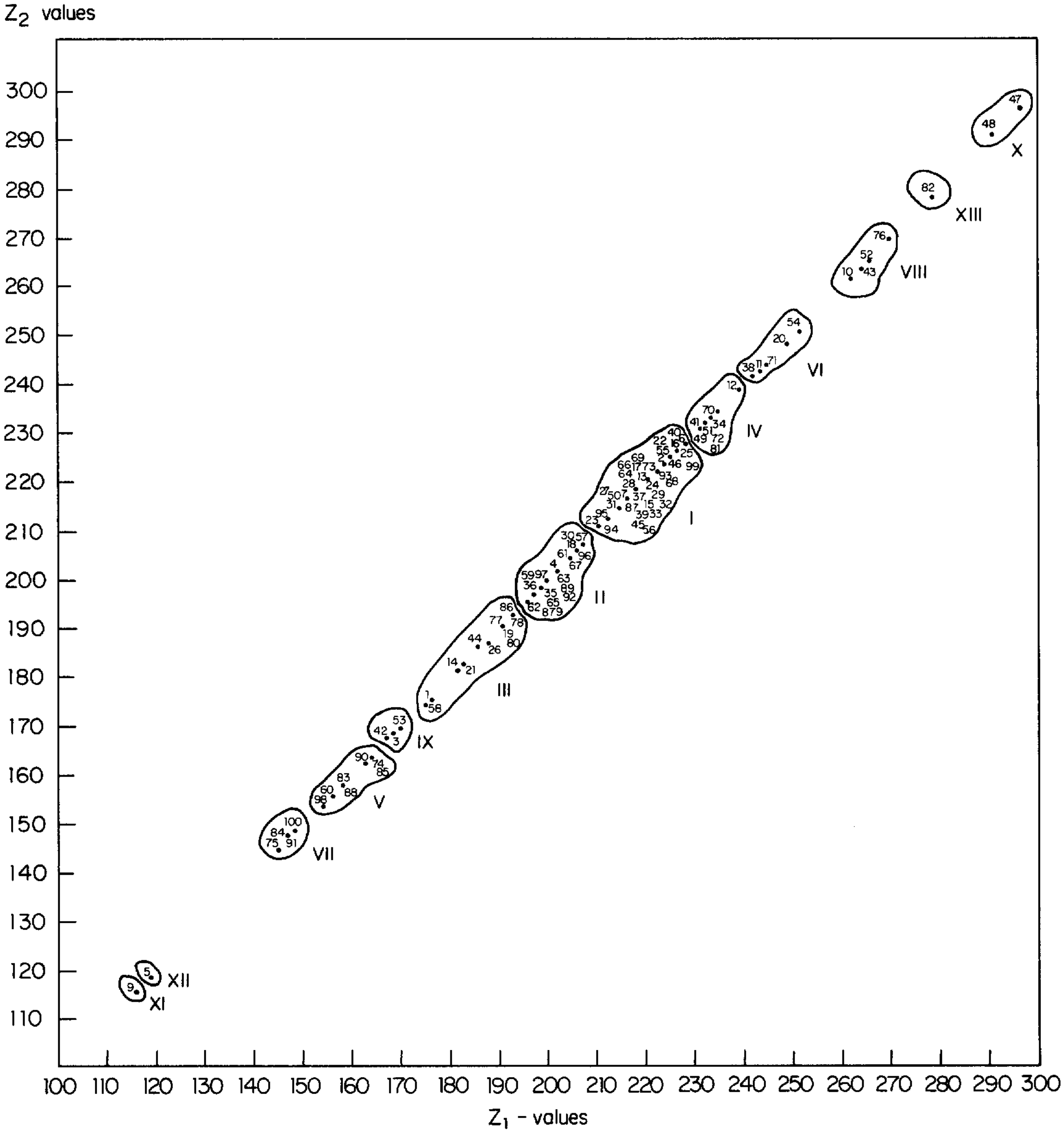

Fig. 1. Disposition of 100 maintainer and restorer lines of rice in Z_1–Z_2 chart

two were common with the percentage of IR10154-23-3-3 having 11 parents in its parentage. Thus, it was assumed that the higher difference in number of parents involved in these two clusters may be another factor for higher D^2-value between them.

The deviation of line number 81 (IR46) from cluster I to its adjacent cluster IV and line number 11 (IR13149-3-2-2) from IV to VI may be due to the clustering done by two different methods.

From the absolute magnitude of the two canonical vectors values (Table 3) it would appear that yield, 1,000-grain weight, days to maturity and plant height were mostly responsible for both primary and secondary differentiation. The remarkable closeness of both the vectors indicated that the characters were equally affected in the course of evolutionary process.

Contribution of individual characters towards divergence

The differences in the transformed uncorrelated mean values for each of the characters were ranked in descending order of magnitude, rank 1 being assigned to the highest value. The total of this rank over all the possible 4,950 comparisons would provide indirect information about the order of priority of the characters for classification. This order of priority of the traits was found to be yield, number of tillers, days to maturity,

Table 3. The canonical vector values for the classification of 100-maintainer and restorer lines in rice

Characters	Canonical vector 1	Canonical vector 2
Plant height at 40 days after transplanting (cm)	−0.005	−0.005
Plant height at maturity (cm)	0.071	0.079
Days to maturity	0.150	0.150
No. of tillers per plant	−0.047	−0.047
No. of panicles per plant	−0.011	−0.011
No. of spikelets per panicle	0.004	0.004
No. of fertile spikelets per panicle	0.034	0.034
1,000-grain wt (gm)	0.152	0.152
Yield/m^2	1.173	1.173
Canonical root value	78,014.67	77,831.58
Contribution to the total divergence (%)	96.4	3.6

Table 4. Number of times the individual characters appeared first in the ranking and their percent contribution towards divergence

Characters	No. of times appearing first in the ranking	Percent contribution towards genetic divergence
Plant height at 40 days after transplanting (cm)	160	3.23
Plant height at maturity (cm)	415	8.38
Days to maturity	574	11.60
No. of tillers per plant	912	18.42
No. of panicles per plant	163	3.29
No. of spikelets per panicle	326	6.59
No. of fertile spikelets per panicle	45	0.91
1,000-grain wt (gm)	526	10.63
Yield/m^2	1,829	37.00
Total	4,950	100

1,000-grain weight, plant height at maturity, number of spikelets per panicle, number of panicles per plant, plant height at 40 DAT and number of fertile spikelets per panicle (Table 4).

The data on both Tables 3 and 4 revealed the importance of major characters responsible for genetic differentiation among the materials although the orders of the characters were different in the two approaches used.

From this study, it was found that yield per se had the highest contribution to the total divergence which also influenced the clustering patterns.

Characterization of individual clusters

Characterization of individual clusters was done by grouping the mean values of all characters for the 13 clusters into low, intermediate and high (Table 5). It was observed that clusters I and II differed from one another only with respect to plant height at maturity, days to maturity and 1,000-grain weight and that these two clusters showed low divergence between them. It can be noted that there was no difference among the means for different characters of clusters II and III. Yet these two clusters could not merge into one cluster, due perhaps, to the difference in mean values of individual lines which were included in a cluster. Clusters V, VII and IX differ from each other only with respect to days to maturity, number of tillers per plant, number of panicles per plant and number of fertile spikelets per panicle. Both custers VII and IX showed a high value for number of fertile spikelets per panicle but a low value for number of tillers per plant and number of panicles per plant. Cluster V showed an intermediate value for the above traits. Clusters V, VII and IX showed low divergence among them. A substantial difference in cluster means was observed in the case of three single variety clusters (XI, XII and XIII) for all the characters except 1,000-grain weight. These clusters showed high divergence among them.

In general, the clusters which showed considerable differences in characters, such as yield, number of tillers per plant, days to maturity and 1,000-grain weight, also showed maximum divergence among them.

Discussion

Genetic divergence analysis is attempted in order to identify specific parents for realizing heterosis and recombination in breeding program. Mahalonobis' D^2-statistics has been followed by several workers on a wide range of crop species, including rice, to measure the genetic distance among their breeding materials and to identify characters responsible for such type of divergence (Ram and Panwar 1970; Vairavan et al. 1973; Maurya and Singh 1977; Rao et al. 1981; Jinfei and Luin 1983).

In the present study the 100 elite lines were found to form 13 distinct clusters, indicating the presence of large amounts of diversity among them. These materials could therefore be successfully used in breeding program to produce F$_1$ hybrids that will give higher magnitudes of heterosis.

Table 5. The mean values of nine characters for 13 clusters obtained by multivariate analysis in selected maintainer and restorer lines in rice

Cluster Character	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
Plant height at 40 days after transplanting (cm)	45.2 (I)	48.1 (I)	46.8 (I)	48.0 (I)	48.0 (I)	48.4 (I)	44.0 (I)	57.6 (H)	42.0 (I)	46.6 (I)	53.3 (H)	32.8 (L)	50.0 (I)
Plant height at maturity (cm)	97.3 (H)	94.3 (I)	95.0 (I)	105.0 (H)	86.0 (I)	103.3 (H)	86.2 (I)	110.1 (H)	88.2 (I)	100.4 (H)	69.0 (L)	85.0 (I)	108.4 (H)
Days to maturity	116 (H)	110 (I)	112 (I)	121 (H)	104 (I)	125 (H)	109 (I)	122 (H)	115 (H)	119 (H)	86 (L)	112 (I)	122 (H)
No. of tillers per plant	17 (I)	18 (I)	13 (I)	14 (L)	17 (I)	15 (L)	16 (L)	17 (I)	16 (L)	14 (L)	21 (H)	21 (H)	18 (I)
No. of panicles per plant	16 (I)	16 (I)	17 (I)	13 (L)	15 (I)	14 (L)	14 (L)	16 (I)	14 (L)	13 (L)	16 (I)	18 (H)	17 (I)
No. of spikelets per panicle	116 (I)	115 (I)	114 (I)	112 (I)	91 (I)	124 (H)	116 (I)	117 (I)	113 (I)	115 (I)	59 (L)	146 (H)	107 (I)
No. of fertile spikelets per panicle	98 (H)	96 (H)	93 (H)	93 (H)	77 (I)	109 (H)	93 (H)	96 (H)	96 (H)	107 (H)	56 (L)	100 (H)	80 (I)
1,000-grain wt (gm)	24.2 (I)	22.7 (L)	22.5 (L)	22.6 (I)	22.6 (L)	24.9 (I)	20.2 (L)	23.6 (I)	21.8 (L)	29.8 (H)	21.7 (L)	18.2 (L)	22.2 (L)
Yield/m^2	632.6 (I)	559.3 (I)	509.3 (I)	653.8 (I)	422.5 (L)	692.8 (H)	354.0 (L)	777.4 (H)	437.6 (L)	872.1 (H)	307.2 (L)	266.8 (L)	830.3 (H)

H = High values; I = Intermediate values; L = Low values

It was revealed from the results that maintainers and restorers derived from the same cross were included in the same cluster showing a close affinity between advanced sister lines. On the other hand, maintainers and restorers derived from the same crosses were also included in different clusters, showing variation among the elite lines derived from the same crosses. This can result from multidirectional selection in early generations. In fact, most of the lines were derived from multiple crosses having several parents in their pedigree. Therefore, even the elite lines derived from the same crosses and also selected in the same regions of cultivation failed to possess stability with respect to yield components in advanced generations which had contributed to its diversity in subsequent selections.

It was interesting to observe that the maintainer BG 379, the only variety from Scri Lanka and the restorer Milyang 46 from Korea were included in cluster I along with other elite maintainer and restorer lines of IR crosses. The two maintainers IET 3257 and MR 365 from India were included in clusters II and VII, respectively. Thus, in the present study, there were no indications of a relationship between geographical diversity and genetic diversity. Ram and Panwar (1970) reported that geographic diversity might be related to genetic diversity in rice. However, Vairavan et al. (1973) did not find any relationship between geographical diversity and genetic diversity in rice. This implies that maintainers and restorers from diverse ecogeographical origins may not give higher heterotic F_1 hybrids if they do not have enough genetic differences.

The most important character contributing to the divergence was found to be yield followed by number of tillers per plant, days to maturity and 1,000-grain weight. It was also observed from the means of clusters that the clusters which showed considerable differences in characters, such as yield, number of tillers per plant, days to maturity and 1,000-grain weight, also showed maximum divergence between them.

In earlier studies on rice, Ram and Panwar (1970) found that height of the plant, number of productive tillers and growth duration were the important traits for differentiation. Maurya and Singh (1977) reported that maturity time, plant height and number of productive tillers contributed most to the divergence in rice. Vairavan et al. (1973) reported the importance of 1,000-grain weight in genetic differentiation.

The above results implied that in order to select genetically diverse parents of heterotic hybrids out of these maintainers and restorers, one should classify the materials on the basis of such traits as yield, number of tillers per plant, 1,000-grain weight, days to maturity and plant height.

It was revealed from this study that yield had the highest contribution to the total divergence which also influenced the clustering pattern. However, materials chosen only on the basis of a single complex character, like yield, may not show transgressive segregates for yield potential. Therefore, if we are interested in heterosis over the best parent then the materials should be discriminated for with respect to yield contributing characters and not yield itself. In addition, discrimination on the basis of more characters along with yield components would also reflect the importance of other characters in genetic differentiation. The number of characters could not be increased in this study due to the large number of entries creating computational complexity. It can be noted that most of the characters chosen in the present study are influenced by the environment and therefore different groupings may be encountered in other regions, especially in the presence of genotype-environment interaction. The fact behind the choice of these characters was that generally plant breeders select their parent materials on the basis of some yield contributing characters which are being sought to be improved through hybridization. Therefore, it was thought proper to classify the materials on the basis of yield component characters prior to selection as parents. However, a follow up experiment through 'isozyme analysis' is underway for the confirmation of the diversity which might give valid information because this technique are free from environmental influences.

On the basis of our findings on extent of genetic diversity among elite maintainer and restorer lines, we can predict prospective parents which shall result in heterotic F_1 rice hybrids. The high divergent clusters were IV, VI, VIII, X and XIII from VII; clusters XI and XII from I, IV, VI, VIII, X and XIII; clusters V from X. Crossing among the maintainer and restorer lines of these clusters is suggested as it may give high heterotic rice hybrids.

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