

## Multivariate analysis in tropical japonica “New plant type” rice (*Oryza sativa* L.)

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### ABSTRACT

*Genetic diversity among thirty-nine “new plant type” tropical japonica lines and three improved cultivars was studied using Mahalanobis D<sup>2</sup> statistic. The genotypes were grouped into 14 clusters. Cluster I with 14 genotypes was the largest while cluster IX, X, XI, XII, XIII, XIV were monogenotypic. Genotypes in cluster II had the highest intra cluster distance. The maximum inter cluster distance (1328.30) was recorded between cluster VI and VII. Harvest index contributed maximum (45.99 %) to the total divergence. Other traits with appreciable contribution to total divergence were biological yield per plant, grain number per panicle and 1000-grain weight whereas panicle length had no contribution towards total divergence. Hybridization among genotypes IR 66736-75-1-3, IR 66792-23-1-2-2, IR 69810-62-1-3, WCR 6 and Govind drawn from widely divergent cluster is likely to produce heterotic combinations and wide variability in segregating generations.*

**Key words:** Genetic diversity, tropical japonica, new plant type, rice

A quantitative assessment of genetic diversity present among selected genotypes of rice will serve 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<sub>1</sub>'s and broad spectrum of variability in the segregating generations (Arunachalam, 1981). 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” lines was investigated using this technique for further choice of donors in the hybridization programme.

### MATERIALS AND METHODS

The experimental material comprised of 39 Tropical Japonica “new plant type” lines and 3 check varieties. These lines were received from International Rice Research Institute (IRRI), Los Banos, Philippines and maintained at G.B. Pant University of Agriculture and Technology, Pantnagar. The experiment was laid out in a randomized complete block design with three

replications during kharif season 2000. Twenty one days old seedlings were transplanted in field. Each plot had two rows of two meter length with an inter and intra row spacing of 20 x 15 cm respectively. The normal cultivars practices (120 N : 60 P : 40 K kg ha<sup>-1</sup>) were followed to raise a healthy crop. Except for days to 50 % flowering which was recorded on plot basis, other characters *i.e.* plant height (cm), number of tillers plant<sup>-1</sup>, panicle number plant<sup>-1</sup>, panicle length (cm), length of flag leaf (cm), width of flag leaf (cm), grain number panicle<sup>-1</sup>, 1000-grain weight (g), biological yield plant<sup>-1</sup> (g), harvest index (%) and grain yield plant<sup>-1</sup> (g) were recorded on the basis five randomly taken competitive plants. The mean values were subjected to analysis of variance and then to multivariate analysis using Mahalanobis D<sup>2</sup> 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 at least on an average, show a smaller intracluster distance than the inter cluster distance. The relative contributions of different

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characters towards genetic divergence were also worked out as the percentage combination in which the characters has been ranked first using Tocher's method (Rao, 1952).

## RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters. The  $D^2$  values in the genotypes ranged from 61.62 to 1328.30 indicating that the material was quite diverse. Based on genetic distance, the 42 genotypes were grouped into 14 clusters (Table 1). The cluster I included 14 genotypes and was the largest. All the genotypes belonging to this cluster were developed at the International Rice Research Institute (IRRI), Philippines and some lines, were developed from the same cross. Cluster IX included genotypes developed at Pantnagar. Five genotypes each were accommodated in cluster II and III, while cluster IX, X, XI, XII, XIII, XIV were represented by a single genotype each. Excepting genotypes in cluster I and IX, the remaining genotypes were grouped into different clusters irrespective of their places of origin or ancestry. Sister lines selected from the same cross also fell into different

clusters. This might be due to different selection pressure and selection criteria applied for specific traits. These observations indicated that genetic diversity was not related to geographical diversity. Similar findings were reported earlier by Kumari and Rangasamy (1997), Kandhala and Panwar (1991) and Rather *et al.* (2001). The average intra cluster distance ranged from 0.0 (cluster IX to XIV) to 111.21 (cluster II). Genotypes in cluster XI and XII had the maximum inter cluster divergence ( $D^2=1328.30$ ) while the closest proximity was observed between clusters IV and XIII (Table 2). Genotypes of distinct clusters separated by high genetic distance could be utilized in the breeding programme for obtaining a wide spectrum of variability in the segregating generations. These results suggested a possibility for obtaining greater variation in the segregating generations derived from hybridization between genotypes of cluster XI and XII because of the maximum genetic distance between these two groups (Table 2 and 3). The relative contributions of different characters towards total divergence ( $D^2$ ) indicated that harvest index had the maximum contribution (45.99 %) and this together with biological yield plant<sup>-1</sup>, grain number panicle<sup>-1</sup>, and 1000-grain weight accounted for 90 % of total divergence. Similar

**Table 1. Clustering pattern of 42 genotypes on basis of  $D^2$  values**

Cluster No.	Genotypes	Number of genotypes
I.	IR 65564-44-5-1, IR 66158-38-3-2-1, IR 65597-17-4-3-3, IR 65600-32-4-6-1, IR 65598-152-1-5-2, IR 66167-27-5-1-6, IR 65605-6-2-3-2, IR 69082-26-2-5-2, IR 66154-48-1-3-1, IR 66774-27-2-3-3, IR 65600-77-4-2-1, IR 65600-42-5-2, IR 69082-49-2-3-2, IR 66738-174-2-1	14
II.	IR 65600-87-2-2-3, IR 67266-52-3-2-2, IR 66155-2-1-1-2, IR 69104-49-2-1-3, IR 66768-42-3-1	5
III.	IR 66159-23-2-2-1, IR 68554-2-2-3-3-2, IR 68516-3-2-2, IR 68011-15-1-1-2-3, IR 69810-15-2-2	5
IV.	IR 65597-29-3-2-3, WCR 21, IR 66159-189-5-2-2, IR 68203-28-2-3-2	4
V.	IR 65597-134-2-3-1, IR 68763-46-1-2-5-2	2
VI.	Pant Dhan-4, Pant Dhan-12	2
VII.	IR 66764-AC4-8, IR 68011-16-1-1-3-2	2
VIII.	IR 67323-46-2-1, IR 69806-1-3-3	2
IX.	IR 66736-75-1-3	1
X.	IR 66792-23-1-2-2	1
XI.	IR 68763-46-1-2-3	1
XII.	IR 69810-62-1-3	1
XIII.	WCR 6	1
XIV.	Govind	1

Table 2. Average intra (diagonal) and inter-cluster D<sup>2</sup> values and distances (in parentheses) for forty-two genotypes of rice

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	81.14 (9.01)	351.31 (18.74)	226.26 (15.04)	175.64 (13.25)	235.60 (15.35)	894.89 (29.19)	128.43 (11.33)	130.63 (11.43)	171.30 (13.09)	295.84 (17.20)	117.50 (10.84)	412.18 (20.30)	172.62 (13.14)	416.35 (20.40)
II		<b>111.21</b> <b>(10.55)</b>	172.42 (13.13)	160.54 (12.68)	446.58 (21.13)	688.29 (26.24)	474.03 (21.77)	254.63 (15.96)	449.40 (21.20)	148.70 (12.19)	495.10 (22.25)	143.68 (11.99)	188.07 (13.71)	308.37 (17.56)
III			83.60 (9.14)	181.80 (13.48)	426.21 (20.64)	937.88 (30.62)	271.52 (16.48)	159.69 (12.64)	458.69 (21.42)	266.55 (16.33)	336.97 (18.36)	257.23 (16.04)	103.97 (10.20)	406.79 (20.17)
IV				66.45 (8.15)	195.87 (14.00)	462.43 (21.50)	339.35 (18.42)	168.44 (12.98)	268.28 (16.38)	135.49 (11.64)	314.46 (17.73)	124.64 (11.16)	<b>93.61</b> <b>(9.68)</b>	134.78 (11.61)
V					93.53 (9.67)	533.29 (23.09)	454.85 (21.33)	249.29 (15.79)	244.85 (15.65)	283.30 (16.83)	313.02 (17.69)	420.90 (20.52)	293.46 (17.13)	231.33 (15.21)
VI						68.15 (8.26)	<b>1328.30</b> <b>(36.45)</b>	851.77 (29.19)	859.05 (29.31)	576.72 (24.01)	1112.84 (33.36)	392.87 (19.82)	642.18 (25.34)	170.91 (13.07)
VII							<b>61.62</b> <b>(7.85)</b>	161.04 (12.69)	246.06 (15.69)	438.14 (20.93)	136.34 (11.68)	605.68 (24.61)	303.18 (17.41)	721.41 (26.86)
VIII								87.21 (9.34)	203.44 (14.26)	190.68 (13.81)	149.74 (12.24)	353.46 (18.80)	148.55 (12.19)	384.19 (19.60)
IX									0.00 (0.00)	275.99 (16.61)	144.92 (12.04)	535.98 (23.15)	360.98 (19.00)	474.61 (21.79)
X										0.00 (0.00)	362.30 (19.03)	175.32 (13.24)	249.75 (15.80)	259.40 (16.11)
XI											0.00 (0.00)	625.91 (25.02)	287.74 (16.96)	613.45 (24.77)
XII												0.00 (0.00)	186.86 (13.64)	127.27 (11.28)
XIII													0.00 (0.00)	202.38 (14.23)
XIV														0.00 (0.00)

**Table 3. Cluster mean values for 12 agronomorphologic characters**

Characters	Days to 50% flowering g (No.)	Plant height (cm)	Number of tiller plant <sup>-1</sup> (No.)	Panicle number plant <sup>-1</sup> (No.)	Panicle length (cm)	Length of flag leaf (cm)	Width of flag leaf (cm)	Grain number panicle <sup>-1</sup> (No.)	1000-grain weight (g)	Biological yield plant <sup>-1</sup> (g)	Harvest index (%)	Grain yield plant <sup>-1</sup> (g)
I	103.305	79.364	5.066	4.854	22.176	25.161	1.645	94.899	24.907	23.666	0.294	6.916
II	104.632	84.886	6.044	5.810	22.686	25.756	1.584	94.532	29.630	23.476	0.552	12.808
III	100.832	86.654	5.074	4.862	21.970	23.160	1.574	94.732	20.994	19.052	0.484	9.228
IV	102.167	83.262	6.670	6.445	22.282	24.542	1.582	106.615	25.395	30.380	0.405	12.353
V	101.250	88.235	6.845	6.550	23.600	23.450	1.680	92.500	26.240	38.415	0.240	9.260
VI	86.960	82.050	8.350	8.125	22.920	24.000	1.500	117.500	25.865	50.840	0.440	22.095
VII	106.000	85.500	4.535	4.250	21.580	30.640	1.670	79.165	23.830	18.205	0.250	4.580
VIII	94.500	88.105	6.025	5.775	24.365	25.850	1.600	64.000	26.400	24.070	0.345	8.170
IX	102.670	84.670	5.270	4.330	23.800	26.800	1.790	76.330	38.330	27.650	0.250	7.990
X	108.670	84.730	8.770	8.530	23.600	22.270	1.390	62.670	33.000	31.500	0.440	13.530
XI	101.170	80.470	5.900	5.630	21.330	19.270	1.300	70.830	28.040	22.000	0.260	5.830
XII	107.000	91.330	6.800	6.550	25.670	25.270	1.520	123.330	22.140	34.070	0.520	17.850
XIII	92.170	85.430	5.500	5.280	23.250	19.670	1.390	121.000	21.100	24.430	0.440	10.950
XIV	94.000	91.430	7.600	7.360	24.430	20.420	1.660	122.500	23.530	41.000	0.420	17.230
% contribution to D <sup>2</sup>	1.858	1.974	1.858	0.000	0.232	1.742	1.510	7.433	6.736	30.081	45.993	0.581

findings were also reported by De *et al.* (1988), Ahmed and Baroh (1999), Singh *et al.* (1996). The present study suggested that biological yield plant<sup>-1</sup>, grain number panicle<sup>-1</sup> and 1000-grain weight should deserve consideration besides harvest index while choosing parents. The results also support the concepts of selecting plants on the basis of harvest index.

The cluster means for different traits varied considerably. Breeding lines of desired plant height (90-100 cm) were grouped in cluster XII and XIV. Cluster XII, XIII and XIV had the genotypes with desired number of grains panicle<sup>-1</sup>.

Considering the importance of genetic distance, relative contributions of characters towards total divergence and yield potential of genotypes, the present investigation suggests that hybridization between cluster XII (for panicle length and grain number panicle<sup>-1</sup>), cluster XI (for 1000 grain weight), cluster X (for panicle number plant<sup>-1</sup>), cluster XI (for flag leaf length) and cluster II (for harvest index) would produce heterotic F<sub>1</sub> combinations. This would also support the corresponding inter cluster D<sup>2</sup> values among these clusters.

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