GENETIC DIVERGENCE IN RICE COLLECTIONS

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Abstract

Deviations observed by Metroglyph method regarding the number of cluster formed, number of genotypes in the cluster and superimposition of the genotypes within the cluster pointed out that genetic improvement for yield and yield components is possible. Metroglyph scatter diagram provided the possibility of 11 groups of rice genotypes. On the basis of this grouping, it can be interpreted that hybridization between group-I and group-II is expected to give better rice varieties.

Introduction

Rice is considered as the stuff of life in Pakistan and covers more than 2.5 million hectares of cropped area with an average paddy yield of 2050 kg/hectare. It accounts for 6.6% of the value added products in agriculture and contributing 1.6% in G.D.P. (Anon., 2000-01). The demand for rice is continuously increasing due to unabated growth of population. To cope with the ever increasing population and to achieve self sufficiency in rice production as well as for maintaining price stability there is need for new genes and improved genetic recombinants not found either in the cultivated varieties or their relatives.

The development of varieties is a continuous process and the success of the plant breeding programme aimed at the evolution of high yielding, better quality, fertilizer responsive, disease and insect resistance varieties depends upon selection of suitable plants to be utilized in breeding programme. The effectiveness of selection depends primarily upon the magnitude of genetic variability in the breeding material at hand. The present study was initiated with the objective to observe variability and select rice genotypes on the basis of quantitative traits and performance.

The study was undertaken to run a classificatory analysis on the rice genotypes by means of Metroglyph statistic, which would enable us to classify the available germplasm into distinct groups on the basis of their genetic diversity. The information, thus obtained, would be helpful to develop an effective rice-breeding programme. Classificatory techniques are being used to quantify the genetic divergence in a given population by Kotaiah *et al*., (1986), Singh *et al.,* (1986[a]), Singh *et al.,* (1986[b]), Kotaiah *et al*., (1987), Gomathinayagam & Natarajan (1988), Vijaykumar & Ramankutty (1988), Ibrahim *et al.,* (1990), Sinha *et al*., (1991), Kharbuli *et al.,* (1992), Mahapatra *et al*., (1995) and Bharadwaj *et al.,* (2001) in rice, Roy & Sharma (1994) in pigeon pea, Ponitha & Raveendram (2000) in cotton. As such a quantification of the degree of divergence would be helpful in choosing suitable genotypes for on-going breeding programme.

Materials and Methods

Seventeen mutants and their respective parents originated from 11 Asian countries (Table 1) used in Regional Rice Mutant Multilocational Trial (RRMMT) were grown at NIAB, Faisalabad during 2002-03. IR-64 was used as a check variety. The experiment was laid out in a randomized complete block design (RCBD) with four replications. Thirty days old seedlings were transplanted in 1.60 x 2.60 sq. m., plot size. Each plot consisted of 13 rows of 1.6 m long with one seedling/hill. Standard agronomic practices and plant protection measures were taken as per schedule. The data were collected on six phenotypic characters viz., days to 50% flowering, plant height (cm), productive tillers/plant, panicle length (cm), spikelets/panicle and yield (kg/ha) (Table 1). Observations were recorded on 5 randomly selected plants of the middle rows excluding the border plants. Their means were used for statistical analysis.

Analysis of variance for all the characters was carried out following the procedure described by Steel & Torrie (1984). Clustering was done according to Metroglyph analysis proposed by Anderson (1957) and used by Singh & Chaudhary (1979) to study the pattern of morphological variation in crop species. The means over replications of the characters were used for this purpose. Two most variable characters which exhibited highest variance (highly significant values of F calculated) were selected and plotted on X and Y-axis using the values of each genotype. Besides the two characters which were taken on X and Y-axis, all the other characters were represented by rays on the glyph. Each ray represents a particular character obtained by dividing the range of variation into three equal classes giving the grades low, medium and high for each character. The length of ray assigned to the characters depends upon the index scores of genotypes for that character (1 for low value, 2 for medium and 3 for highest value). The performance of genotype was indicated by total index scores of genotype, which was the sum of the index values with regards to all characters. The grouping of the genotypes was carried out on the basis of sum of index scores of all the genotypes in that group.

Results and Discussions

The analysis of variance for means indicted that the differences among the genotypes were significant for all the characters studied (Table 2). Bharadwaj *et el.,* (2001) found the significant mean squares results for 9 quantitative characters in 50 genotypes of rice. Kotaiah *et al.,* (1986) and Bharadwaj *et al.,* (2001) reported that the significant differences among the rice genotypes indicated the necessity to group them into clusters to identify the divergent groups. Mehdi & Asghar (1999) also classified the sorghum grenotypes in five distinct groups.

According to Anderson's Metroglyph technique (1957), the index score was allotted to each character of the 30 diverse rice genotype, which indicated the worth of the genotype regarding the character (Tables 3 & 4). Similarly, Gomathinayagam & Natarajan (1988) used index scores for studying the morphological variations of 40 rice entries tested at the upland rice sites. The same thing is represented as rays on the glyph (Fig. 1). Ibrahim *et al.,* (1990) plotted a scatter diagram by using the glyph between the plant height and single plant yield. The traits i.e., days to 50% flowering and plant height are required for desirability in a lower magnitude. Das & Borthakur (1973) and Maurya & Singh (1977) observed that flowering time and plant height were the important contributors to genetic divergence in rice. Therefore, higher score was given to the genotypes, which showed a low magnitude of that character.

Table 1. Mean phenotypic values of characters contributing to genetic divergence in 30 genotypes of rice.

Code No.	Genotypes		Origin	Days to 50% flowering	Plant height (cm)	Productive tillers/Plant	Panicle length (cm)	Spikelets/Panicle	Yield Kg/ha
1.	Cisadane	(P)	Indonesia	135.0	105.0	16.5	22.5	120.8	5294
2.	Atomita 4	(M)	"	121.0	106.1	12.6	25.2	142.0	6275
3.	MutSM-268/PSJIR36	(P)	"	127.0	110.2	14.0	27.6	127.8	4095
4.	Cilosari	(M)	"	122.0	104.1	13.4	25.9	144.5	6176
7.	Q 31 Acc. 9338	(P)	Malaysia	123.8	118.7	10.6	28.7	213.0	5056
8.	Y 1281 (Q31-60-2)	(M)	"	111.5	92.0	14.3	29.7	229.5	6560
9.	Hwacheon-byeo	(P)	Korea	75.3	65.6	31.3	16.3	72.7	3953
10.	Huacheong du-1	(M)	"	73.3	68.2	33.4	15.7	45.0	3382
11.	Huacheong du-2	M)	"	78.0	72.1	37.9	19.0	98.9	3669
12.	Tainan 3	(P)	India	92.5	101.9	9.1	24.4	201.5	6144
13.	PNR 381	(M)	"	91.5	106.4	15.9	25.3	189.5	5374
14.	PNR 519	M)	India	106.8	96.5	14.3	28.6	175.8	7137
15.	IR 8	(P)	"	110.0	88.2	13.5	24.0	169.3	6694
16.	PNR 166	(M)	"	105.0	100.8	11.6	25.8	192.3	6078
18.	TNDB-100	(M)	Vietnam	104.8	96.0	19.0	27.3	154.8	6524
21.	RD 25'86 G₁Cs- PTT- 31-1-2-1-1	(M)	Thailand	105.8	117.1	14.7	29.7	164.3	7339
22.	RD25		"	82.0	102.2	11.1	25.4	175.0	3924
23.	Sigadis Milagrosa	(P)	Philippines	115.8	95.6	14.8	28.8	160.3	5262
24.	PR 26305-M32	(M)	"	101.5	100.0	13.6	30.9	155.3	6863
25.	IR 22 m-1	(P)	"	98.8	84.8	16.7	26.2	177.5	7096
26.	PR 26768-PJ (T) 4	(M)	"	105.0	92.8	14.0	25.5	174.0	6451
28.	Binadhan 4	(M)	Bangladesh	107.8	118.6	11.8	28.7	189.0	7958
29.	IRATOM 24	(P)	"	98.0	91.1	10.5	25.3	184.8	6601
30.	Binadhan 6	(M)	"	108.5	119.1	12.7	25.0	205.0	7470
31.	Basmati 370	(P)	Pakistan	110.3	174.5	11.4	34.0	188.5	5072
32.	Kashmir Basmati	(M)	"	84.8	149.7	11.4	31.4	139.5	3365
33.	DM 25	(M)	"	117.8	131.7	13.1	31.2	166.3	4123
34.	3027	(P)	China	94.8	98.5	10.3	27.2	252.5	5058
35.	R 3027	(M)	"	94.8	92.5	10.8	27.3	157.5	5709
36.	IR-64 (IRRIs Local check)		IRRI	98.0	96.1	16.6	26.8	112.5	4703

(P): Parent   (M):   Mutant

Table 2. Mean squares for quantitative traits among 30 rice genotypes in RRMMT

S.O.V	df	Days to 50 % flowering	Plant height (cm)	Productive tillers/ plant	Panicle length (cm)	Spikelets/ panicle	Yield (kg/ha)
Replication	3	2.2	1.4	11.4	1.1	62.4	42706.3
Genotypes	29	945.4**	1925.1**	186.1**	66.0**	7654.6**	6865618.6**
Error	87	1.1	2.3	2.6	0.6	106.2	232976.6

Table 3. Range of means and index scores for quantitative traits of 30 rice genotypes in RRMMT

Characters	Range of means	Score-I		Score-II		Score-III	
		Value more than	Sign	Value from to	Sign	Value less than	Sign
Days to 50% flowering	73.3-135.0	114.44	○	93.86-114.44		93.86	
Plant height (cm)	65.6-175.4	138.80	○	102.20-138.80		102.20	

Characters	Range of means	Score-I		Score-II		Score-III	
		Value less than Sign		Value from to	Sign	Value more than	Sign
Productive tillers/plant	9.1-37.9	18.70	○	18.70-28.30		28.30	
Panicle length (cm)	15.7-34.0	21.80	○	21.80-27.90		27.90	
Spikelets/panicle	45.0-252.5	114.20	○	114.20-183.30		183.30	
Yield Kg/ha	3365-7958	4896.0	○	4896.0-6427.0		6427.0	

Table 4. Score of the six quantitative traits of thirty rice genotypes in RRMMT

| Code No.	Genotypes		Origin	Days to 50 % flowering	Plant height (cm)	Productive tillers/ Plant	Panicle length (cm)	Spikelets /Panicle	Yield Kg/ha	Total
1.	Cisadane	(P)	Indonesia	1	2	1	2	2	2	10
2.	Atomita 4	(M)	"	1	2	1	2	2	2	10
3.	MutSM-268/PSJIR36	(P)	"	1	2	1	2	2	1	9
4.	Cilosari	(M)	"	1	2	1	2	2	2	10
7.	Q 31 Acc. 9338	(P)	Malaysia	1	2	1	3	3	2	12
8.	Y 1281 (Q31-60-2)	(M)	"	2	3	1	3	3	3	15
9.	Hwacheon-byeo	(P)	Korea	3	3	3	1	1	1	12
10.	Huacheong du-1	(M)	"	3	3	3	1	1	1	12
11.	Huacheong du-2	M)	"	3	3	3	1	1	1	12
12.	Tainan 3	(P)	India	3	3	1	2	3	2	14
13.	PNR 381	(M)	"	3	2	1	2	3	2	13
14.	PNR 519	M)	India	2	3	1	3	2	3	14
15.	IR 8	(P)	"	2	3	1	2	2	3	13
16.	PNR 166	(M)	"	2	3	1	2	3	2	13
18.	TNDB-100	(M)	Vietnam	2	3	2	2	2	3	14
21.	RD 25'86 G_1Cs- PTT- 31-1-2-1-1	(M)	Thailand	2	2	1	3	2	3	13
22.	RD25	(P)	"	3	2	1	2	2	1	11
23.	Sigadis Milagrosa	(P)	Philippines	1	3	1	3	2	2	12
24.	PR 26305-M32	(M)	"	2	3	1	3	2	3	14
25.	IR 22 m-1	(P)	"	2	3	1	2	2	3	13
26.	PR 26768-PJ (T) 4	(M)	"	2	3	1	2	2	3	13
28.	Binadhan 4	(M)	Bangladesh	2	2	1	3	3	3	14
29.	IRATOM 24	(P)	"	2	3	1	2	3	3	14
30.	Binadhan 6	(M)	"	2	2	1	2	3	3	13
31.	Basmati 370	(P)	Pakistan	2	1	1	3	3	2	12
32.	Kashmir Basmati	(M)	"	3	1	1	3	2	1	11
33.	DM 25	(M)	"	1	2	1	3	2	1	10
34.	3027	(P)	China	2	3	1	2	3	2	13
35.	R 3027	(M)	"	2	3	1	2	2	2	12
36.	IR-64	(IRRIs Local check)	IRRI	2	3	1	2	1	1	10

(P): Parent   (M): Mutant
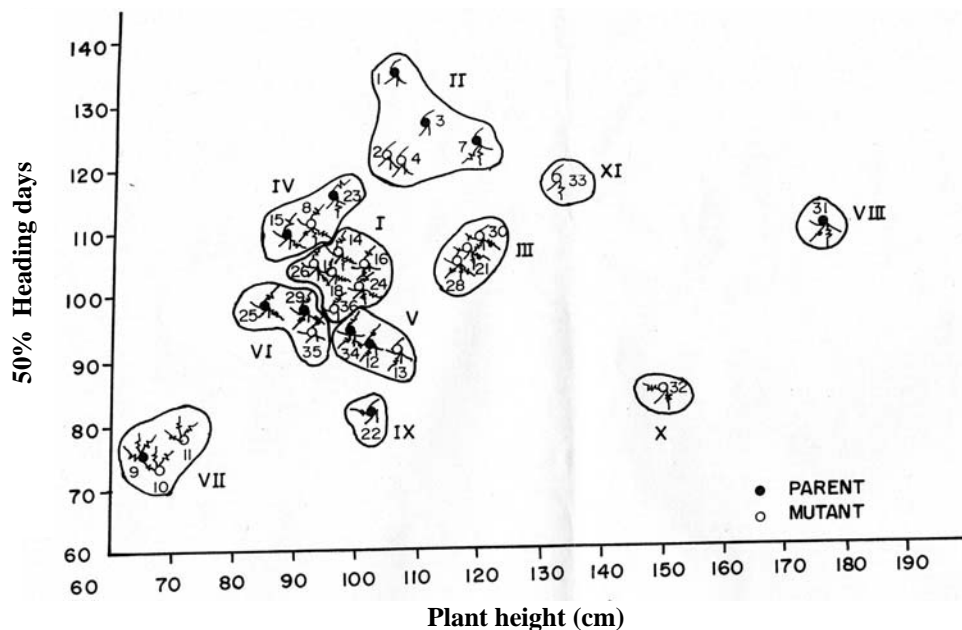
Table 5. Group number, index scores and rice genotypes included in each cluster following metroglyph technique.

Group number	Genotypes	Group index scores
I	14, 16, 18, 24, 26, 36	78
II	1, 2, 3, 4, 7.	51
III	21, 28, 30	40
IV	8, 15, 23	40
V	12, 13, 34	40
VI	25, 29, 35	39
VII	9, 10, 11	36
VIII	31	12
IX	22	11
X	32	11
XI	33	10

Among genotypes, genotypes number 8, 12, 14, 18, 24, 28 and 29 had the highest index scores as total (Table 4). Genotype number 3 scored the minimum index score of 9. Rice genotypes formed eleven groups (Fig. 1) on the basis of relative dispositioning of genotypes on the graph. The results suggested that the metroglyph analysis would be suitable for grouping the genotypes as reported by Chandra (1977). The number to each group was allotted on the basis of net index scores of the group in ascending order. Genotypes number 31, 22, 32, and 33 formed the group number VIII, IX, X and XI respectively (Table 5). Group-I included 6 genotypes, likewise group-II, has 5 genotypes. This grouping can be used in the future hybrid-breeding programme for the improvement of rice population. Hybridization between group-I and group-II is expected to give better types. The group with lowest of 10 index score was group number 11 which included a single genotype 33.

From these results, one can easily foresee that those genotypes, which had high index scores and fell into different groups, can be crossed to have maximum variability of good combinations of characters. Similarly, if one is interested in improving a character, which is undesirable or otherwise weak on a genotype, this information will be helpful in identifying the cross (es) that could be attempted to obtain the desired results. Similar suggestions about the technique were given by Ibrahim *et al.,* (1990), Kotaiah *et al.,* (1986) and Bharadwaj *et al.,* (2001).

Acknowledgement

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