

## Genetic Divergence, Character Association and Selection Criteria in Irrigated Rice

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**Abstract:** Genetic divergence, correlation and path coefficient analysis among 19 genotypes of irrigated rice were studied for grain yield and yield contributing characters. The genotypes under study fell into five clusters. The inter cluster distances were higher than the intra cluster distances indicating wider genetic diversity among the genotypes of different clusters. The intra cluster distances were lower in all the cases reflecting homogeneity of the genotypes within each of the clusters. Regarding inter cluster distance, cluster II showed high genetic distance from all other four clusters. The genotypes from cluster II could be hybridized with the genotypes of any other clusters for producing transgressive segregants. Clustering pattern was not influenced by the geographic origin rather it was influenced by the pedigree of the breeding lines. Harvest index, panicle length and 1000 grain weight showed significant positive correlation with grain yield. Highest direct effect on grain yield was exhibited by spikelets/panicle followed by plant height, harvest index, 1000 grain weight and panicle length respectively. Grains/panicle, spikelets/panicle, flag leaf area, 1000 grain weight and plant height had highest contribution towards divergence respectively. Considering the relative contribution of different characters towards diversity and the effect of correlation and path coefficient all together; the characters like plant height, spikelets/panicle, grains/panicle, 1000 grain weight, flag leaf area and grain yield were found important. Genotypes having these characters of respective cluster would offer a good scope for the improvement of irrigated rice through rational selection.

**Key words:** Genetic divergence, character association, selection criteria, path analysis

### Introduction

Genetic divergence analysis quantifies the genetical distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence. Within a certain limit, hybridization between the more diverged parents is expected to enhance the level of heterosis in hybrids and generate wide range of variability in segregating generations (Joshi and Dhawan, 1966). However, maximum heterosis is generally expressed through crossing between moderately diverged parents. The necessity of principal component analysis (PCA), principal coordinate analysis (PCO), non-hierarchical clustering and canonical vector analysis (CVA) for measuring the degree of divergence has been established by several investigators in rice (Selvakumar *et al.*, 1989; De *et al.*, 1988; Sun and Xu, 1988; Buu and Tuan, 1989; Pathan *et al.*, 1993).

Selection of desirable recombinants in the segregating generations is highly essential in a successful breeding program. As rice yield is a complex polygenically controlled trait influenced by its component traits, direct selection for yield often misleads the plant breeder. Character association of various component traits with yield and among themselves is therefore very important. But correlation coefficients between yield and yield components traits usually exhibit a complex chain of interacting relationship. Path coefficient analysis partitions the genetic correlation between yield and its component traits into the direct and indirect effects of the later. Efforts on establishing selection criteria in rice on the basis of path coefficient analysis were undertaken by a number of scientists (Mirza *et al.*, 1992; Das *et al.*, 1992; Haque *et al.*, 1991; Mehetre *et al.*, 1994). So the investigation has been undertaken with a view to find out the genetic divergence of the irrigated rice genotypes, character association among different traits and constructing selection criteria on the basis of these traits for having high yielding irrigated rice.

### Materials and Methods

The experiment was conducted at Regional Station, Bangladesh Rice Research Institute, Comilla duration Boro season in 2000-01, with 19 irrigated rice genotypes of different origins. The genotypes were tested in a randomized complete block design. Thirty days old seedlings were transplanted in 12 m<sup>2</sup> plot with a spacing of 20 × 15 cm<sup>2</sup> using single seedling per hill. Fertilizers were applied @120:27:60:12.6:2 kg N, P, K, S and Zn per hectare. Except nitrogen all other recommended nutrients were applied at final land preparation. Nitrogen was applied in three equal splits, at

15 days after transplanting (DAT), 45 DAT and just before panicle initiation. Intercultural operations and pest control measures were done as and when necessary. At maturity, grain yield, t ha<sup>-1</sup> was taken and adjusted at 14% moisture level. Grain yield along with plant height (cm), days to maturity, panicles/plant, spikelets/panicle, grains/panicle, panicle length (cm), 1000 grain weight (g), harvest index and flag leaf area (cm<sup>2</sup>) were recorded and used in the analysis. Flag leaf area was calculated according to Gomez (1983). The data were subjected to principal component, principal coordinate, non-hierarchical clustering, canonical vector, correlation and path coefficient analysis using respective programs from computer.

### Results and Discussion

**Cluster analysis:** Significant variations were recorded among the genotypes for all the ten characters. The principal component analysis showed that the first two components accounted for 98.06% of the total variation. The D<sup>2</sup> values ranged from 2.96 to 22.07 and PCA scores also indicated a high degree of genetic diversity among the genotypes. Therefore, scores obtained for the first two components were plotted against two main axes and then super-imposed with clustering (Fig. 1). This clustering pattern confirmed the results obtained by D<sup>2</sup> analysis. Masud *et al.* (1995) reported the same trend. On the basis of D<sup>2</sup> analysis, 19 genotypes of rice were grouped into five clusters (Table 1). The distribution patterns revealed that maximum number of genotypes (6) were included in cluster IV, while cluster II included the minimum (2). Cluster I, III and V included 3, 5 and 3 genotypes respectively. The clustering pattern of the genotypes under this study revealed that the genotypes constellated in single cluster were not originated from same country or geographic distribution, which might be due to continuous exchange of genetic material among the countries of the world. Similar results were reported by Sheriffa and Shivashankar (1992) and Shew *et al.* (1972). The inter cluster distances were higher than the intra cluster distances in all of the cases reflecting wider diversity among the genotypes of the distant group (Table 2). The results agreed with Rahaman *et al.* (1998). The intra cluster distances were low for all the 5 clusters with the range 0.153 in cluster II and 1.01 in cluster IV that indicated the homogeneous nature of the genotypes within the clusters. Regarding inter cluster distance, cluster II showed maximum genetic distance from cluster V followed by from IV, III and I suggesting wider diversity between them and

Iftekharruddaula *et al.*: Genetic divergence, character association, selection criteria, path analysis

Table 1: Rice genotypes in different clusters with grain shape and origin

Clusters	Genotype Sl. no.	Designation	Grain shape	Origin
I	4	BR6018-45-4-1-4	Very long medium	Bangladesh
	6	Zhengui-Ai-1	Long medium	China
	19	BRRIdhan29	Medium slender	Bangladesh
II	3	IR45912-9-1-2-2	Long medium	Philippines
	5	Qingliali No. 1	Very long slender	China
III	2	BR5877-21-2-3	Very long medium	Bangladesh
	9	D3	Very long slender	Malaysia
	10	IR71604-4-4-3-4-3-3-3	''	Philippines
	14	IR71604-4-4-3-8-7-3-3-3	''	Philippines
	18	BRRIdhan28	Medium slender	Bangladesh
IV	1	BR4828-54-4-1-4-9	Very long medium	Bangladesh
	7	IR60832-187-2-2-2	Very long slender	Philippines
	11	IR63896-60-3-12	''	Philippines
	12	IR68068-99-1-3-3-3	''	Philippines
	13	IR68440-61-1-3-2	''	Philippines
	15	IR71600-4-12-1-3	''	Philippines
V	8	IR72101-4-159-1-3-3	''	Philippines
	16	IR65621-116-2-3-2-3	''	Philippines
	17	IR71601-3-4-2-3	''	Philippines

Table 2: Intra (diagonal value) and inter-cluster D<sup>2</sup> values

Clusters	I	II	III	IV	V
I	<b>0.390</b>	12.643	5.772	9.837	11.228
II		<b>0.153</b>	16.806	21.696	22.066
III			<b>0.761</b>	4.955	5.552
IV				<b>1.011</b>	2.966
V					<b>0.287</b>

Table 3: Cluster means with inter cluster CV (%) for ten characters in 19 rice genotypes

Characters	Clusters					% CV
	I	II	III	IV	V	
Days to maturity	159.7	161.0	155.0	163.7	159.3	1.98
Plant height (cm)	99.4	94.7	92.2	93.0	81.1	7.32
Panicles/plant	11.9	11.7	11.1	12.6	11.4	4.84
Spikelets/panicle	189.3	253.5	153.2	126.0	110.7	34.25
Grains/panicle	161.0	215.5	123.4	101.7	81.0	38.92
Panicle length (cm)	22.2	22.0	23.2	23.8	23.2	3.30
1000 grains weight (g)	21.79	21.51	24.28	23.74	25.59	7.36
Harvest index	0.52	0.57	0.56	0.55	0.56	3.48
Flag leaf area (cm <sup>2</sup> )	30.90	35.53	31.48	26.16	24.22	15.19
Grain yield (t ha <sup>-1</sup> )	6.27	7.05	6.72	6.55	6.23	5.16

Table 4: Genotypic (G) and phenotypic (P) correlation among 10 characters in 19 rice genotypes

Character	Types	PH	PN	SN	GN	PL	GW	HI	FLA	GY
DM	G	0.280	0.279	-0.069	-0.055	0.526*	-0.109	-0.008	-0.388	0.365
	P	0.257	0.211	-0.070	-0.062	0.494*	-0.105	-0.004	-0.349	0.323
PH	G		-0.112	0.437	0.417	0.100	-0.242	-0.475*	0.509*	0.159
	P		-0.099	0.387	0.370	0.092	-0.230	-0.220	0.476*	0.146
PN	G			-0.091	0.012	-0.159	-0.570	-0.188	0.134	-0.531*
	P			-0.028	0.022	-0.120	-0.407	0.083	0.050	-0.303
SN	G				0.987**	-0.408	-0.304	0.049	0.737**	0.151
	P				0.982**	-0.346	-0.266	-0.003	0.559*	0.153
GN	G					-0.407	-0.352	0.118	0.717**	0.182
	P					-0.345	-0.320	0.012	0.569*	0.177
PL	G						-0.014	0.175	-0.548*	0.485*
	P						0.016	0.127	-0.415	0.389
GW	G							0.339	-0.265	0.461*
	P							0.133	-0.177	0.368
HI	G								-0.243	0.686**
	P								-0.148	0.330
FLA	G									-0.194
	P									-0.141

\* Significant at 5% level of significance, \*\* Significant at 1% level of significance  
 DM = Days to maturity, PH = Plant height, SN = Spikelets/panicle, GN = Grains/panicle, PL = Panicle length, GW = 1000-grain weight, HI = Harvest index, PN = Panicles/plant, FLA = Flag leaf area, Gy = Grain yield  
 G = Genotypic P = Phenotypic

Table 5: Path coefficient analysis showing direct (bold) and indirect effects of 10 characters on grain yield in 19 rice genotypes

Character	Effect through										Genotypic correlation with yield
	DM	PH	PN	SN	GN	PL	GW	HI	FLA		
DM	<b>-0.302</b>	0.213	0.095	-0.064	0.016	0.211	-0.064	-0.005	0.265	0.365	
PH	-0.084	<b>0.761</b>	-0.038	0.406	-0.122	0.040	-0.142	-0.315	-0.348	0.159	
PN	-0.084	-0.085	<b>0.340</b>	-0.085	-0.003	-0.064	-0.334	-0.125	-0.091	-0.531*	
SN	0.021	0.332	-0.031	<b>0.930</b>	-0.289	-0.164	-0.178	0.033	-0.503	0.151	
GN	0.017	0.317	0.004	0.918	<b>-0.293</b>	-0.163	-0.206	0.078	-0.490	0.182	
PL	-0.158	0.076	-0.054	-0.380	0.119	<b>0.401</b>	-0.008	0.116	0.374	0.485*	
GW	0.033	-0.184	-0.194	-0.283	0.103	-0.006	<b>0.585</b>	0.225	0.181	0.461*	
HI	0.002	-0.361	-0.064	0.046	-0.034	0.070	0.199	<b>0.663</b>	0.166	0.686**	
FLA	0.117	0.387	0.045	0.685	-0.210	-0.220	-0.155	-0.161	<b>-0.683</b>	-0.194	

\* Significant at 5% level of significance; \*\* Significant at 1% level of significance Residual effect, R = 0.180  
 DM = Days to maturity, PH = Plant height, SN = Spikelets/panicle, GN = Grains/panicle, PL = Panicle length, GW = 1000-grain weight, HI = Harvest index, PN = Panicles/plant, FLA = Flag leaf area, Gy = Grain yield

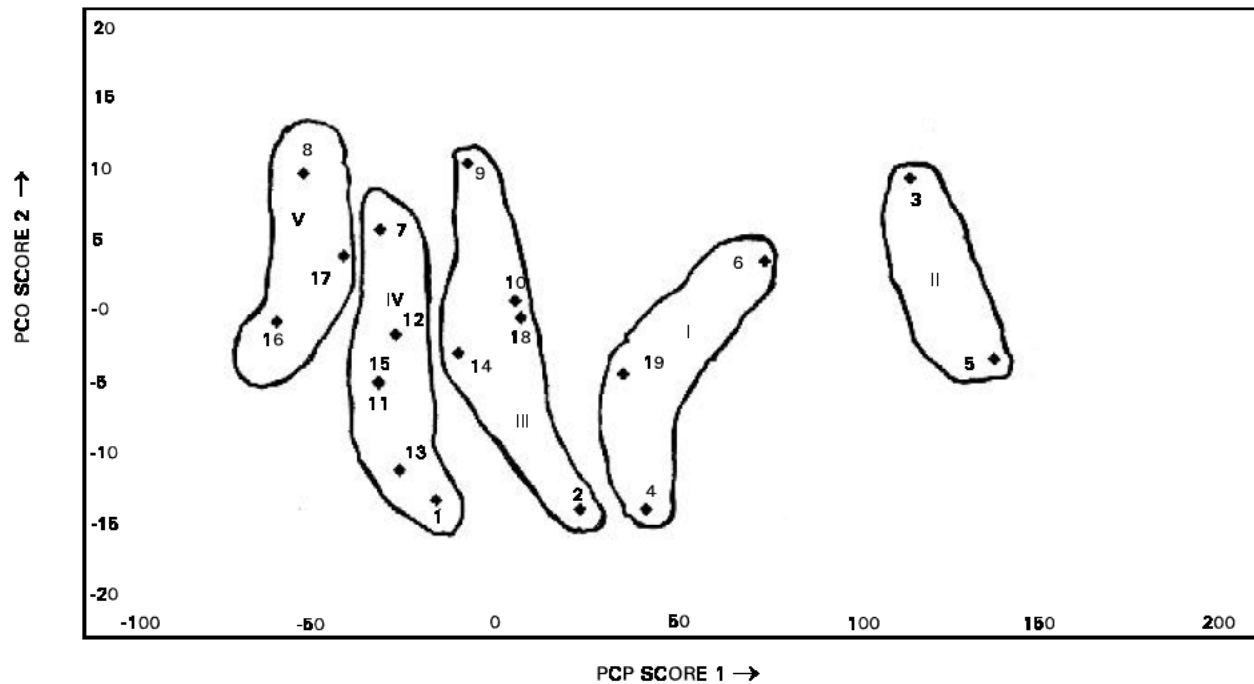


Fig. 1: Distribution of 19 rice genotypes in a two-dimensional scatter diagram based on PCA scores superimposed with clusters.

the genotypes in these clusters could be used as parents in hybridization program for getting transgressive segregants. Intermediate or moderate inter cluster divergence was observed between cluster V and I followed by cluster IV and I and the minimum inter cluster divergence was observed between V and IV. Cluster V showed low divergence from cluster III and IV. This might be due to low spikelets/panicle and grains /panicle. Most of the BRR1 developed breeding lines were constellated in cluster IV and V except few other genotypes in different clusters. This is due to homogeneity in parental sources or pedigree lines. Bansal *et al.* (1990) also reported that clustering pattern was influenced by the pedigree of breeding lines. Cluster III had low D<sup>2</sup> values with I and IV indicating the genotypes in these clusters to be close in genetic make-up.

The relative contribution of different characters towards divergence is demonstrated by CV(%) values at inter cluster level (Sharma, 1998). Grains/panicle, spikelets/panicle, flag leaf area, 1000 grain weight and plant height were the potential contributors to genetic divergence in the genotypes (Table 3). Selvakumar *et al.* (1989) and De *et al.* (1988) reported the highest contribution of grains/panicle towards the genetic divergence between the genotypes. Highest mean performance of plant

height was found in cluster I, whereas cluster II included highest spikelets/panicle, grains/panicle, flag leaf area and grain yield. On the other hand cluster V showed lowest intra cluster mean values in plant height, spikelets/panicle, grains/panicle and flag leaf area indicating maximum contribution of these characters towards divergence between cluster II and V. Similarly cluster IV had high divergence with II for distant mean values of spikelets/panicle, grains/panicle and flag leaf area. Cluster III was also distant with II for the same characters. The characters contributing maximum to the divergence should be given higher emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization (Jagadev *et al.*, 1991)

**Character association:** Genotypic and phenotypic correlation coefficients among yield and yield contributing traits for 19 irrigated rice genotypes are presented in Table 4. In most of the cases, the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficient values, which suggested that the character association had not been largely influenced by environmental factors. Bai *et al.* (1992) reported the similar results in rice. Grain yield was found positively and significantly associated with harvest index, panicle length and

1000 grain weight while grain yield was negatively but significantly associated with panicles/plant. Bhatti *et al.* (1998) reported significant positive association of grain yield with panicle length and 1000 grain weight in rice. Kennedy and Rangasamy (1998) reported significant positive correlation of grain yield with 1000-grain weight and harvest index in rice. Significant negative correlation of panicles/plant with grain yield was obtained by Haque *et al.* (1988) in rice.

Days to maturity showed significant correlation with panicle length both at genotypic and phenotypic level. There was significant negative association of plant height with harvest index but positive with flag leaf area. Significant negative correlation was obtained between panicles/plant and 1000 grain weight. Haque *et al.* (1988) also obtained significant negative correlation between panicles/plant and 1000 grain weight in rice. Spikelets/panicle was found strongly correlated with grains/panicle and flag leaf area both at genotypic and phenotypic level. Highly significant positive correlation between spikelets/panicle and grains/panicle was reported by Das *et al.* (1992). Again there were significant positive correlation between grains/panicle and flag leaf area while significant negative correlation between panicle length and flag leaf area in this study.

**Path coefficient analysis:** From the path coefficient analysis (Table 5) it was revealed that the highest positive direct effect on grain yield was obtained by of spikelets/panicle followed by plant height, harvest index, 1000 grain weight and panicle length. Panwar *et al.* (1989) reported highest direct effect of spikelets/panicle and Gomathinayagam *et al.* (1988) reported highest direct effect of plant height on grain yield in rice. Higher positive indirect effects on grain yield were obtained by grains/panicle, flag leaf area and plant height through spikelets/panicle followed by flag leaf area through plant height and panicle length through flag leaf area. Similarly Das *et al.* (1992) obtained highest positive indirect effect of grains/panicle on grain yield through spikelets/panicle. Higher positive indirect effect of grains/panicle and flag leaf area through spikelets/panicle might be due to significant positive correlation of grains/panicle and flag leaf area with spikelets/panicle. The results suggested that while using grains/panicle and flag leaf area as selection criteria, spikelets/panicle should be given due importance. The genetic correlation of harvest index with grain yield was almost equal to its direct effect, indicating that this trait had true relationship with grain yield and direct selection through this trait will be most effective for improving the yield of irrigated rice. The residual effect was 0.18, indicating that 82 % of the variability in grain yield was contributed by the nine characters studied in the path analysis. This gave an idea that a few other characters than those involved in the present study might also contributed to grain yield.

The findings of genetic diversity, character association and path coefficient analysis revealed that the characters plant height, spikelets/panicle, grains/panicle, 1000 grain weight, flag leaf area and grain yield were found important in respect of genetic diversity, correlation and path coefficient analysis. The greater divergence in the genotypes due to these characters in clusters would offer a prime scope for the development of high yielding irrigated rice through rational selection in the segregating generations.

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