Genetic diversity among rice varieties cultivated in Punjab

Monika A. Joshi*, Pritpal Singh, N. K. Sarao, R.C. Sharma and T.S. Bharaj

Seed Technology Centre, Punjab Agricultural University, Ludhiana

ABSTRACT

The assessment of genetic diversity among the rice varieties cultivated in Punjab was done using Mahalanobis D^2 statistics based on eleven agro-morphological traits. Nineteen cultivars were grouped into four different clusters revealing sufficient amount of variability among the genotypes. The clustering pattern revealed non-correspondence of geographic diversity with genetic divergence. Days to 50% flowering and plant height contributed considerably, accounting for 61% of total divergence. The highest inter-cluster divergence (76.33) between clusters I and II maybe utilized in heterosis as well as in recombination breeding. Further, selection within cluster IV, having maximum intra-cluster distance (11.64), maybe exercised based on the highest mean for the desirable traits, which could be used for improvement through inter-varietal hybridization.

Key words: Genetic diversity, rice, clustering pattern, Punjab

The success of any breeding programme depends on the selection of parents for hybridization. In any crop, the germplasm serves as a valuable source of base population and provides immense scope for wide variability. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parent for breeding programmes. In Punjab, generally the harvesting of rice gets delayed in long duration genotypes due to untimely rain which leads to further delay in sowing of the subsequent *rabi* crops. As a result, the late maturing varieties also get trapped in untimely rains during September-October, leading to a considerable deterioration in the seed quality. Another important parameter that needs to be taken into account is the plant height since short-statured genotypes are preferred as they are less prone to lodging. Hence, the present study was focused to assess the genetic diversity for early maturing and short-statured varieties using Mahalanobis D^2 statistics among the cultivated genotypes in Punjab.

MATERIALS AND METHODS

The experimental material consisted of 19 varieties of rice belonging to non-Basmati (Pusa 44, IR 8, Jaya, PR 106, PR 108, PR 109, PR 110, PR 111, PR 113, PR 114, PR 115, PR 116 and PR 118) and Basmati group (Basmati 370, Basmati 385, Basmati 386, Pusa Basmati 1, Pusa Sugandh 2 and Super Basmati). The genotypes were raised during wet season 2006 and 2007 at the Seed Technology Farm in plot size of ten rows with each row of 5 meter length. Row-to-row and plant-to-plant spacing was maintained at 20 x 15 cm. The material was replicated thrice and all the agronomic practices were followed to raise a good crop. The diversity among the above 19 genotypes was analysed with respect to eleven agro-morphological traits viz. length and width of leaf blade, days to 50% flowering, plant height (excluding panicle), panicle length, number of tillers per plant, 1000 grain weight and length and width of grain as well as the decorticated grain. Observations were recorded on ten randomly selected plants for each trait and the genetic distance between the individual genotypes was worked out using Mahalanobis D^2 statistics and the grouping of genotypes was done following the Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant variability among the genotypes for all the characters studied. Based on the relative magnitude of D^2 values, 19 genotypes were grouped into four clusters (Table1). Maximum number of genotypes (eight) were

Table 1. Clustering pattern of 19 rice genotypes

Cluster	No. of genotypes	Name of genotypes
I	3	Basmati 370, Basmati 385, Basmati 386
II	5	PR 109, PR 110, PR 111, PR 113, PR 115
III	8	Pusa 44, Jaya, IR 8, PR 106, PR 108, PR 114, PR 116, PR 118
IV	3	Pusa Basmati 1, Pusa Sugandh 2, Super Basmati

included in cluster III. The cluster II had five genotypes while clusters I and IV had three genotypes each. Further, the overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Hence, the kind of genetic diversity found among the genotypes belonging to the same geographic origin might be due to change in selection for different objectives, utilizing new germplasm and adopting different methodology for evolving rice varieties (Vivekanandan and Subramanian, 1993). Similar findings of non-correspondence of geographic diversity with genetic divergence were also reported in rice by Kaw 1995, Shanmugasundaram (2000) and Nayak *et al* (2004).

A perusal of results on cluster means (Table 2) revealed that the cluster I could be characterized by tallest genotypes (132.92 cm) but with least number of tillers per plant (10) while Cluster II had genotypes with shortest length (61.08 cm) and maximum tillers (13). Highest value for days to 50% flowering (117.50 days; late flowering) and maximum 1000-grain weight (22.87g) were characteristic features of cluster III whereas, early flowering genotypes (100 days) with maximum panicle length (31.50 cm) grouped

into Cluster IV. Further, the genotype PR 111 in cluster II had the shortest length while PR 109 in the same cluster had high value for number of tillers per plant. Similarly, genotype Pusa Sugandh 2 in cluster IV matured earliest and Pusa Basmati 1 had the maximum value for panicle length. A critical appraisal of the observations suggested that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Interestingly, all the minimum and maximum cluster mean values were distributed in relatively distant clusters. Similar results were also reported by Bose and Pradhan (2005) while studying the divergence in deep water rice genotypes, thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Hence, depending on the *per se* performance of the best genotypes within the clusters, they may be directly used for adaptation or maybe used as parents in future hybridization programmes.

The inter-cluster distance (Table 3) ranged from 17.67 to 76.33 between cluster II and III and between clusters I and II, respectively. Pradhan and Roy (1990) and De and Rao (1987) pointed out that selection of parents should be done from the two clusters having

Table 2. Cluster mean values for 11 morphological traits

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Length of leaf blade (cm)	59.03	33.79	29.08	43.56
Width of leaf blade (cm)	1.05	1.17	0.90	1.33
Days to 50% flowering	103.66	105.00	117.50	100.00
Plant height (cm)	132.92	61.08	72.44	88.97
Panicle length (cm)	31.07	26.76	24.81	31.50
Tiller number per plant	10	13	12	12
1000 grain weight (gm)	21.76	22.22	22.87	22.66
Grain length (mm)	9.73	8.98	9.01	11.00
Grain breadth (mm)	2.10	2.34	2.46	2.13
Decorticated grain length (mm)	7.23	6.88	6.70	8.16
Decorticated grain breadth (mm)	1.70	1.96	2.06	1.83

Table 3. Average intra (Bold) and inter cluster distance values

Cluster No.	I	II	III	IV
I	**7.710**	76.33	69.22	46.80
II		**9.13**	17.67	30.46
III			**7.91**	28.99
IV				**11.64**

wider inter-cluster distance to get more variability and high heterotic effect. Hence, the highest divergence between clusters I and II (76.33) maybe made use of in heterosis as well as in recombination breeding. Minimum inter-cluster distance (17.67) between clusters II and III indicated close relationship between the two. Unidirectional selection practiced in the past to meet certain edapho-climatic exigencies might have resulted in uniform features with limited divergence among the genotypes. Further, the maximum intra-cluster distance (11.64) was observed in cluster IV. Hence, selection within this cluster maybe exercised based on the highest mean for the desirable traits, which could be made use of in improvement through inter-varietal hybridization.

The utility of D^2 analysis, which is a potent tool to quantify the extent of divergence in biological

Table 4. Relative contribution of different characters to genetic divergence

Character	Percentage of total
Length of leaf blade	11.97
Width of leaf blade	0.34
Days to 50% flowering	35.05
Plant height	26.18
Panicle length	8.78
Tiller number plant^{-1}	3.79
1000- grain weight	7.22
Grain length	3.02
Grain breadth	0.75
Decorticated grain length	2.27
Decorticated grain breadth	0.63

populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The present study revealed that days to 50% flowering and plant height contributed to 61.23% of total divergence (Table 4). Similarly, Bisht *et al*, (2007) also reported that the greatest contributors to genetic diversity in grain crops were the flowering time, plant height and tiller number per plant. Hence, it is suggested to consider these traits in transgressive breeding, in this particular set of germplasm lines to get early flowering, short-statured rice genotypes.

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