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Short Communication

Genetic divergence in elite genotypes of basmati rice (*Oryza sativa* L.)

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Genetic diversity of the parental lines is a good indicator of performance of the progeny. Success through hybridization and subsequent selection depends primarily on the selection of parents having high genetic variability for various agronomic traits [1, 2].

In the present study an attempt has been made to find out the degree and nature of genetic divergence among a set of 61 elite basmati rice genotypes with the objective of selecting genetically divergent parental lines for hybridization and development of high yielding basmati varieties. The above genotypes were collected from different parts of India and abroad. These were grown in randomized complete block design in three replications during *kharif*, 2000 at the Crop Research Centre, G.B.P.U.A.&T., Pantnagar, India. Each genotype was grown in two rows of 3 m length in each replication. All the recommended cultural practices for basmati rice in the region were followed. Observations were recorded on five randomly selected competitive plants to study the days to 50% flowering, plant height (cm), number of panicles/plant, panicle length (cm), length of flag leaf (cm), width of flag leaf (cm), grain yield/plant (g), number of spike lets/panicle, 1000-grain weight (gm), length of brown rice (mm) and breadth of brown rice (mm). The mean over three replications was used for the statistical analysis. The analysis of genetic divergence was carried out using Mahalanobis's D^2 statistic. Tocher's method [3] was followed for clustering of genotypes.

The analysis of variance revealed significant differences among basmati rice genotypes for all the eleven characters, indicating high genetic variability present in the population.

All the genotypes were grouped into four clusters, indicating wide diversity in the experimental material for majority of the characters. Maximum number of genotypes (43) were included in cluster I. This was followed by cluster II (13) and cluster III (4). Only one genotype appeared in cluster IV (Table 1). Clusters I, II and III included genotypes from India (U.P, Delhi, Haryana and Uttaranchal), Pakistan, IRRI, Iran and Thailand. This pattern of clustering indicated that there was no association between eco-geographical distribution of genotypes and genetic divergence as genotypes selected under diverse locations clustered together. On the other hand genotypes from the same geographic region but different breeding programmes (other parts of the country) were distributed in different clusters. This kind of genetic diversity (genotypes belonging to same geographic region) might be due to differential adaptation, selection criteria, selection pressure and environment [4]. This indicated that genetic drift and selection in different environments can produce greater diversity than the geographic diversity [5, 6].

Table 1. Clustering of basmati rice genotypes using Tocher's method

Cluster	Genotypes	No. of genotypes
I	IR 68281, UPR 2268-5-1, UPR 2268-3-1, UPRI 93-76, UPRI 93-77-1, TDC 16-1-1, UPR 2268-5-2, UPR 1854-17-1, UPR 2268-3-3, IET 13846, UPPI 93-74, IET 15373, UPR 1954-22-1, Kbao Dawk Mali, UPRI 93-77-2, IET 15390, DR-33, Haryana Basmati, Basmati 123, UPR 93-104, UPR 2268-3-2, IET 15805, UPRI 93-60, UPR 1840-31-1-1, IET 14131, Basmati 242, UPRBS 92-4-1, DR-30, UPRI 93-63-2, IET 15392, UPRI 93-62-2, PK 1501-9-2-8-1, UPRI 93-66, Azucena, PK 1379-91-1, Basmati Kamon, IET 15391, Basmati 410, UPRI 93-68-3, Pusa Basmati-1, PK 1427-8-1-1-1, DR-31, Super Basmati	43
II	IET 14707, Basmati 6113, Basmati 386, VL Basmati-2, Binam, Karnal Local, Type-3, IET 15388, Basmati 6129, Basmati 334, IET 14720, PK-1521-4-1-1-3, Basmati 5888	13
III	UPR I854-14-1-1, UPRI 93-60-2, DR-28, DM 38	4
IV	Basmati Aman	1

Cluster III contained only four genotypes, but it showed maximum intra cluster distance, because the genotypes originated from breeding programme in three different countries (India, Philippines and Pakistan). Thus these four genotypes in cluster III were most heterogeneous and this cluster was best for within group hybridization. Genotypes from this cluster could also be exploited in hybrid development programme, due to their wide within the group genetic distances. On the other hand cluster II contained 13 genotypes but it showed minimum intracluster distance due to the common origin of many genotypes.

As regards inter-cluster distance (Table 2), cluster III showed maximum genetic distance from cluster IV (33.00) suggesting wide diversity between these groups. Hybridization between parental lines selected from these clusters are likely to produce most variable progeny.

Table 2. Average intra and inter-cluster D^2 values (Bold) and distance ($\sqrt{D^2}$)

Cluster	I	II	III	IV
I	**87.29**	**247.88**	**139.43**	**761.61**
	9.34	15.74	11.81	27.60
II		**85.03**	**420.63**	**324.30**
		9.22	20.51	18.01
III			**142.27**	**1088.82**
			11.93	33.00
IV				**0.00**
				0.00

Pradhan and Roy [7] have also pointed out that selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability. Cluster II and cluster III had the minimum genetic distance (11.81) between them which showed that these genotypes were somewhat similar in genetic constitution and hybridization between these groups may not result in sufficient variability.

As far as cluster means are concerned, there was a wide range of variation for all the characters, except width of flag leaf (Table 3). Cluster IV (variety Basmati Aman) had high mean values for days to 50% flowering (131.33), plant height (144.33), number of panicles/plant (14.67) and number of spikelets/panicle (171.0). Cluster II had high mean values for panicle length (28.33), length of flag leaf (32.49), 1000-grain weight (22.50), length of brown rice (7.50) and width of brown rice (1.85). Cluster III had high value of grain yield/plant. This indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Recombination breeding between genotypes of different clusters has been suggested by Singh *et al.* [6].

The observations revealed that the plant height contributed maximum towards genetic divergence (52.24%). It was followed by days to 50% flowering (22.56%) and grain yield per plant (8.63%). This is in conformity with the observations of Murty and Arunachalam [1] that the greatest contributors to genetic diversity in grain crops are flowering time, plant height, primary branches or tiller number/plant. The importance of plant height and days to maturity as main contributors to genetic diversity in rice has also been emphasized by Kanwal *et al.* [8].

On the basis of observations recorded on a diverse group of basmati genotypes it may be concluded that hybridization between genotypes of variable clusters may produce a wide spectrum of variation in the segregating progeny.

Table 3. Cluster means of morphological traits based on standard taxonomic distances

Clusters	Days to 50% flowering	Plant height (cm)	No. of panicles/ plant	Panicle length (cm)	Length of flag leaf (cm)	Width of flag leaf (cm)	No. of spikelets/ panicle	Grain yield/ plant (g)	1000-grain weight (g)	Length of brown rice (mm)	Breadth of brown rice (mm)
I	104.57	89.46	11.74	26.79	31.52	1.20	142.37	14.43	19.99	7.44	1.73
II	109.59	124.12	11.46	28.33	32.49	1.23	135.10	15.34	22.50	7.50	1.85
III	97.58	81.16	12.66	25.55	30.08	1.24	164.50	18.00	21.38	7.19	1.81
IV	131.33	144.33	14.67	25.87	27.00	1.20	171.00	13.67	13.33	5.60	1.63

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