SHORT COMMUNICATION

Studies on Genetic Divergence in Aromatic Rice

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Nature of genetic divergence among the thirty aromatic rice genotypes was measured using Mahalanobis D^2 analysis for eleven agronomic characters. Significant variation was observed for all the characters studied. On the basis of D^2 values the genotypes were grouped into five clusters. The cluster I was the largest with 10 genotypes and cluster V had the least 3 genotypes. No relationship was observed between clustering pattern and the geographic distribution of the genotypes. The characters like grain yield/plant and plant height showed maximum contribution towards divergence. The cluster III and V showed maximum and II and III minimum inter cluster distance. So the genotypes from these clusters are suggested as parental donors to obtain high heterotic combination.

Key Words: Aromatic rice, Cluster analysis, Genetic divergence

Aromatic rice germplasm collected from different parts of India provides a good genetic diversity due to presence of high degree of phenotypic variability. Crosses between the parents with maximum divergence has been found to be most effective for genetic improvement. The importance of nature and magnitude of genetic divergence in aromatic rice and its utilization for selection of desirable parents or donors. Either exploitation of hybrid vigour or to get desirable recombinations the multivariate analysis developed by Mahalanobis D^2 analysis is a valuable tool to quantify the degree of divergence among the population. The present study was undertaken to know the nature and magnitude of genetic divergence among the aromatic rice collected from different parts of India.

The experimental material comprised thirty aromatic genotypes collected from different parts of India. The experiment was conducted in a Randomised Block Design in *kharif* season-2002 at Central Rice Research Institute, Cuttack with three replications. Thirty days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and between plants respectively. Onservations were recorded on ten randomly selected plants of eleven quantitative characters *viz.* days to 50% flowering, plant height, panicle number, plant panicle length, spikelets/ panicle, grains/panicle, 1000-grain weight, grain length, grain breadth, length/breadth ratio and grain yield/plant. The mean values over three replications were used for statistical analysis. The analysis of genetic divergence using Mahalanobis D^2 analysis was carried out and grouping of the genotypes into different clusters by Tocher's method (Rao 1952).

The analysis of variance showed significant variability among the genotypes for all the characters studied indicating adequate scope for selection of superior and diverse genotypes. On the basis of D^2 values the thirty genotypes were grouped into five clusters. The cluster I consisted of maximum number of ten genotypes. Cluster II have seven genotypes, Cluster III consisted of four genotypes, Cluster IV consisted of six genotypes and Cluster V consisted of three genotypes. Though PPS-50, PPS-55, PPS-58, PPS-85 and Punjab basmati-1

Table 1. Clustering pattern of aromatic rice genotypes

Cluster	No. of Genotypes	Origin	Genotypes
I	10	Haryana,	Pusa basmati, HKR-228
		M.P.	Kalimochi
		U.P.	Basmati-370, Kalajira-286
		Punjab	PPS-55, PPS-85
		Tamil Nadu	Pusa-33, ADT-9
		Bihar	Kamini
II	7	Punjab	PPS-50
		M.P.	Vishnubhog
		Haryana	Karnal basmati, HKR-241
		Bihar	Kamod
		Orissa	CRM-8-30
		Assam	Tulsibhog
III	4	Orissa	Sugandha
		Karnataka	Kusum
		M.P.	Madhuri
		Rajasthan	BK-79
IV	6	Tamil Nadu	ADT-32, ADT-41
		U.P.	Narendra-118
		Maharashtra	PBN-1
		Punjab	Punjab basmati-1
		M.P.	Basmatibahar
V	3	Orissa	IET-12016
		M.P.	Dubaraj
		Punjab	PPS-58

Table 2. Cluster mean values for eleven characters in aromatic rice

	Days to 50% flowering	Plant height (cm).	Panicle number/ plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	1000-grain weight (gm)	Grain length (mm)	Grain breadth (mm)	Length/ breadth ratio	Grain Yield/ plant (g)
I	106.0	**140**	6.2	24.2	**60.2**	**40.4**	20.2	10.2	1.96	5.2	**4.5**
II	**117.0**	125	7.5	**22.1**	90.5	65.2	18.5	9.7	**2.11**	4.6	6.2
III	**98.0**	**112**	**8.2**	23.5	93.4	60.1	19.8	10.8	1.96	5.5	8.7
IV	115.0	130	6.0	22.3	**160.3**	**120.4**	**16.3**	**7.6**	**1.85**	**4.1**	**15.3**
V	108.0	128	**5.6**	**24.6**	98.2	55.3	**21.8**	**11.0**	1.96	**5.6**	7.2

Bold figures indicate highest and lowest values for each character

originated in Punjab but they are placed in different clusters. Vivekanandan and Subramanian (1993) viewed that this clustering pattern may due to varied agroclimatic region prevailing in different states of India. The genotypes in cluster I originated from six different states showed maximum diversity and grouped in one cluster. There is no parallalism existing between the genetic diversity and geographical distribution. Similar reports have been reported by Ushakumari and Rangaswamy (1997) and Gupta *et al.* (1998). Selvakumar *et al.* (1989) also reported that the genetic drift and selection in different environments can produce greater diversity than geographic diversity.

The contribution of different characters towards divergence have greater emphasis on clustering pattern of genotypes and best choice of parents in hybridization programme. It was observed that grain yield/plant contributed maximum (28.2%) followed by plant height (15.2%) whereas lowest contribution was observed by length/breadth ratio (2.5%) towards total divergence. Vivekanandan and Subramanian (1993), Ushakumari and Rangaswamy (1997) also emphasized the greater contribution of grain yield/plant and plant height towards total divergence.

The intracluster distance varied from 6.1(II) to 21.7(V). The maximum intercluster distance 24.4 was observed between cluster III and V. Since the genotypes found in cluster III and V are more divergent, so the selection of parents from these two cluster for hybridization programme to obatin high heterotic combination and desirable transgressive segregants which was supported by Soni *et al.* (1999).

The genetic divergence among the clusters are reflected in the cluster mean values. The cluster mean values (Table 2) showed wide difference for various characters studied. Cluster I showed highest values for plant height (140.0 cm) and lowest values for spikelets per panicle (60.2), grains/panicle (40.4) and grain yield per plant (4.5 g). The cluster II have highest mean values for days to 50% flowering (117 days), grain breadth (2.11 cm) and lowest for panicle length (22.1 cm). The cluster III have highest panicle number (8.2) and lowest for days to 50% flowering (98 days), plant height (112 cm). The cluster IV have highest value for spikelets/panicle (160.3), grains/panicle (120.4), grain yield/plant (15.3 g) and lowest values for 1000 grain weight (16.3 g), grain length (7.6 mm), grain breadth (1.85 cm) and length/breadth ratio (4.1). Cluster V have highest values for panicle length (24.6 cm), 1000-grain weight (21.8 g), grain length (11.0 mm), length/breadth ratio (5.6) and lowest for panicle number (5.6). The genotypes with high mean values can be directly used for adaptation or can be used as parents in hybridization programme through recombination breeding. Among the clusters, cluster V is the best cluster for genotypes.

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

	I	II	III	IV	V
I	**12.7**	13.8	12.8	11.2	19.6
II		**6.1**	7.0	15.4	22.8
III			**7.3**	14.5	24.4
IV				**7.1**	16.6
V					21.7

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