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Genetic Divergence of Some Quality Rice Germplasm for Morphological and Quality Characters

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Abstract

Success in improving the quality of rice to meet the growing demand for special purpose rice can be achieved by selecting suitable parents from the rich source of rice germplasm for breeding program. In this study 28 quality rice genotypes were evaluated for genetic divergence study. Chi-square test indicated that the population was divergent. Based on relative magnitude and D^2 estimates the genotypes were grouped into four clusters. Members from cluster II recorded higher mean values for number of panicles/plant, panicle weight, length of panicle, grains/panicle, HI, cooked kernel length, cooked kernel L/B ratio, kernel elongation index and seed yield/plant. Cluster III had high values for grains/panicle, brown kernel L/B ratio, 1,000-seed weight and lowest mean value for amylase content. While, cluster I possessed the highest values for brown kernel L/B ratio, 1,000-seed weight, cooked kernel L/B ratio and amylase content. Seed yield/plant contributed major portion to the total divergence followed by amylase content, cooked kernel length and 1,000-seed weight in this regard.
Key words : Quality rice, Cluster analysis, Genetic divergence, Morphological characters.

Selection of parents based on the degree of genetic divergence has been successfully utilized in various breeding programs (Murthy and Anand 1966, Sandha and Sangha 1974, Nadef et al. 1986). Mahalanobis generalized distance (D^2) as an important statistical tool to measure this divergence among the genotypes. Selection of the parents on the basis of individual characters may not be fruitful as the one based on a number of important component traits simultaneously, especially if the aim is to seek improvement in complex character like yield and quality of the produce. In this context, the present study was carried out to estimate the nature and magnitude of genetic diversity in 16 morpho physico-chemical characters in a set of 28 genotypes of quality rice.

Methods

Twenty eight quality rice genotypes were evaluated at Regional Research station, New Alluvial Zone, Bidhan Chandra Krishi Viswavidyalaya, Sub-center Chakdah, Nadia, West Bengal. The genotypes were raised in a randomized block design with two replications during *kharif* season of 2006. Normal agronomic practices were followed to obtain a good harvest. Observations on different biometrical characters were recorded from five randomly selected plants from each entry. The quality parameters i.e., physico-chemical parameters viz. brown grain length and breadth, L/B ratio of brown grain, cooked kernel length and breadth, cooked kernel L/B ratio and kernel elongation index were studied to estimate the genetic divergence among the tested materials. The quality parameters were estimated following standard procedures as suggested by Hussain et al. (1987)and alkali digestion value and amylase content were estimated following techniques of Little et al. (1958) and Sadasivam and Manikkam (1992) respectively. The analysis of genetic divergence was done by using Mahalanobis D^2 (Mahalanobis 1936) statistics as described by Spark (1973) and the genotypes were grouped into different clusters following Tochers method.

Results and Discussion

The divergence of the population was confirmed by Chi-square test. Based on relative magnitude of D^2 values 28 genotypes were grouped into 4 clusters (Table 1). Cluster II comprising 12 genotypes was the largest, followed by cluster IV with eight genotypes, cluster II with six genotypes and cluster I with two genotypes respectively. The clustering pattern of the

Table 1. Clustering pattern of 28 quality rice germplasm.

Cluster no.	No. of genotypes	Genotypes
I	2	Madhuri, Sitadhan
II	12	Sitabhog, Kalikhasa, Badshabhog, Dudheswar, Gayasur, Pusa Basmati, IET 4786, Chandrakanti, Tulaipanji, Basmati T3, Haryana Basmati, Hansaraj
III	6	Shantibhog, Madhumati, Samba mashuri, Kalobhog, Tulshibhog, Taroari Basmati
IV	8	Radhunipagal, Chamormoni, Mashino, Basmati 385, Basmati 370, Sitasail, Narsinghajata, Baldhar Basmati

genotypes indicated that no particular pattern was followed with respect to their quality or choice of farmers, as Sitabhog, Chandrakanti, Badshabhog which are less preferred local cultivars was grouped into the same cluster with popular genotypes like, Pusa Basmati, IET 4786 and Haryana Basmati.

For almost all the characters, considerable differences in cluster means were observed (Table 2). Chuster I had highest mean values against eight characters viz. length of brown grain, L/B ratio of brown grain, 1,000-seed weight, cooked kernel length, L/B ratio of cooked kernel, gelatinization temperature and amylase content and minimum values for rest of the characters. Cluster II possessed maximum mean values for six characters viz. panicle weight, length of panicle, grains/panicle, breadth of brown grain, harvest index, seed yield/plant and minimum mean values for L/B ratio of brown grain only. Maximum mean values for number of panicle/plant was observed in cluster III and it had minimum mean values for cooked kernel length, L/B ratio of cooked kernel length, kernel elongation index and amylase content. Therefore, it was observed that desirable characters that i.e., quality parameters were mainly distributed in cluster I and yield and yield related traits were mainly distributed in cluster II. The major contribution to the divergence was imparted by seed yield/plant followed by amylase content, cooked kernel length and 1,000-seed weight respectively. Therefore during the selection of parents for hybridization program and during selection of superior segregants in segregating generation, all of these characters should be considered (De et al. 1992).

Highest and lowest intra-cluster distance were observed in cluster III and cluster I respectively (Table 3). This indicated that cluster III was the most heterogeneous group and two genotypes of cluster I revealed their proximity between them. The maximum inter cluster distance observed between cluster II and cluster III suggested wide diversity between them. The minimum inter cluster distance between cluster I and cluster IV indicated the close relationship among the genotypes included in these two groups. A considerable inter cluster distance was also observed between cluster I and cluster II and cluster III and cluster IV. In this context, Mishra et al. (2003) recommended that parents for hybridization program should be selected from clusters having wider inter-cluster distances. So, hybridization can be done by selecting

Table 2. Cluster mean values for 16 morphological and quality parameters. NP = No. of panicles ; PW=Panicle weight (g) ; LP = Length of panicle (cm) ; GP = Grains/panicle ; LG = Length of brown grain (mm) ; BG = Breadth of brown grain (mm) ; L/B = Length/breadth of brown grain ; SW =1000-seed weight (g) ; HI = harvest index ; CKL = Cooked kernel length (mm), CKB = Cooked kernel breadth (mm) ; CL/B = Cooked kernel length/breadth ; KEI = Kernel elongation index ; GT = Gelatinization temperature (C) ; AC = Amylase content (%) ; SYP = Seed yield/plant (g).

	NP	PW	LP	GP	LG	BG	L/B	SW	HI	CKL	CKB	CL/B	KEI	GT	AC	SYP
I	9.60	1.48	19.60	67.50	6.77	1.83	3.73	20.85	0.32	9.05	2.88	3.15	1.34	3.5	24.55	11.65
II	12.33	1.92	24.98	112.38	6.04	1.94	3.13	17.35	0.36	8.34	2.76	3.02	1.42	3.25	23.17	16.83
III	13.59	1.55	21.07	71.95	6.52	1.86	3.55	19.44	0.34	8.13	2.83	2.87	1.26	3.17	21.22	14.78
IV	11.84	1.59	24.32	92.33	5.74	1.87	3.16	17.11	0.32	8.39	2.74	3.07	1.47	2.75	23.43	15.49
Mean	11.84	1.64	22.49	86.04	6.27	1.88	3.39	18.69	0.34	8.48	2.80	3.03	1.37	3.17	23.09	14.69
No. of first rank	7	0	0	1	0	2	2	12	7	20	2	5	5	2	28	285
Percent contribution to divergence	1.85	0.00	0.00	0.26	0.00	0.53	0.53	3.17	1.85	5.29	0.53	1.32	1.32	0.53	7.41	75.39

Table 3. Intra and inter cluster D^2 values for 28 genotypes. Values in parentheses are square roots of D^2 values.

Cluster no.	I	II	III	IV
I	61.530 **(7.844)**	1942.581 (44.075)	1585.130 (39.814)	1341.157 (36.622)
II		2427.673 **(49.271)**	2742.587 (52.370)	1973.421 (44.423)
III			3169.216 **(56.296)**	2431.419 (49.309)
IV				1629.546 **(40.368)**

parents from cluster II having high mean values for most of the important morphological traits including seed yield/plant and cluster II having high and desired mean values for number of panicles per plant.

Therefore the present investigation revealed that considerable diversity, both within and between clusters, was always observed. Out of 16 characters studied seed yield/plant, amylase content, cooked kernel length and 1,000-seed weight contributed more than 90% to the divergence. Hence, selection for divergent parents based on these characters would be useful for heterosis breeding and to obtain high yielding segregants in succeeding generations. Based on cluster analysis and mean performance of the clusters, that cluster I, II and III were found to be distinct and genotypes belonging to these groups can be utilized for recombine the yield and quality characters to obtain desirable genotypes in segregating generations.

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