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Genetic divergence analysis using quality traits in rice genotypes (*Oryza sativa* L.)

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ABSTRACT

Genetic divergence was studied for different quality traits in 70 rice genotypes. These genotypes were collected from different rice eco-geographical regions of India. The analysis of variance revealed significant differences among the genotypes for each character studied. Based on genetic distance, 70 genotypes were grouped into nine different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like water uptake, gel consistency and head rice recovery percentage contributed maximum towards genetic diversity. The maximum inter-cluster distance was recorded between cluster VI and cluster VIII. The genotypes in these clusters may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield coupled with desirable grain quality.

Key words: *Oryza sativa L, genetic divergence, rice grain quality, D^2 analysis*

Genetic improvement mainly depends on the amount of genetic variability present in the population. Information on the nature and degree of divergence would help the plant breeder in choosing the right type of parents for future breeding programme to improve the quality characters. Hence, estimation of genetic diversity for grain quality parameters among genotypes is important for planning the future crossing programme. In the present study, an attempt was made to classify and understand the nature and magnitude of genetic diversity by using Mahalanobis (1936) D^2 statistics.

MATERIALS AND METHODS

The material for this study consisted of 70 rice genotypes from different rice eco-geographical regions of India. The material was grown in randomized block design with three replications during wet season 2004-05. Thirty days old seedlings were transplanted 20 cm apart between rows and 15 cm within the row. All recommended package of practices were adopted besides providing necessary prophylactic plant protection measures to raise a good crop. Observations were recorded on eleven grain quality characters *viz.*, hulling percentage, milling percentage, head rice recovery percentage, kernel L/B ratio, kernel length after cooking, elongation ratio, volume expansion ratio, water uptake, amylose content, alkali spreading value and gel consistency.

Two hundred gram paddy of each genotype was taken and shelled in a Satake Dehusker (type THU 35A) and milled in Satake grain testing mill (Type-TM 05) under standard condition to obtain uniformly 5-6 percent polish. Milled samples were sieved to separate whole kernels from the broken ones. Full rice and three-fourth kernels were taken as whole milled rice for computation. Kernal length and kernel breadth were measured with Satake grain shape tester as indicated by Murthy and Govindaswamy (1967). L/B ratio was calculated as the ratio of mean kernel length to mean kernel breadth. Kernel length after cooking was determined by following the procedure described by Verghese (1950). Elongation ratio was calculated as the ratio of mean cooked kernel length to mean uncooked kernel length. Alkali spreading value, an indirect measure of gelatinization temperature was estimated by following the method by Little *et al.* (1958). Estimation of amylose was determined following the procedure described by Juliano (1965). Water uptake was recorded by following the procedure described by Beachell and Stansel (1963).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all characters indicating existence of variability among the genotypes for the characters studied. Based on the relative magnitude of D^2 values, 70 genotypes were grouped into nine clusters (Table 1). The cluster I was the biggest cluster consisting of 40 genotypes followed by cluster V consisting of 12 genotypes.

The clustering pattern of genotypes revealed that the genotypes originated in different states were clubbed together or genotypes originated from the same state were distributed in different clusters. As observed from the clusters, the genotypes included in cluster I originated from Gujarat, Andhra Pradesh, Tamil Nadu and West Bengal indicating that there was no relationship between clustering pattern and geographical distribution of genotypes (Manonmani *et al*., 2003, Vanaja *et al*., 2003).

The distribution also indicated that the genotypes originated from similar geographic regions were distributed in different clusters. Therefore, the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions (Nayak *et. al* ., 2004). Perusal of Table 2 showed that the maximum intra-cluster distance was observed in cluster V (1323.90) followed by cluster IV and the minimum intra cluster distance 0.00 in five clusters (cluster II, III, VII, VIII, IX) indicating limited genetic diversity among these genotypes. The relative divergence of each cluster

Table 1. Distribution of 70 genotypes in different clusters

Clusters Number	No. of lines	Genotypes
I	40	Suraksha, Tilakchandan, PTB 39, MTU 1001, GR 11, Cottondora Sannalu, IR 30864, Sabita, Poornima, NDR 359, SGT 1, Krishna Kamod, RAU 3030, MTU 3626, GR 103, NLR 30491, Khitish, Kalanamak, Atmashital, Chittimutyalu, IET 8116, NLR 145, Gurjari, Vasumati, PR 111, Badshabhog, Satabdi, Pant dhan 14, Type 3, RAU 3045, Tella Hamsa, Mandya Vijaya, KRH 2, White Ponni, Rasi, Sashi, PR 116, GR 104, Basmati 370, Pusa Basmati 1
II	1	PNR 519
III	1	Dhandi
IV	11	IET 16775, PR 114, Triguna, PR 113, Taroari Basmati, Vijetha, Vikas, Giri, Ranbir Basmati, BPT 5204, IR 64,
V	12	Basmati 386, Yamini, ADT 41, Karjat 3, ADT 43, Kranthi, Amritbhog, GR 7, Jaya, Mugad sugandha, Pant dhan 16, BPT 11711
VI	2	NLR 33654, VRS 3
VII	1	Mahamaya
VIII	1	Kasturi
IX	1	ADT 36

Table 2. Intra (diagonal) and inter cluster average D^2 values of different genotypes of rice under study

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
I	763.74	1173.06	1180.74	1526.40	1567.54	1516.75	2323.14	3360.77	2147.83
II		.000	2590.71	1687.84	809.71	3321.72	768.96	923.03	2287.26
III			0.00	1258.27	3041.93	753.05	3468.75	5514.22	2112.55
IV				1131.92	2508.07	2553.66	1995.32	3384.49	2094.19
V					1323.90	3559.27	1839.03	2251.74	2695.61
VI						229.59	4834.66	6681.28	2993.13
VII							0.00	630.29	2180.81
VIII								0.00	3835.68
IX									0.00

from other clusters (inter - cluster distance) indicated greater divergence between cluster VI and VIII (6681.28) followed by cluster III and VIII (5514.22). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability of quality traits which may enable further selection and genetic improvement.The hybrids developed from the selected genotypes within the limits of compatibility of these clusters may produce desirable transgressive segregates that would be productive in a rice breeding programme.

The average cluster means revealed (Table 3) that genotypes with slender grains (L / B > 3.0) were grouped into clusters II, IV and V. The genotypes in cluster III and VI had high head rice recovery percentage. The cluster V showed the highest mean kernel length after cooking (12.38 mm) and elongation ratio (1.85). The genotypes in the clusters V, VII and VIII had soft gel consistence and intermediate amylose content, preferred grain qualities. The genotypes with high water uptake (>300 ml) fell in the cluster IX. The present study suggested that hybridization among genotypes included in the diverse clusters (VI, VIII and III) and the clusters having high mean value for quality traits such as high elongation (V), high head rice recovery (III, VI) and intermediate amounts of amylose contents (V, VII, VIII) would give high heterotic combinations and thus produce large variability and better segregates in the segregating generations.

Table 3. Cluster means for quality characters in different rice genotypes (cluster analysis)

	Character I	Character II	Character III	Character IV	Character V	Character VI	Character VII	Character VIII	Character IX	Character X	Character XI
Cluster 1	78.12	70.05	64.78	2.91	9.97	1.77	4.62	185.94	21.82	6.01	58.43
Cluster II	78.03	69.90	48.00	3.57	11.10	1.73	4.40	165.00	20.17	6.20	80.67
Cluster III	79.23	75.13	70.63	2.82	11.30	1.70	4.46	274.33	21.63	6.53	44.00
Cluster IV	76.01	67.78	57.47	3.69	10.75	1.55	4.60	284.21	20.22	6.74	62.89
Cluster V	77.50	68.75	55.66	3.44	12.38	1.85	4.47	160.39	22.88	5.14	78.74
Cluster VI	82.73	77.85	73.98	2.73	9.32	1.62	5.56	175.00	21.06	6.11	26.17
Cluster VII	80.13	67.57	38.13	2.55	11.30	1.71	5.35	255.00	25.04	6.27	94.00
Cluster VIII	78.70	66.03	29.47	2.69	9.27	1.50	4.38	166.67	24.50	7.00	96.33
Cluster IX	80.20	72.13	57.37	2.63	10.40	1.65	4.21	301.33	23.70	2.10	69.40

I. Hulling percentage, II. Milling percentage, III. Head rice recovery (%), IV. L/B ratio, V. Kernel length after cooking (mm), VI. Elongation ratio, VII. Volume expansion ratio, VIII. Water uptake (ml), IX. Amylose content (%), X. Alkali spreading value (Gelatinization temperature), XI. Gel consistency (mm).

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