Oryza Vol. 45. No.4, 2008 (263-267)

Divergence analysis for quality traits in some indigenous Basmati rice genotypes

Yogendra Singh*, D.R. Pani, S.K. Pradhan, Anita Bajpai and U.S. Singh

Department of Molecular Biology and Genetic Engineering, G.B. Pant University of Agriculture and Technology, Pantnagar-263145, Uttaranchal, India

ABSTRACT

Forty five genotypes of Basmati rice (Oryza sativa L.) representing different regions of India were studied for genetic diversity on the basis of quality characteristics utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2 values), the rice genotypes were grouped into eight clusters. Of the eight clusters formed, cluster I consisted of maximum 25 genotypes followed by cluster II accommodating five genotypes. The results indicated that there was some degree of similarity of genotypes clubbed together in a cluster on the basis of their origin. The highest genetic divergence was observed between cluster V and VI exhibiting wide diversity between the groups. The maximum intra-cluster divergence was observed for cluster VI and least for cluster VII and VIII. It was observed that all the minimum and maximum cluster mean values were distributed in relatively distant clusters. Among different traits, grain and kernel length, grain breadth and milling recovery had maximum contribution towards total divergence The genotypes from these clusters may be used as potential donors for future hybridizations programme to develop varieties with more grain as well as kernel length.

Key words: *Basmati rice, genetic divergence, quality traits*

Aromatic rices form a separate group and are nature's gift, exclusive to Indian sub continent (Glaszman, 1987). Among aromatic rices Basmati is accepted as the best scented, longest and slenderest rice in the world. However, little effort has been done for genetic enhancement in consumer's quality traits of the grain. The role of genetic diversity and its significance has been recognized for selection of desirable parents in breeding programme. Therefore, it is essential to know the relatedness among different long-grain basmati rices grown in the country as quite often same variety is called by different names in different parts of the country or *vice-versa.* Present study was undertaken to assess the genetic diversity based on fourteen consumers quality traits among forty five Basmati rice genotypes.

MATERIALS AND METHODS

Forty five genotypes of Basmati rice were evaluated at Seed Production Center, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttaranchal, India, in a randomized block design with two replications in wet seasons of 2004-05. Transplanting was done after one month of sowing of seeds in nursery bed in a $6m^2$ plot with a spacing of 15cm x 20cm plant-to-plant and row-to-row, respectively. Recommended package of practices were followed to raise a healthy crop. Observations were recorded on fourteen grain quality characters *viz.*, hulling percentage, milling percentage, head rice recovery percentage, grain length, grain breadth, kernel L/B ratio, kernel length and breadth after cooking, elongation ratio, volume expansion ratio, amylase content, alkali spreading value, gel consistency after harvesting of seeds.

Two hundred gram seeds of each genotype were taken, shelled and milled under standard condition to obtain uniformly 5-6% polish. Milled samples were sieved to separate whole kernels from broken ones. Kernel length and breadth were measured (Murthy and Govindaswamy, 1967). Kernel length after cooking was determined (Vergese, 1950). Alkali spreading value was estimated (Little *et al.*, 1958). Estimation of amylase content was determined (Juliano *et al.,* 1965). The mean values of two replications were used for statistical

analysis. The analysis of genetic divergence using D^2-statistics of Mahalanobis (1936) and grouping of genotypes into different clusters were done following Tocher's method (Rao, 1952) and (Arunachalam, 1981).

RESULTS AND DISCUSSIONS

The analysis of variance revealed highly significant differences among all the genotypes for the fourteen quality traits indicating the existence of significant amount of variability among the values for the characters studied (Table 1). Forty five genotypes were grouped into 8 clusters (Table 2). Twenty five genotypes were accommodated in the largest cluster i.e. cluster I; 5 genotypes in Cluster II; 4 genotypes each in cluster III and IV; 3 genotypes in Cluster V while two genotypes namely Taraori and Basmati 433 were in cluster VI. Cluster VII and VIII were mono-genotypic clusters having Basmati Uzerpka and Hansraj 3078, respectively. Clustering pattern based on D^2 values included Tilak Chandan 3048 and Kalanamak 3121 in the same cluster which was also confirmed by dendrogram (Fig. 1) prepared by UPGMA (Unweighted Pair Group Method Arithmetic averages) based on Jaccards similarity coefficient may be due to their source of origin and similarity in some of the grain characters. Some genotypes from user soil (resented by "U" suffix) were clustered in same group, i.e. 3032 AR 575 (U) and Pokkali (U) in cluster III by quality traits. All Hansraj and Basmati genotypes were distributed in 2-3 clusters. At 20 % similarity all genotypes except Bindali 3317 were grouped in three major groups comprising 5, 36, 3 genotypes, respectively. The group A' included all four Hansraj genotypes in one sub group, isolating Basmati Mohan-381, into a separate sub group probably due to the variability in grain characters. Similarly the group B' comprising 36 genotypes was further classified into two subgroups with 18 genotypes in each cluster. All the 36 genotypes in two sub groups were almost similar in grain morphology except six Hansraj genotypes. However, the subgroup I under group B' having 18 genotypes were separated from subgroup II and placed together with Hansraj genotypes since they were closely similar in some of the quality traits with Hansraj and also the origin of the material i.e. selected from single breeding programme. The group C comprising 3 genotypes viz. Tilak Chadan-3048, Kalanamak, Basmati-6129 were isolated from other two groups may

Table1. Analysis of variance for quality traits

Sources of variation	D.F.	Grain length	Grain breadth	L/B ratio of grain	Hulling recovery	Milling recovery	Kernel length	Kernel breadth	L/B ratio of kernel	Cooked kernel length	Cooked kernel breadth	Elongation ratio	Gel length	Alkali score	Amylose content
Replication	1	0.0310	0.0004	0.0114	23.1152	7.789	0.0115	0.2190	0.0747	0.2196	0.0585	0.0017	16.0472	20.0753	4.9444
Treatment	44	1.0130	0.0248	0.3067	12.9190	18.3586	0.4197	0.0182	0.1923	2.1261	0.0261	0.0188	684.196	5.5375	16.506
Error	44	0.0111	0.0009	0.0092	1.6337	1.7121	0.0058	0.0015	0.0087	0.1451	0.0035	0.0006	4.0440	0.0635	0.4278
$CD_{1\%}$		0.2840	0.0811	0.2594	3.4414	3.5230	0.2059	0.1057	0.2519	0.3243	0.1605	0.0682	5.4146	0.6785	1.7611

Table 2. Clustering composition of genotypes using quality characters

Cluster	Number ofgenotypes	Genotypes
I	25	Basmati 370, Hansraj 3074 (U), Dehradun Basmati3020, Hansraj 3077, Basmati Mohan 381, Basmati 6129, Hansraj 3086,Type 3, Basmati 375 A, Basmati C 622, Basmati Sufaid 100, Basmati 127, Hansraj 3067, 3065 AR 771(U), Basmati 376, Basmati Sathi, Bindali 3317, Hansraj3072-1, Dehradun Basmati 3020 (U), Hansraj 3074, Basmati 5836, Basmati 106, Basmati 3085, Basmati 124-10, & Hansraj 3072-2(U).
II	5	Basmati 217, Basmati 5875, Basmati 122, Basmati 136, Basmati 134.
III	4	3032AR 575 (U), Basmati 107, Basmati 43 A, Pokkali (U).
IV	4	Basmati 3034, 3065AR 1409 (U), Hansraj 3072-2, Basmati1-1 A.
V	3	Tilak Chandan 3048, Kalanamak 3121 , Basmati Nepal.
VI	2	Taraori, Basmati 433.
VII	1	Basmati Uzerpka (U).
VIII	1	Hansraj 3078.

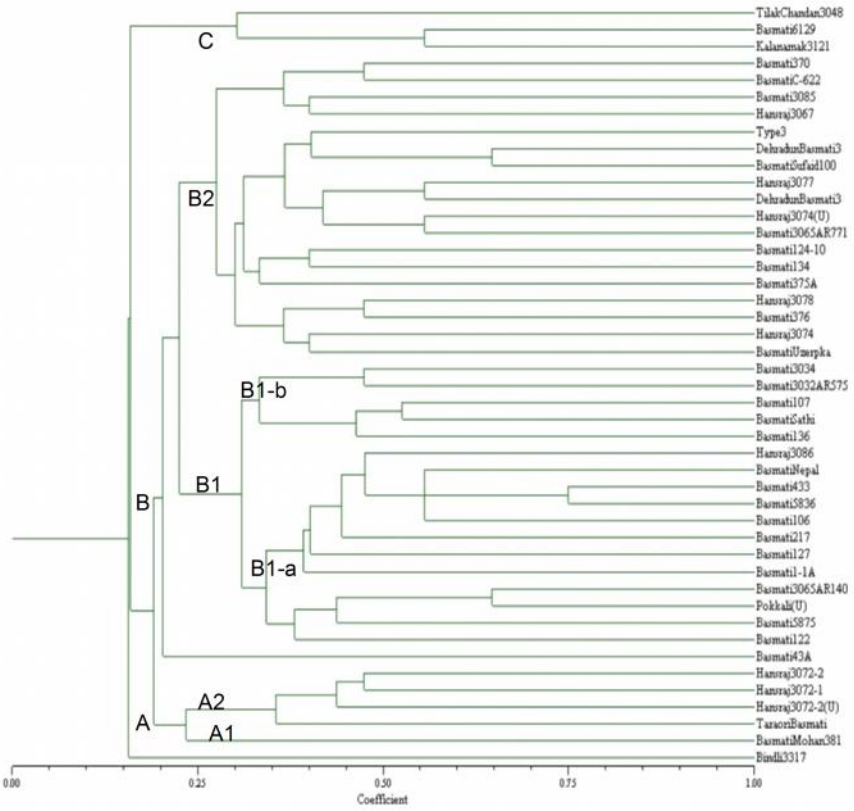

Fig. 1. Dendrogram depicting genetic diversity among indigenous Basmati rice genotypes

be due to their difference in grain size, shape, husk colour etc. from rest of the genotypes studied. The results indicated that geographical distribution and the source of the genotypes played major role in clustering along with the similarity and differences in their adaptation, selection criteria, selection pressure and environmental conditions (Nayak *et al*., 2004; Bose and Pradhan, 2005).

The average intra and inter-cluster D^2values and average genetic distance between and within cluster for quality traits are presented in Table 3**.** The maximum intra cluster divergence was observed for cluster VI and least intra cluster divergence was recorded for cluster VII and VIII. Therefore, maximum care should be taken while selecting the members of the cluster VI and least priority may be given to the members of

clusters VII and VIII. The maximum inter-cluster divergence was observed between cluster V and VI followed by cluster VII –VIII and Cluster V-VIII. The hybrids developed from the selected members on the basis of D^2 matrix value would produce highly variable population in the segregating generations.

The cluster means of various quality traits are present in Table 4. Twenty five genotypes were accommodated in cluster I, exhibited lowest mean value for hulling recovery (76.30 %), kernel breadth (1.69 cm).Cluster II, with 5 genotypes, exhibited lowest mean value for grain breadth (2.08 mm). Cluster III, with 4 genotypes in the cluster, exhibited highest mean value for grain breadth (2.38 mm), kernel breadth (1.95 mm), gel length (83.37 mm), amylose content (27.56 %) and lowest mean values for alkali digestion score (2.54). Cluster IV with 4 genotypes, did not displayed any lowest or highest mean value. Cluster V consisting of 3 genotypes, displayed highest mean value for hulling recovery (79.57 %), elongation ratio (1.93) and lowest mean value for grain length (7.43 mm), L/B ratio of grain (3050), kernel length (5.25mm), L/B ratio of kernel (2.97), cooked kernel breadth (2.10mm). Cluster VI, having two genotypes ,displayed highest mean value for grain length (10.18mm), kernel length (7.27mm), L/B ratio of kernel (4.05), Cooked kernel length (13.58 mm). Cluster VII having only one genotype, displayed highest mean value for milling recovery (65.50) and lowest mean value for elongation ratio (1.7), gel length (63.50mm), amylose content (22.55%). Cluster VIII consisting of only one genotype, exhibited highest mean value for L/B ratio of grain (4.80), cooked kernel breadth (2.40mm), alkali digestion score (6.9) and lowest mean value for milling recovery (57.50%). The results indicated that all the minimum and maximum cluster mean values were distributed in relatively distant clusters (Bose and Pradhan, 2005). It is observed that no clusters contained the majority of the quality features in its member. Hence, directly a genotype can not be selected for direct use as cultivar. Therefore, hybridization programme between the diverse clusters is suggested to get majority of the superior quality traits

Table 3. Intra (diagonal) and inter cluster average D^2 of 45 Basmati rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	86.74	181.39	218.04	137.05	731.01	198.80	333.59	226.91
II		85.51	228.54	224.84	380.46	383.63	158.31	439.81
III			113.51	237.36	671.51	261.05	307.56	448.84
IV				104.93	640.94	347.92	493.46	140.43
V					128.56	1254.24	645.52	821.04
VI						132.01	361.05	529.52
VII							0.00	889.18
VIII								0.00

Table 4. Cluster mean for different quality characters in Basmati genotypes

C.N.	G.L (mm)	G.B (mm)	L/B ratio	H.R %	M.R%	K.L (mm)	K.B (mm)	L/ B ratio	C.K.L (mm)	C.K.B (mm)	E.R	G.L (mm)	A.S	A.C.%
I	9.63	2.10	4.60	76.30	61.86	6.65	1.69	3.93	12.60	2.14	1.89	70.00	3.65	24.64
II	8.76	2.08	4.17	78.60	63.60	6.37	1.74	3.68	11.76	2.12	1.86	78.10	3.65	23.60
III	9.35	2.38	3.94	78.13	62.63	6.62	1.95	3.40	11.78	2.25	1.77	83.37	2.54	27.56
IV	9.73	2.15	4.50	78.29	57.81	5.57	1.75	3.74	12.26	2.14	1.86	68.00	3.44	23.56
V	7.43	2.13	3.50	79.57	61.50	5.25	1.77	2.97	10.20	2.10	1.93	71.50	3.88	23.17
VI	10.18	2.20	4.63	75.25	64.50	7.27	1.80	4.05	13.58	2.17	1.85	75.50	4.65	27.13
VII	8.05	2.10	4.05	77.00	65.50	6.75	1.70	3.95	11.70	2.15	1.70	63.50	3.15	22.55
VIII	10.05	2.10	4.80	76.50	57.50	6.25	1.70	3.65	11.25	2.40	1.80	72.00	6.90	23.75

C.N=Cluster Number, G.L= Grain Length, G.B =Grain Breadth, L/B=Ratio of Length & Breadth, H.R = Hulling Recovery, M.R= Milling Recovery, K.L= Kernel Length, K.B=Kernel Breadth, C.K.L= Cooked Kernel length, C.K.B= Cooked Kernel breadth, E.R =Elongation Ratio, G.L =Gel Length, A.S= Alkali Score, A.C= Amylose Content

in the segregating population.

Contribution of different quality characters to the genetic divergence among indigenous rice germplasm under study is presented in Table 5**.** It was observed that grain length (30.263 per cent), grain breadth (13.455 per cent), kernel length (25.394 per cent), milling recovery (11.313 per cent) were among the major contributing factors towards genetic diversity among 45 Basmati rice genotypes. The hulling recovery (3.737 per cent), kernel breadth (3.434 per cent), L/B ratio of kernel (1.235 per cent), cooked kernel length (1.465 per cent), elongation ratio (1.800 per cent), gel consistency (1.155 per cent), alkali digestions score (3.025 per cent) and amylose content (2.885 per cent) were moderate contributing traits towards genetic divergence. Least contribution was given by traits cooked kernel breadth (0.435 per cent), L/B ratio of grain (0.404 per cent) towards the total genetic divergence. Hence, the traits like grain length, grain breadth, kernel length and milling recovery may be used as selection parameters in the segregating generations.

Table 5. Percentage contribution of quality characters towards total divergence

Character	Contribution percentage
Grain length	30.263
Grain breadth	13.455
L/B ratio of Grain	0.404
Hulling recovery	3.737
Milling recovery	11.313
Kernel length	25.394
Kernel breadth	3.434
L/B ratio of kernel	1.235
Cooked kernel length	1.465
Cooked kernel breadth	0.435
Elongation ratio	1.800
Gel consistency	1.155
Alkali digestion score	3.025
Amylose content	2.885

REFERENCES

Arunachalam V 1981. Genetic distance in plant breeding .Indian J. Genet. 41:226-236

Bose LK and Pradhan SK 2005. Genetic divergence in deepwater rice genotypes. J of Central European agriculture 6(4):641-646

Glaszman JJC 1987. Isozyme and classification of Asian rice varieties**.** Theor.App.genet.74:21-30

Juliano BO, Onate LU and Del Mundo AM 1965. Relation of starch composition, protein content and gelatinization temperature to cooking and eating qualities of milled rice. Food Technology 19:116-121

Little RR, Hilder GB and Dawson EH 1958. Differential effect of dilute alkali on 25 varieties of milled white rice. Cereal Chemistry 35:111-126

Mahalanobis PC 1936. On the generalized distance in statistics. Proceeding of National Institute of Sciences, India. 12**:** 49-55

Murthy PSN and Govindaswamy S 1967. Inheritance of grain size and its correlation with the hulling and cooking qualities. Oryza 4(1):12-21

Nayak AR,Chaudhary D and Reddy JN 2004. Genetic divergence in scented rice. Oryza 41(3&4):79-82

Rao CR 1952. Advance statistical method in biometrical research. John Willy and Sons, Inc. New York**.**

Vergese EJ 1950. A standard procedure for cooking rice for experimental purposes. The Madras Agric. J 37:217-221