Genetic Diversity in Traditional Aromatic Rices of India

R Prasad*, LC Prasad and RK Agrawal
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221 005, India

Fifty-two traditional aromatic rice genotypes of India were evaluated along with three checks for quantitative characters to study genetic diversity employing D^2 analysis. Based on D^2 analysis with respect to grain yield and 14 other related traits, genotypes were classified in to four clusters and four ungrouped genotypes. Genotypes, namely, P 1174-91-4-1-1-1, Lalmati, HUR-BL-6 AR and KLS 27 belonged to four ungrouped clusters V to VIII. Genotype allocated to ungrouped cluster V was earliest for days to 50% flowering and exhibited highest mean performance fertile grain and spikelets per panicle. The genotype KLS 27 (ungrouped cluster VIII) was best for high density grain, grain length and L/B ratio. The maximum inter-cluster distance was observed between ungrouped clusters VI and VII followed by between clusters III and VIII. Tilak Chandan was promising genotype for high grain weight; Ganga Barud was local cultivar for grain yield per plant (cluster I). The genotypes having higher mean performance for various traits and diversity exhibited by their allocation in distant cluster could be considered for their inclusion in hybridization programmes to obtain desirable segregants.

Key Words: Rice, Aromatic, Genetic diversity, D^2 analysis

Introduction

Rice (*Oryza sativa* L.) is the world's single most important food crop and a primary food source for more than a third of world's population (Singh and Singh, 2008). India which is endowed with a great diversity of rice germplasm in its vast territorial land area is also known for a large number of cultivated varietal types. Amongst them, a variety of special quality rices are of great significance which deserve better premium in the domestic as well export market. So far, only basmati and long grain non-basmati varieties of rice have succeeded in the export market. Recently, after realizing the export potentiality and also the domestic demand of basmati varieties, more attention has been given to increase the yield of basmati varieties in the country. India is, however, endowed with a variety of short, slender aromatic rice varieties which are popular in different traditional rice growing pockets and commend premium no less than the traditional basmati rice. Bringing such varieties to the knowledge of consumers abroad would certainly find small but assured market for them (Siddiq, 2002). However, meager attempts have been made for the improvement of such rice genotypes. Therefore, it is very much essential to asses the extent of genetic diversity present in the aromatic rice lines of our country in order to undertake further crop improvement programmes. In the present investigation, an attempt has been made to study the nature of diversity using Mahalanobis D^2 statistic in set of traditional aromatic rice germplasm obtained from different parts of India.

Materials and Methods

The material for the present investigation consisted of 52 traditional aromatic rice varieties/lines procured from the Directorate of Rice Research Institute, Hyderabad, India. They included the entries of Aromatic Fine Grained Observational Nursery of the All India Coordinated Rice Improvement Programme (AICRIP), India along with three checks *viz.*, Pusa Basmati I, Mahisugandha and Type 3 (Local check). The experiment was conducted at the Agricultural Research Farm of Institute of Agricultural Sciences Banaras Hindu University, Varanasi, which represents eastern region of Uttar Pradesh in India. This site is situated at 25.2^{o}N latitude and 83^{o}E longitude and an altitude of 75.6 msl. The experiment was laid out in a Randomized Block Design with the two replications. Each plot consisted of six rows of two meters length. Row to row and plant to plant spacing was maintained at 20 x 15 cm. All the recommended agronomic practices were followed to raise a good crop. Observations were recorded for grain yield and 14 other traits. From each plot ten random plants were tagged for taking observations. D^2 analysis was done followed by Mahalanobis (1936). Clustering of genotypes was done by Tocher's method as detailed by Rao (1952).

Results and Discussion

In the present study, V (stat.) calculated for D^2 analysis and tested by the significance of Ç^2, revealed significant difference between the means in respect of the pooled effect of 15 characters among 52 aromatic rice genotypes. Clustering pattern along with inter- and intra- cluster

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*Author for correspondence: E-mail: rprasadbhugpb@gmail.com

Table 1. Average inter and intra-cluster D values among eight clusters of 52 aromatic rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	48.37	81.40	111.25	106.51	93.58	99.23	118.32	115.56
II		39.78	65.61	78.87	102.41	100.45	113.40	104.32
III			36.56	80.53	90.18	95.61	106.24	120.68
IV				32.16	85.67	88.74	96.35	110.40
V					0.00	50.45	119.50	113.63
VI						0.00	125.24	102.34
VII							0.00	85.24
VIII								0.00

Cluster numbers V to VIII are assigned to ungrouped genotypes

distances have been presented in Table 1. The 52 genotypes could be divided into four clusters (Table 2). Cluster I was the largest with 34 genotypes and maximum intra-cluster distance (48.37), indicating diversity within the group but not to the extent so that they can form separate clusters as there existed genetic similarities among themselves on the basis of multiple characters causing them to belong into a single cluster. Cluster II consisted of four genotypes, while cluster III and IV contained five genotypes each. The ungrouped clusters represented by numbers V, VI, VII and VIII were assigned to four single ungrouped genotypes, namely, P 1174-91-4-1-1-1, Lalmati, HUR-BL-6 AR and KLS 27. The maximum distance (125.24) was observed between the ungrouped genotypes Lalmati and HUR-BL-6AR with contrasting mean performances for plant height, panicle weight, grain length, high density grain index, and grain yield per plant. Similarly, the ungrouped genotype KLS 27 showed the next highest inter- cluster distance (120.68) with cluster III, and exhibited higher mean performance for plant height and high density grain index compared to the mean performance of genotypes contained in cluster III (Table 2).

Among the genotypes that could be grouped into four different clusters the maximum inter-cluster distance (111.25) was observed between cluster I and III which exhibited contrasting mean performances for the characters namely, filled grain per panicle and spikelets per panicle. The next higher inter-cluster distance (106.51) was observed between cluster I and IV were as, the smallest inter cluster distance (65.61) was observed between cluster II and III. The cultivar Punjab Basmati, a well known genotype, belonged to cluster III and exhibited difference in performance with the Kariga Javile (cluster II) *per se* in respect of characters, namely, grain maturity duration, plant height, spikelets per panicle and L/B ratio. Both of these have been a collection from Amritsar district of Punjab.

In the present study, hybridization between genotypes having higher inter D-distances are expected to generate exploitable variability for the improvement in the yield and yield related traits as well as are likely to through desirable transgressive segregants in later generations of hybridization. D^2 analysis is an efficient statistical tool to assess the genetic diversity and has been employed by many workers in various crops, such as Brassica (Murty and Quary, 1996), cotton (Singh and Bains, 1988), linseed (Anand and Murthy, 1968) rice (Shiva Kumar *et al.*, 1989; Subramaniam and Vivekanandan, 1993; (Sarma and Richharia, 1995 and Sarma *et al.*, 1996, 1997). In the present study, D^2 analysis revealed presence of considerable diversity among the genotypes investigated and the genotypes were observed to be distributed into four different clusters. Since, the genotypes present in the same cluster indicate their close relationship as compared to others (Table 1), it could be expected that all the 34 genotypes present in the cluster I were some how genetically related among themselves and were diverse from the genotypes belonging to others classes. It was interesting to note that the aromatic fine-grained check varieties included in the experiment also belonged to this cluster. This might be due to similar selection pressure applied for this group of genotypes in favour of grain quality attributes. The genotypes that were found in this cluster are the indigenous aromatic fine-grained rice varieties of different locations of our country, which generally commend premium prices in the local markets.

The two selected lines from Karnal Local, *i.e.*, KLS-5 and KLS-27 were observed to belong to cluster II and ungrouped cluster VIII. This indicates the effectiveness of selections in the local land races in generating genetic variability for utilization in the crop improvement programme. The clustering pattern indicated wide diversity between different groups of genotypes. The greater the distance between two clusters, wider is the expected

Table 2. Cluster mean values for fifteen traits of 52 aromatic rices

Cluster	Traits														
	DF	DM	GMD	PH	TN	PL	PW	FG	SP	GW	GL	GB	L/B	HDI	GY
I	112.67	145.64	28.31	117.81	11.07	23.57	2.28	145.98	160.39	1.63	7.07	2.54	2.79	20.71	10.78
II	112.25	145.73	33.00	81.88	8.00	23.83	2.05	95.18	111.70	1.95	9.93	2.79	3.43	19.97	9.90
III	104.72	132.50	27.42	80.20	8.76	22.09	1.82	81.06	93.82	1.78	10.12	2.52	4.14	27.72	8.36
IV	118.90	140.46	29.48	83.60	8.88	21.18	1.96	111.15	126.31	2.22	8.48	2.97	2.97	20.27	8.59
V	95.10	123.70	28.60	84.10	7.50	21.70	2.38	163.40	180.95	1.50	8.80	2.41	3.60	24.51	8.18
VI	100.30	130.10	29.80	79.30	8.80	21.38	1.52	95.35	114.75	1.35	6.61	2.46	2.68	34.90	4.96
VII	102.00	136.20	34.70	127.50	8.60	24.85	2.61	112.75	125.45	2.35	10.46	2.68	3.84	14.09	8.49
VIII	107.20	134.20	27.10	121.80	9.70	23.38	1.91	89.80	112.00	1.35	10.69	2.64	4.06	56.73	8.42

Abbreviations:— DF = Days to 50% flowering, DM = Days to maturity, GMD = Grain maturity duration, PH = Plant height, TN = Effective tiller number^{-1}, PL = Panicle length, PW = Panicle weight, FG = Filled grains panicle^{-1}, SP = Spikelets panicle^{-1}, GW = Grain weight, GL = Grain length, GB = Grain breadth, L/B = Length breadth ratio of grain, HDI = High density grain index (%), GY= Grain yield^{-1}.

genetic distance between the genotypes. This has also been suggested by aromatic rice workers such as (Kole 2000; Sharma *et al.*, 2002). The genetic distance among the parents largely governs the variability spectrum generated in the segregating generations and also heterosis in the F$_1$s. Therefore, identification of genetically diverse genotypes would help in selecting desirable parents for hybridization programmes. However, it has been suggested that while selecting parents for hybridization programme their yield potential should not be overlooked (Singh *et al.*, 1987).

The characters which contributed maximum towards the total diversity in the present study were; grain maturity duration (24.03%), plant height (19.94%), panicle weight (17.18%), high density grain index (14.10%), grain weight (6.22%), and grain yield per plant (5.7%). Kole (2000) studying the genetic divergence in 20 aromatic rice genotypes including mutants reported that grain length, panicle number, grain weight, and days to flowering were the measure contributors towards the total diversity.

The diverse genotypes identified (belonging to distant clusters) with desirable performances for different traits, if are utilized into multiple crossing programmes would yield promising results in bringing together different desirable genes into the common genetic background. Sarawgi and Rastogi (2001) in aromatic rice have also advocated crossing of diverse genotypes for evolving semi-dwarf, high yielding and early maturing lines with good grain quality.

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