

## Genetic diversity in Indian germplasm of aromatic rice

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### ABSTRACT

*Fifty-two traditional aromatic rice genotypes of India were studied for genetic variability, heritability and genetic advance with respect to grain yield and 14 related traits. Considerable diversity was observed among these aromatic rice cultivars. Based on per se performance, the cultivar Punjab Basmati appeared as a promising genotype for earliness, long grain size and length/breadth ratio. Highest GCV was observed for grain yield per plant followed by high-density grain index. Heritability estimates was highest for plant height.  $D^2$ -analysis classified the fifty two genotypes into eight diverse clusters. The largest cluster included most of the indigenous aromatic fine-grained rice varieties of India. The maximum inter-cluster distance was observed between cluster VI and VII followed by clusters III and VIII. Characters namely grain maturity duration, plant height and panicle weight contributed maximum towards divergence. On the basis of  $D^2$ -inter cluster distance the cross namely; Lalmati (cluster VI) X HUR-BL-6AR (cluster VII) exhibiting contrasting differences for a large number of traits is expected result in desirable segregants on hybridization.*

**Key words:** genetic diversity, aromatic rice, heritability, variability

India is endowed with a great diversity of rice germplasm in its vast territorial land area. A large number of aromatic rice genotypes are known to exist in this country. Amongst them, a variety of special quality rices are of great significance which deserve better premium in the domestic as well export market. Rice is one of the most important food crop and a primary food source for more than one third of world's population (Singh and Singh, 2008). So far, only basmati and long grain non-Basmati rice have shown promise for 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 command premium no less than the traditional Basmati rice. Bringing such varieties to the knowledge of consumers in abroad would help to find small but assured market for them (Siddiq, 2002). However, meager attempts have been made for the improvement of such rice genotypes (Kole, 2000; Sarawagi and Rastogi, 2001). In the present investigation, an attempt has been made to

study the genetic variability and diversity in a set of traditional aromatic rice genotypes obtained from different part of India.

### MATERIALS AND METHODS

The material for the present investigation consisted of 52 aromatic rice cultivars (Table 1) procured from the Directorate of Rice Research, Hyderabad, India. The experiment was conducted at the Agricultural Research Farm of the Institute of Agricultural Sciences Banaras Hindu University, Varanasi, Uttar Pradesh, India. The experiment was laid out in a randomized block design with two replications. Each plot consisted of six rows of 2m length. Row to row and plant to plant spacings were maintained at 20x15 cm. All the recommended agronomic practices were followed to raise a good crop. Observations were recorded for grain yield and 14 other traits viz., days to 50% flowering (DF), days to maturity (DM), grain maturity duration (GMD), plant height (PH), effective tiller number<sup>-1</sup> (TN), panicle length (PL), panicle weight (PW), filled grain panicle<sup>-1</sup> (FG), spikelets panicle<sup>-1</sup> (SP), grain weight (GW), grain length (GL), grain breadth (GB), length breadth ratio of grain (L/B), high density grain index in per cent (HDI), grain

**Table 1. Germplasm lines of aromatic rice and their sources**

Cultivars	Cluster position	Source
Ganga Barud	I	Traditional
Laxmi Bhog	I	Traditional
Krishna Bhog	I	Traditional
Lakhan Bhog	I	Traditional
Kapoor Kranti	I	Traditional
Jawa Pool	I	Traditional
Thurun Bhog	I	Traditional
Atma Sital	I	Traditional
Amrit Bhog	I	Traditional
Badsah Bhog	I	Traditional
Cini Kapoor	I	Traditional
Jira Sankar	I	Traditional
Tulasi Amrit	I	Traditional
Elayichi	I	Traditional
Lokti Machhi	I	Traditional
Shri Kamal	I	Traditional
Jeeriga Sambha	I	Traditional
Gandha Sali	I	Traditional
Kali Kamod	I	Traditional
Punjab Basmati	III	Collected from Amritsar District, Punjab
Kariga Javile	II	Amritsar District, Punjab
Huggi Bhatta	I	Collection from Belgaum
HUR 71	IV	Induced mutant of Basmati
HUR 72	IV	Induced mutant of Basmati
HUR 77		Induced mutant of Basmati
PNR 546	III	KLM/615-14-1-1/IR 72
P 1173-91-4-2-2	III	BM 34/Asomiya Basmati
P 1176-91-1-3-2-1	III	KLM 5/Pusa 615-14-1-1/IR-72
P 1442-98-3-5-1	II	IR 72/IR 64
P 1433-98-14-1-1	IV	BM 34/ Asomiya Basmati
P 1176-91-1-2-9-3-1	III	KLM 5/Pusa 615-14-1-1/IR 72
P 1173-91-1-2-3	IV	KLM-2/ Asomiya Basmati
P 1174-91-4-1-1-1-1	V	KLM-2/ Asomiya Basmati
Dhania	I	Local selection
Lalmati	VI	Local selection
Kalanamak	I	Local selection
Vishnu Parag	II	Local selection
Laung Choor	I	Local selection
HUR-BL-181 AR	I	Natural mutant of Adamchini
HUR-BL-6 AR	VII	Selection of Lanjhi, local collection from Jhansi
HUR-BL-152 AR	I	Tulaiparia mutant
HUR-BL-149 AR	I	Govind mutant
HUR-BL-137 AR	I	Selection of Lalchandani, local collection from Robertsganj
HUR-BL-135 AR	I	Collection from Robertsganj
Tilak Chandan	IV	Land race
Kalanamak	I	Land race
KLS 5	II	Selection from Karnal Local
KLS 27	VIII	Selection from Karnal Local
Chinoor	I	Traditional
Dubraj	I	Traditional
Mahisugandha	I	Traditional
Type 3	I	Traditional

yield<sup>-1</sup>(GY). Ten random plants/replication/genotype were tagged for recording observations. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense and genetic advance as percent of mean were calculated as followed by Singh and Chaudhary (1985). Aanalysis of variance was done following Panse and Sukhatme, (1995) and D<sup>2</sup>-analysis was carried out following Mahalanobis (1936). Clustering of genotypes was done by Tocher's method as detailed by Rao (1952).

## RESULT AND DISCUSSION

The analysis of variance indicated highly significant differences between the genotypes for all the traits under study. Considerable range of variation was observed for the all the fifteen traits under study (Table 2). Phenotypic coefficient of variation was highest for grain yield plant<sup>-1</sup> (47.13%), followed by high-density grain index (40.20%) and panicle weight (37.14%). The presence of significant phenotypic variation in the set of aromatic rice genotypes. Justifies the scope of further improvement or utilization of the aromatic rice genotypes under study. Large amount of variability in aromatic rices was also reported by many other workers (Bhattacharyya, 1978; Subha Rao *et al.*, 2001; Pandey and Awasthi, 2002). The substantial variability obtained for high density grains appear to be of importance in rice breeding. Selection based on high density grain index has been emphasized by many workers to break the yield barrier in rice (Angrish and Panwar, 1992; Padmaja Rao *et al.*, 1985; Chauhan, 2000). In the present study days to 50% flowering, days to maturity and panicle length exhibited small amount of phenotypic variation and thus poor scope of their exploitation. Broad sense heritability estimate was highest for the plant height (98.7%) followed by grain length (98.4%), total spikelets panicle<sup>-1</sup> (97.8%), high density grain index, fertile grain and days to maturity. Whereas, panicle weight recorded the poorest heritability estimate (29.9%). In the present investigation highest genetic advance as percent of mean was observed for grain yield plant<sup>-1</sup> (80.59) followed by high-density grain index (79.66). Considerable magnitude of genetic advance was also observed for fertile grain panicle<sup>-1</sup>, spikelet panicle<sup>-1</sup>, grain maturity duration, plant height, tillers plant<sup>-1</sup>, and L/B ratio. Among these, grain yield plant<sup>-1</sup> and high-density grain index exhibited high heritability, and high

genetic coefficient of variation along with high value of genetic advance. This suggests that selection would be most effective for these two traits.

In the present study utilizing Wilk's criteria, calculated 'V' stat. <sub>(1495,32)</sub> tested by the significance of  $F^2$  revealed significant difference between the means in respect of the pooled effect of 15 characters among 52 aromatic rice genotypes. The characters which contributed maximum to words the diversity 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 plant<sup>-1</sup> (5.7%). The 52 genotypes could be grouped into eight different clusters. Clustering pattern along with inters and intra cluster distances have been presented in Table 3. Cluster I was the largest containing 34 genotypes. Cluster II consisted of four genotypes, while cluster III and IV contained five genotypes each. The maximum inter-cluster distance was observed between cluster VI and VII. The next two diverse clusters were II and VI, followed by IV and V. Observation on cluster mean values (Table 4) indicated that the clusters exhibited differences in mean values for different traits.

Since, the genotypes present in the same cluster indicate their close relationship as compared to the others, it could be expected that all the 34 genotypes present in the cluster I were genetically related with each other 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 fetch premium prices in the local markets.

The two selected lines from Karnal Local i.e. KLS-5 and KLS-7 were observed to belong to two different clusters. This indicates the effectiveness of selections in the local land races in generating genetic variability for utilization in the crop improvement programme. The maximum inter-cluster distance observed between cluster VI and VII indicated that hybridization between genotypes viz., Lalmati (cluster VI) and HUR-BL-6AR (cluster VII) exhibiting contrasting differences for the traits namely plant height,

**Table 2. Variability parameters for 15 traits in 52 aromatic rices of India**

Parameters	Traits														
	DF	DM	GMD	PH	TN	PL	PW	FG	SP	GW	GL	GB	L/B	HDI	GY
Range: Min	95.05	121.80	19.85	68.55	6.15	16.78	1.28	69.05	73.25	1.25	5.57	2.15	2.05	9.27	4.96
Max	121.80	148.90	41.65	138.55	23.15	288.12	2.93	199.75	210.85	2.85	11.61	3.59	4.36	56.73	14.85
Mean	112.44	142.44	28.85	108.16	10.18	93.15	2.15	130.98	145.97	1.71	7.88	9.58	3.06	21.98	10.66
Sem ( $\pm$ )	1.08	1.80	1.72	2.14	2.19	1.11	0.67	7.19	5.10	0.12	0.20	0.20	0.42	1.76	2.04
PCV (%)	6.02	8.03	18.15	17.47	29.77	9.67	37.14	25.64	23.75	24.60	20.10	13.96	23.10	40.20	47.13
GCV (%)	5.94	7.77	17.14	17.36	20.66	8.31	20.32	25.05	23.49	23.71	19.94	11.61	18.50	39.43	43.06
Heritability (%)	97.40	94.22	89.20	98.70	48.12	74.80	29.90	95.40	97.80	91.40	98.40	69.40	64.10	96.20	83.44
Genetic advance	13.58	22.05	9.62	38.42	2.99	3.43	0.49	66.01	69.74	0.80	3.21	0.51	0.93	17.61	8.59
Genetic advance (% of mean)	12.08	15.48	34.29	35.52	29.37	3.68	22.79	50.39	46.53	4.68	4.07	5.32	30.39	79.66	80.59
CV (%)	0.96	1.27	5.97	1.98	21.43	4.82	31.08	5.49	3.50	7.27	2.53	7.74	13.84	7.85	19.17
CD (P=0.05)	3.06	9.36	3.86	4.31	4.34	3.10	2.40	7.89	6.69	1.03	1.32	1.32	1.92	3.88	8.45

Table 3. Inter and Intra-cluster values among eight clusters of 52 aromatic rice genotypes

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

\* Intra cluster distance

Table 4. 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	20.05	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
Contribution towards divergence (%)	1.20	3.66	24.03	19.94	3.72	0.62	17.18	0.21	0.74	6.22	1.72	0.73	0.22	14.10	5.70

panicle weight, grain weight, grain length, high density grain index and grain yield plant<sup>-1</sup> is expected to generate desirable segregants. Hybridization of distant genotypes as indicated by D<sup>2</sup> analysis for generating variability and desirable segregants have also been advocated by earlier aromatic rice workers (Kole, 2000; Sarawgi and Rastogi, 2001; Sharma et al., 2002).

The genetic distance between the parents largely govern the variability spectrum generated in the segregating generations and also heterosis in the F<sub>1</sub>s. Therefore, identification of genetically diverse genotypes helps 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). Based on mean performance and their inter-cluster distances, the promising genotypes identified were Punjab Basmati for earliness, grain length and L/B ratio; HUR 71 for plant height; HUR-BL-181 AR for effective tillers plant<sup>-1</sup>; Tilak Chandan for high grain weight and Ganga Barud for grain yield plant<sup>-1</sup>. These genotypes can be used for improvement of the respective traits. Diverse genotypes with desirable values for different traits and crossing them in to multiple crossing programme would be expected to yield desirable segregants and be helpful in bringing together different desirable genes into the common genetic background.

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