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## Genetic Divergence Studies in Some Indigenous Scented Rice (*Oryza sativa* L.) Accessions of Central India

Deepak Naik, Abhinav Sao, A.K. Sarawgi and Pushpendra Singh  
Department of Plant Breeding and Genetics, Indira Gandhi Agricultural University,  
Raipur-492 006 (C.G.) India

**Abstract:** The genetic divergence study was conducted to estimate the nature and magnitude of diversity in fifty aromatic rice accessions including five scented improved varieties viz., Pusa Basmati, Taraori Basmati, Indira 9, Dubraj and Madhuri 11 as checks during wet season, 2001. The D<sup>2</sup> analysis indicated the presence of appreciable amount of genetic diversity in the material. The fifty genotypes were grouped in to seven clusters. The cluster VI had the highest mean for grain yield per plant and for biological yield per plant. Inter cluster distance was recorded highest between cluster 3 and cluster 4. The least distance was recorded in between cluster 1 and cluster 5. The conclusion drawn by the cluster analysis is that in the studied population high variability observed between the genotypes in different clusters for different characters. The genotypes Taraori Basmati, Jaigundhi, Krishnabhog, Samunderphool, Sansari, Amtma Shital, Bhataphool, Ghodapunchi, Tulsimala, Dumerphool, Loktimachii and Elaychi can be used as potential donors for future hybridization programme to develop scented rice variety with good grain yield and quality traits.

**Key words:** Scented rice, genetic divergence, cluster analysis

### INTRODUCTION

Rice (*Oryza sativa* L.) is the main staple food crop of Asia and is being consumed by more than half of the population of the developing countries in the world. It provides 35-37% of the calories consumed by more than 3 billion Asians. It is an important food crop of the world both in terms of area (147 million ha) and production (525 million tons). In India, rice contributes around 45% of cereal production and is the main food source for more than 60% of population in the country (Siddiq, 2002).

Genetic diversity is pre-requisite for any crop improvement programme, as it helps in the development of superior recombinants (Manonmani and Fazlullah Khan, 2003). Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different characters (Nayak *et al.*, 2004). Genetic diversity can be evaluated with morphological traits, seed proteins, isozymes and DNA markers. Conventionally it is estimated by the D<sup>2</sup> analysis, metroglyph and principle component analysis using morphological traits (Manonmani and Fazlullah Khan, 2003). Genetic divergence analysis quantifies the genetical distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence (Iftekharuddaula *et al.*, 2002). The crosses

between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981).

Central India is well known for its native wealth of rice genetic resources and among these the large number of indigenous short grained, scented varieties cultivated in different pockets of the Madhya Pradesh and Chhattisgarh states. These varieties in general are tall and photoperiod sensitive with aromatic, short and medium grains. Despite of low yield, they possess valuable genes for aroma and excellent cooking quality traits and enjoy immense consumer preference within and outside the state. Therefore, genetic improvement in the yield potential of these scented accessions is needed through crossing programmes.

Thus, keeping in view the above facts, present study was conducted to estimate the nature and magnitude of genetic divergence and characters contributing to the genetic divergence were studied in fifty selected traditional aromatic rice accessions along with improved aromatic varieties as checks viz., Pusa Basmati, Taraori Basmati, Indira 9, Dubraj and Madhuri 11 to assess the genetic diversity among these genotypes. This study will help in selection of more distantly related parents for crossing programme to develop high yielding scented rice varieties.

## MATERIALS AND METHODS

The experimental material consisted of 45 scented local rice genotypes along with 5 scented varieties of rice (Table 1), collected from different districts of Chhattisgarh and Madhya Pradesh. The experiment was conducted in a Randomized Block Design with two replications at Research Farm, Department of Plant Breeding and Genetics, Indira Gandhi Agricultural University, Raipur (C.G.) during wet season, 2001. Twenty

Table 1: List of used scented rice genotypes

Genotypes	Accession No.	Source		
		District	State	Country
Aama Gohi	A:349	Balaghat	M.P.	India
Amtra Shital	A:3287	Dantewara	C.G.	India
Aziyasal	A:367 II	Sarguja	C.G.	India
Barang	B:1166	Raipur	C.G.	India
Badshahbhog	B:1209	Shahdol	M.P.	India
Badshahbhog	B:1727	Bastar	C.G.	India
Bisnubhog	B:1094 II	Durg	C.G.	India
Rajabhog	R:509	Bastar	C.G.	India
Vishnubhog	V:9	Bilaspur	C.G.	India
Bikoni	B:525 II	Rajnandgaon	C.G.	India
Urai Butta	U:78 II	Jabalpur	M.P.	India
Chinnore	C:334 I	Raipur	C.G.	India
Dubraj	D:191	Raipur	C.G.	India
Dubraj	D:743	Bilaspur	C.G.	India
Dubraj Scent	D:234	Raigarh	C.G.	India
Moti Dubraj	M:576 II	Bastar	C.G.	India
Dudgi	D:1205	Raigarh	C.G.	India
Ganga Baru	G:39	Bastar	C.G.	India
Ganga Prasad	G:230	Durg	C.G.	India
Jai Gundhi	J:248	Raipur	C.G.	India
Jilli Safri	J:109 IV	Rajnandgaon	C.G.	India
Bhataphool	B:1087	Sidhi	M.P.	India
Dumerphool	J:1004	Bastar	C.G.	India
Jandri Nagi	J:403	Bastar	C.G.	India
Rajim-12	R:169 II	Raipur	C.G.	India
Ramkali	R:273 III	Raipur	C.G.	India
Krishnabhog	K:1019	Durg	C.G.	India
Samunderphool	S:6721	Durg	C.G.	India
Sansari	S:1049	Raigarh	C.G.	India
Tulsimala	T:237	Rajnandgaon	C.G.	India
Tulsi manjari	T:247	Raipur	C.G.	India
Chhatribhog	C:539	Bastar	C.G.	India
Mohanbhog	M:873	Raipur	C.G.	India
Kali muchh	K:1056	Morena	M.P.	India
Lokti machhi	L:748	Bastar	C.G.	India
Ghoda puchi	G:821	Raipur	C.G.	India
Sonth	S:715	Shahdol	M.P.	India
Ramjira	R:397	Bilaspur	C.G.	India
Shrikamal	S:715	Shahdol	M.P.	India
Anterved	A:219	Damoh	M.P.	India
Chote Dubraj	K:796	Bastar	C.G.	India
Elaychi	E:15	Raipur	C.G.	India
Chinikapoor	C:459	Bastar	C.G.	India
Bagmucchha	B:1689	Seoni	M.P.	India
Jaigundhi	J:248	Raipur	C.G.	India
Madhuri 11	Check			India
Pusa Basmati	Check			India
Dubraj	Check			India
Indira 9	Check			India
Taraori Basmati	Check			India

C.G. -Chhattisgarh; M.P. -Madhya Pradesh

five days old seedlings were transplanted with a spacing of 20×15 cm between rows and between plants, respectively. Observations were recorded on five plants for 11 morphological and quality characters viz., Plant height, panicle length, Effective tillers per plant, biological yield per plant, paddy length, paddy breadth, paddy L:B (Length: Breadth) ratio, kernel length, kernel breadth, kernel L:B ratio and grain yield per plant. The mean values over replications were used for statistical analysis. The analysis of genetic divergence using Mahalanobis D<sup>2</sup> statistics was done as described by Rao (1952) and grouping of genotypes into a number of clusters as per the standard procedure described by Spark (1973).

## RESULTS AND DISCUSSION

A clear understanding of the extent of variability prevails for each trait in germplasm would simply the job for improvement of characters through selection. But in hybridization programme where selection of genetically diverse parent is important to set wide array of recombinants, the knowledge of genetic diversity among the accession of germplasm is necessary. The Wilks test indicated highly significant differences among 50 genotypes for all the 11 characters.

The 50 genotypes were grouped into seven clusters by using D<sup>2</sup> values in such a way that the genotypes within a cluster had small or low D<sup>2</sup> values than those of in between the characters. The composition of clusters has been presented in Table 2.

The maximum inter cluster distance was observed in between 3 and 4 (10.957) followed by cluster 3 and 6 (9.625), cluster 2 and 3 (8.441) and cluster 3 and 7 (7.845), whereas, minimum distance was observed in between cluster 1 and cluster 5 (2.541). The inter cluster distance varied from 2.541 to 10.957 (Table 3).

The maximum intra-cluster distance was observed for cluster 3 (2.160) followed by cluster 4 (2.051), cluster 7 (1.855) and cluster 2 (1.830) whereas, cluster 6 (1.294) observed the minimum cluster distance. Maximum number of 17 genotype were accommodated in cluster 2 followed by 12 in cluster 5, 7 in cluster 7, 6 in cluster 1 and 4 in cluster 6 and 3 in cluster 4. The minimum number of genotype 1 included in cluster 3 (Table 3).

The cluster mean for plant height was highest for cluster 6 (154.42) and lowest for cluster 3 (124.30). For effective tillers per plant cluster mean was highest to cluster 6 (8.66) while lowest for cluster 4 (4.47). The cluster mean for panicle length was highest for cluster 4 (27.93) and lowest for cluster 5 (22.24). Cluster 6 (48.51) had the highest cluster mean values biological yield per plant whereas, cluster 3 (26.41) exhibited lowest value. The

Table 2: Genotypes included in different clusters

Cluster No.	No. of genotypes included in each cluster	Name of genotypes
1	6	Dubraj scented (15), Chhatribhog (32), Anterved (40), Chote Dubraj (41), Chinikapoor (43), Indira 9 (49)
2	17	Aama Gohi (1), Amtma Shital (2), Aziyasai (3), Barang (4), Badshahbhog (5), Badshahbhog (6), Bishnubhog (7), Bikoni (10), Urai Butta (11), Bhantaphool (22), Jandri nadgi (24), Tulsimala (30), Tulsimanjari (31), Ghoda Punchi (36), Ramjira (38), Shrikamal (39), Jaigundhi (45)
3	1	Taraori Basmati (50)
4	3	Dumerphool (23), Lokti machi (35), Elaychi (42)
5	12	Dubraj (14), Moti Dubraj (16), Gangaprasad (19), Jhilli Safri (21), Rajim-12 (25), Ramkali (26), Mohanbhog (33), Kali Muchh (34), Bagmuchha (44), Madhuri 11 (46), Pusa Basmati-1 (47), Dubraj (48)
6	4	Jaigundhi (20), Krishnabhog (27), Samunderphool (28), Sansari (29)
7	7	Rajabhog (8), Vishnubhog (9), Chinnore (12), Dubraj (13), Dudgi (17), Gangabaru (18), Sonth (37)

Table 3: Average intra and inter cluster D<sup>2</sup> values

Cluster	1	2	3	4	5	6	7
1	1.762	3.773	4.892	6.688	2.541	5.485	3.144
2		1.830	8.441	5.110	4.272	3.611	2.617
3			2.160	10.957	5.989	9.625	7.845
4				2.051	7.225	7.330	4.481
5					1.482	4.786	3.055
6						1.294	4.390
7							1.855

Note: Intra-cluster D<sup>2</sup>- Bold and Diagonal values; Inter values are inter-cluster D<sup>2</sup> values

Table 4: Cluster mean for morphological and quality traits

Cluster No.	No. of genotypes in each cluster	Characters										
		1	2	3	4	5	6	7	8	9	10	11
1	6	128.52	6.56	25.67	31.92	8.39	2.26	3.70	5.53	2.01	2.74	8.95
2	17	142.59	5.86	27.88	33.72	6.27	2.27	2.76	4.27	2.05	2.08	10.20
3	1	124.30	6.00	25.68	26.41	9.98*	2.17	5.40*	6.87*	1.72*	3.99	7.37
4	3	137.86*	4.47	27.97	30.38	6.79	3.11	2.17	4.49	2.80	1.60	9.80
5	12	126.73	6.22	22.24	39.43	8.23	2.20	3.67	5.46	1.98	2.71	13.99
6	4	154.42	8.66*	27.62	48.51*	6.10	2.15*	2.84	4.23	1.96	2.17	14.29*
7	7	135.79	5.89	22.33	36.35	7.23	2.52	2.86	4.98	2.24	2.22	11.31

\*Significance at 0.05 level, 1. Plant height (cm) 2. Effective tillers/plant 3. Panicle length (cm) 4. Biological yield/plant (g), 5. Paddy length (mm) 6. Paddy breadth (mm) 7. Paddy L:B ratio 8. Kernel length (mm), 9. Kernel breadth (mm) 10. Kernel L:B ratio 11. Grain yield/plant (g)

Table 5: Desirable genotypes for different traits

Characters	Genotypes		
	I	II	III
Grain yield per plant	Sansari (29) (16.22)	Samunder phool (28) (16.05)	Jhilli Safri (21) (15.51)
Plant height	Dubraj (13) (123.40)	Gangaprasad (19) (124.20)	Elaychi (42) (124.81)
Effective tillers per plant	Krishnabhog (27) (9.50)	Aama Gohi (1) (9.45)	Samunder phool (28) (9.4)
Panicle length	Dumerphool (23) (34.22)	Bhantaphool (22) (32.22)	Amtma Shital (2) (31.84)
Biological yield per plant	Krishnabhog (27) (51.01)	Sansari (29) (49.42)	Jaigundhi (20) (47.50)
Paddy length	Taraori Basmati (50) (9.98)	Sonth (37) (8.85)	Chote Dubraj (41) (8.85)
Paddy breadth	Ramkali (26) (2.09)	Krishnabhog (27) (2.11)	Moti Dubraj (16) (2.12)
Paddy L:B ratio	Taraori Basmati (50) (5.40)	Rajim-12 (25) (4.10)	Madhuri 11 (46) (4.01)
Kernel length	Taraori Basmati (50) (6.87)	Chote Dubraj (41) (5.97)	Madhuri 11 (46) (5.91)
Kernel breadth	Taraori Basmati (50) (1.72)	Ramkali (26) (1.87)	Moti Dubraj (16) (1.90)
Kernel L:B ratio	Taraori Basmati (50) (3.99)	Dubraj scented (15) (2.87)	Chote Dubraj (41) (2.86)

L:B ratio – Length: Breadth ratio

highest cluster mean for paddy length was exhibited by cluster 3 (9.98) and lowest cluster mean value was observed for cluster 6 (6.10) (Table 4).

For quality characters, highest mean value recorded for paddy breadth was cluster 4 (3.11) and lowest for the cluster 6 (2.15) whereas, for L: B ratio of paddy highest cluster mean was shown by cluster 3 (5.40) and lowest for cluster 4 (2.17). The highest cluster mean for kernel length was shown by cluster 3 (6.87) and lowest value recorded

for cluster 6 (4.23). For kernel L: B ratio the highest cluster mean value was recorded by the cluster 3 (3.99) and lowest by cluster 4 (1.60). The highest cluster mean value for grain yield per plant was exhibited by cluster 6 (14.29) and lowest by cluster 3 (7.37).

The relative divergence of each cluster from other cluster (inter cluster distance) indicated greater divergence between cluster 3 and cluster 4 followed by cluster 3 and 6, cluster 2 and cluster 3 and 3 and cluster 7

(Table 5). The selection of diverse genotype for above cluster would produce a broad spectrum of variability for morphological and quality traits studied which may enable further selection and improvement. The hybrid developed from the selected genotypes within the limits of compatibility of these cluster may produce high magnitude of heterosis or desired transgressive segregants. This would be rewarding in rice breeding programme. Sarawgi and Shrivastava (1996), Sarawgi and Rastogi (2000), Ray *et al.* (2002) and Nayak *et al.* (2004) also found similar degree of diversity in rice.

For the grain yield per plant the selected genotypes was Sansari (29), Samunderphool (28) and Jhilli Safri (21). The Genotype Dubraj (13), Gangaprasad (19) and Elaychi (42) for plant height. For effective tillers per plant the selected genotypes were Krishnabhog (27), Aama Gohi (1) and Samunderphool (28). For the panicle length the genotypes selected were Dumerphool (23) Bhataphool (22) and Amtma Shital (2).

For quality characters like Kernel length the genotypes selected were Taraori Basmati (50), Chote Dubraj (41) and Madhuri 11 (46). Chote Dubraj (41) was selected for kernel length: breadth ratio of paddy.

The above grouping indicates the existence of wide genetic divergence among constituent genotypes. Such high degree of divergence were found in local collection by Gupta *et al.* (1999), Sarawgi and Rastogi (2000) and Nayak *et al.* (2004) as well as in international collections by Usha Kumari and Rangaswamy (1997).

These observations suggest that inter crossing of genotypes from different cluster showing good mean performance may help in obtaining high yielding with good grain quality genotypes. The genotypes Tarori Basmati from cluster 3; Jaigundhi, Krishnabhog, Samunderphool and Sansari from cluster VI, Amtma Shital, Bhataphool, Ghoda Pucchi and Tulsimala from cluster 2; Dumerphool, Loktimachii and Elayachi from cluster 5 were selected. The genotypes from above different cluster can be utilized as parents in crossing programme to isolate desirable genotypes for yield and quality traits.

Sarawgi and Shrivastava (1991) reported that selection of genotypes as parents for hybridization or in crop improvement programme need not necessarily be based on geographical diversity, the genetic diversity may prove sound base for the purpose. This is in accordance to the present findings.

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