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Research Note

Genetic diversity among some traditional aromatic Rice (*Oryza sativa* L.) landraces of Chhattisgarh

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Abstract

The nature and magnitude of genetic diversity in thirty eight aromatic rice accessions collected from different places of Chhattisgarh were evaluated for their performance. Data generated on nine quantitative characters were subjected to D^2 statistics and result indicated the presence of appreciable amount of genetic diversity in the material. The 38 genotypes were grouped into five clusters. Cluster II was the biggest one consisting of eleven genotypes and cluster III, the smallest one consisting of four genotypes. The intra-cluster distance varied from 1.828 for cluster III to 2.338 for cluster I and the inter-cluster distance ranged from 2.534 between clusters IV and V to 4.765 between clusters III and V indicating closeness and diversity between the clusters respectively. The highest inter-cluster distance between clusters III and V revealed highly divergent group. Therefore, it is suggested that the parents should be chosen from clusters III and V for hybridization to get high grain yield.

Keywords
Aromatic rice, Genetic divergence, D^2 analysis, Cluster analysis

Rice (*Oryza sativa* L.) is one of the most important staple food crops of Chhattisgarh. In Chhattisgarh, it is mainly grown under rainfed ecosystem, which covers about 74, 97 and 95 per cent cropped area of Chhattisgarh plain, Bastar plateau and Northern hill zones, respectively. The central plains of Chhattisgarh are known as rice bowl of central India. Besides basmati types which get high price in international market, the country also bounds with hundreds of indigenous short grain aromatic cultivars and landraces grown in pockets of different states. Almost every state of India has its own collection of aromatic rice that performs well in native areas. These aromatic rice cultivars also possess exemplary quality traits like aroma, fluffiness and taste. However, the improvement of these rice varieties very much neglected as they lacked export value per se. The short and medium grained aromatic rice varieties are generally low yielders, susceptible to lodging, pest and diseases. Some of these genotypes are being gradually eroded from their respective place of origin and are on the verge of becoming extinct due to competition from high yielding varieties (Ram *et al*., 2007). Hence, there is a need to catalogue, characterize and conserve the non-basmati traditional aromatic rice landraces, which are in extricably integrated with culture and traditional knowledge of nation.

Although genetic diversity analysis has been done by several workers, limited information is available on traditional aromatic rice. Such studies have especially become essential for initiating genetic improvement efforts of short grain aromatic rice, as meager attention has been paid for their improvement (Singh, 1996). Assessment of genetic diversity is an integral part of crop improvement as exploitation of the genetic diversity helps the plant breeder to develop new varieties (Manonmani and Fazlullah Khan, 2003). Genetic diversity can be evaluated with morphological traits, seed proteins, isozymes and DNA markers. Conventionally, it is estimated by the D^2 analysis, metroglyph and principle component analysis using morphological traits (Manonmani and Fazlullah Khan, 2003).

For the assessment of variation on multivariate scale, The D2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity, it helps to quantify the degree of divergence between populations and to choose genetically diverse parents for obtaining desirable recombination (Thomas and Lal, 2012). Mahalanobis D^2 statistics has proved to be a powerful technique (Murty and Arumachalam, 1966). 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 in thirty eight selected aromatic rice landraces. This study will help in selection of elite genotypes for crossing programme and also they can be released as a variety.

The experiment was conducted during the *Kharif* 2011 at the Research cum Instructional Farm of Indira Gandhi Krishi Vishwavidyalay, Raipur. Thirty eight aromatic land races of rice collected from different places of Chhattisgarh were selected for this study (Table 1). Twenty one days old seedlings were subsequently transplanted in the field, in Randomized Block Design (RBD) with three replications. Net plot size was 3 m x 15 m. Row to row distance was 25 cm and plant to plant distance was 25 cm. Observations were recorded on five plants for 9 morphological and quality characters *viz.*, Days to 50 % flowering, Days to maturity, Plant height, Panicle length, Number of tillers per plant, Number of panicles per plant, Number of grains per plant, Grain yield per plants and 1000 seed weight. The mean values over replications were used for statistical analysis. The analysis of genetic divergence using Mahalanobis D^2 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).

One of the main objectives of any breeding program is to produce high yielding and better quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is the presence of sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. For identifying such desired lines for crossing, Mahalanobis's D^2 statistic has been used in several crops. It is a powerful tool used to quantify the genetic divergence between the genotypes and to relate clustering pattern. In the present investigation, thirty eight genotypes of rice were considered for assessment of nature of genetic diversity by adopting Mahalanobis's D^2 statistic (1936) considering nine characters.

Thirty eight aromatic rice genotypes were grouped into five clusters. Maximum divergence observed between clusters III and V (4.765) while, minimum divergence was observed between clusters IV and V (2.534). Cluster II was the biggest cluster consisting of 11 genotypes *viz.,* Shyamjeera, Gopalbhog, Jawaphool, Kasturi, Vishnubhog-1, Dubraj-1, Kubrimohar-1, Jaigundhi, Shrikamal, Tilkasturi, and Vishnubhog-2 followed by cluster I, comprised of nine genotypes *viz.,* Kapoorsar, Kalikamod, Jeeradhan, Sukulphool, Elaychi, Tulsiprasad, Samudrafan, Badhashahbhog and Kharigilas followed by cluster V, comprised of eight genotypes *viz.,* Jeeraphool, Chinnor-1, Tulsimanjari, Atmasheetal, Gangabaru, Keraghul, Jaophool and Katarnibhog followed by cluster IV, comprised of six genotypes *viz.,* Dujai, Chinnor-2, Kubrimohar-2, Dubraj-2, Dubraj-3 and Maidubraj. The cluster III contained only four genotypes *viz.,* Bisni, Londhi, Anterved and Lalloo-14. The patterns of distribution of genotypes into various clusters are given in the Table 2.

The intra and inter-cluster values in terms of D^2 values among the five clusters are given in Table 3 and represented in Fig. 1.The inter-cluster D^2 exhibited that cluster I (2.338) had the maximum genetic diversity followed by cluster IV (2.200) and cluster II (2.138). The inter-cluster D^2 values of the five clusters that had the highest inter-cluster D^2 value was between cluster III and V (4.765) while, the lowest was between cluster IV and V (2.534). From the above, it could be concluded that, considerable diversity existed among genotypes included in the present study. This could be the result of selection in different direction by nature and human forces.

The mean values of nine characters studied in thirty eight genotypes for five clusters are presented in Table 4. The cluster III (91.92 days) had the early flowering genotypes whereas cluster V (121.21days) had the late flowering genotypes. The genotypes of cluster II (115.25 cm) were dwarfest while, genotypes of cluster IV (146.72cm) were tallest compared to other clusters. Cluster II had the genotypes with lowest number of tillers per plant (14.88) and number of panicles per plant (11.79) on contrary, the cluster V had the genotypes with highest number of tillers per plant (16.58) and number of panicles per plant (19.04). The genotypes lying in the cluster IV had shortest panicle length (24.56 cm) while, the genotypes in cluster I had longest panicle length (32.78 cm). The number of grains per panicle was lowest in cluster I (108.07) and highest in cluster V (186.50). The genotypes of cluster V had lowest grain yield (1982.33 kg/ha) while, cluster V had highest grain yield (5730.33 kg/ha). The 1000 seed weight was lowest in cluster V (13.06 gm) and highest weight in cluster IV (19.44 gm).

The above grouping indicates the existence of broad genetic divergence among present 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 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 Jeeraphool, Chinnor-1, Tulsimanjari, Atmashital, Gangabaru, Keraghul, Jouphool, and Katarnibhog from cluster 5 and Dujai, Chinnor-2, Kubrimohar-2, Dubraj-2, Dubraj-3 and Maidubraj from cluster 4 can be utilized as parents in crossing programme to isolate desirable genotypes for yield.
The maximum per cent contribution towards genetic divergence was of grain yield followed by number of grains per panicle and days to 50% flowering. Roy and Panwar (1993), Sardana *et al.*(1997), Shanmugsundaram *et al.* (2000), Roy *et al.* (2002), Datta and Mani (2003), Senapati and Sarkar (2005), Anand Kumar and Indubala (2005),Ovung *et al.*, (2012)observed grain yield per plant to be main contributor towards diversity. Shukla *et al.* (2006) observed biological yield and harvest index to be main contributors towards genetic diversity.

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Table1. List of aromatic rice landraces used in present investigation during *kharif* 2011-2012

S.No.	Variety	Sources	S.No.	Variety	Sources
1.	Anterved	Chhuriya/ Rajnandgaon	20.	Kapoorsar	Jabera / Damoh
2.	Atmasheetal	Chhindgarh/ Bastar	21.	Kasturi	Bakawand/ Bastar
3.	Badshahbhog	Jagadalpur	22.	Kharigilas	Charama/ Bastar
4.	Bisni	Surajpur	23.	Katarnibhog	Sabour (Bihar)
5.	Chinnor –I	Balaghat	24.	Kheraghul	Gharghoda/ Raigarh
6.	Chinnor-II	Tilda / Raipur	25.	Kubrimohar-I	Bemetra
7.	Dubraj-I	Nagari	26.	Kubrimohar-II	Magarload/ Raipur
8.	Dubraj-II	Balaodabazar/ Raipur	27.	Lalloo-14	Mandla
9.	Dubraj-III	Nagri	28.	Londhi	Pendra
10.	Dujai	Pendra	29.	Mai Dubraj	Bastar
11.	Elaychi	Phingeshwar/ Raipur	30.	Samudrafan	Pandariya/ Bilaspur
12.	Gopalbhog	Bagicha, Sarguja	31.	Shyamjeera	Surajpur
13.	Gangabaru	Chhindgarh/Bastar	32.	Srikamal	Raipur/Naikin/ Sidhi
14.	Jaigundi	Saraypali / Raipur	33.	Sukalaphool	Jaijepur/ Bilaspur
15.	Javaphool	Raigarh	34.	Tilkasturi	Pithora / Raipur
16.	Jeeradhan	Tilda / Raipur	35.	Tulasiprasad	Aarang / Raipur
17.	Jeeraphool	Bageecha, Sarguja	36.	Tulsimanjari	Sabour / Bihar
18.	Jaophool	Lallunga / Raigarh	37.	Vishnubhog-I	Pendra
19.	Kalikamod	Aarang / Raipur	38.	Vishnubhog-II	Badrafnagar/ Sarguja

Table 2. Distribution of aromatic rice landraces in various groups based on D^2 analysis

Cluster	Number of entries	Entries numbers
I	09	Kapoorsar (14), Kalikamod (15), Jiradhan (17), Sukulaphool (19), Elaychi (20), Tulsiprasad (24), Sar Badhshahbhog (34), Karigilas (35).
II	11	Shyamjeera (1), Gopalbhog (6), Jawaphool (7), Kasturi (8), Vishnubhog-1 (9), Dubraj-1 (10), Kubrimohar-1 (11), Jaigundhi (22), Shrikamal (36), Tilkasturi (37), Vishnubhog-2 (38).
III	04	Bisni (2), Londhi (4), Anterved (23), Lallu-14 (32).
IV	06	Dujai (5), Chinnor-2 (18), Kubrimohar-2 (25), Dubraj-2 (29), Dubraj-3 (30), Maidubraj (31).
V	08	Jeeraphool (3), Chinnor-1 (12), Tulsimanjari (13), Atmashital (16), Gangabaru (21), Keraghul (26), Jouphool (28), Katarnibhog (33).

Table 3. Average intra and inter cluster D^2 values in aromatic rice landraces

	I	II	III	IV	V
I	**2.338**				
II	2.701	**2.138**			
III	3.633	4.198	**1.828**		
IV	3.251	3.000	4.268	**2.200**	
V	3.297	2.849	4.765	2.534	**1.951**

***Bold values are intra-cluster value**

Table 4. The mean values of clusters for nine characters in thirty eight aromatic rice landraces

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of tillers/plant	Number of panicles/plant	nicle length (cm)	Number of grains/panicle	Grain yield (Kg/ha)	1000 seed weight (gm)
I	112.59	138.00	137.85	15.00	16.67	32.78	108.07	1982.33	19.25
II	116.36	140.18	115.25	14.88	11.79	26.88	137.52	3610.36	17.29
III	91.92	116.92	141.00	16.42	17.67	27.83	126.00	4115.42	17.23
IV	120.56	142.33	146.72	16.56	18.72	24.56	180.94	4788.33	19.44
V	121.21	146.08	123.00	16.58	19.04	29.75	186.50	5730.33	13.06

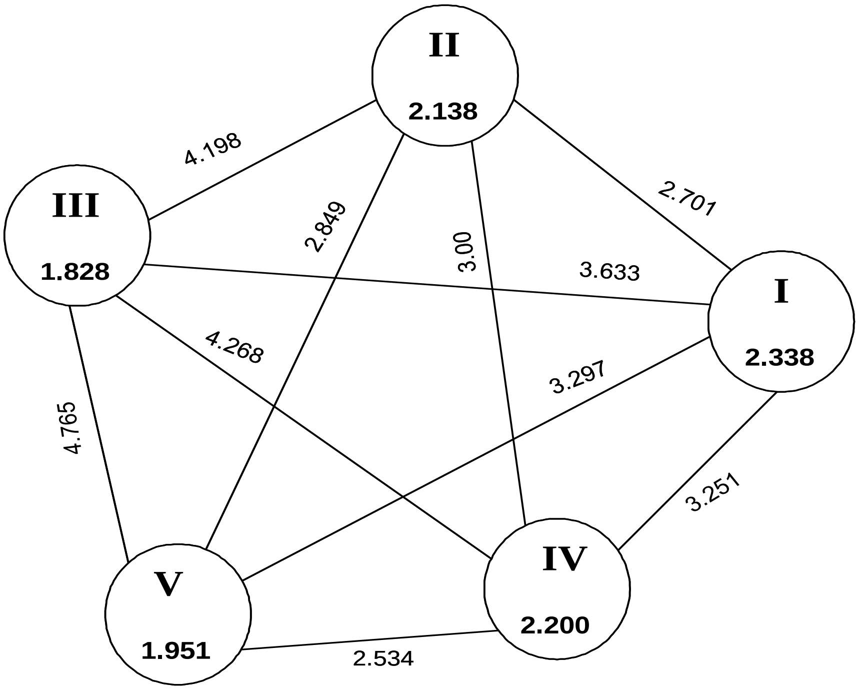

Fig. 1 : D^2 Diagrammatic representation of intra and inter cluster values.