# Genetic Diversity in Farmers' Varieties and Some Advanced Lines of Aromatic Rice (*Oryza sativa* L.) from West Bengal

**Bidhan Roy**

*Department of Genetics and Plant Breeding, Regional Research Station, Terai Zone, Pundibari, Cooch Behar-736165, West Bengal*

(Received: 1 March 2013; Revised: 19 June 2013; Accepted: 25 June 2013)

The nature and magnitude of genetic diversity were estimated in 37 aromatic rice genotypes during the *kharif* (Aman) season under humid sub-tropic Terai Zone of West Bengal using Mahalanobis $D^2$ statistics. The genotypes were grouped into 10 clusters. The pattern of distribution of genotypes into different cluster is random and independent of geographical origin or region of adoption. The relative divergence of each cluster from other clusters displayed higher order of divergence between cluster VIII and X followed by clusters VII and VIII, clusters IX and X, and clusters III and IX. Maximum intra-cluster distance was observed among the genotypes, viz., Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1, Nunia in cluster X, indicating existence of wide genetic divergence among the constituent genotypes in it. Considerable variation in cluster mean values was observed for all the characters except seed thickness. Genotypes of clusters IX (KNS-6/2 and Chini Atap) and III [KNS-3-9(N) and KNS-2-1] exhibiting high seed yield may be directly used for adoption or in hybridization programme for yield improvement. Seed length, seed thickness, seed breadth, panicle length and seed yield were major contributing characters towards the total genetic divergence which may be used in selecting genetically diverse parents, particularly to exploit maximum heterosis or to execute efficient selection in highly segregating generations.

**Key Words: Aromatic rice, Farmers' varieties, Genetic diversity**

## Introduction

Rice is the most important staple food grain and stands next to wheat in the global food grain production. India has the largest acreage under rice, about 44.6 m ha of land with a production of about 90.15 mt (Anonymous, 2009). The biodiversity of scented and non-scented rice in India is the largest in the world. The Indian subcontinent has the *natural gift* of basmati rice that has been accepted as the best scented, long and slender grain in the international markets and gets high price. In addition to the basmati rice, a large number of local landraces of scented rice perform equally in terms of aroma, cooking quality and yield as well. Most of these genotypes have short-bold to medium-bold grain. Their demand in the domestic market is greater than that of basmati. These are mainly used for special culinary preparation (such as *khir* in Bengal). Unfortunately, these have somehow not got the attention of the rice scientists, which has led to decline and/or extinction of this valuable wealth. Many patches of West Bengal and Assam are endowed with non-basmati rice cultivars which are cultivated casually, as way of life, with almost no bent towards their commercial exploitation. And this is not uncommon in the northern districts of West Bengal, wherein a score of outstanding landraces of such category, viz., Tulaipanji, Kataribhog, Kalobhog, Tulsibhog, Badshabhog, Khasha etc. are grown. These local cultivars posses the ability to tolerate biotic and abiotic stresses.

Germplasm constitute the foundation of any genetic improvement programme of crop. The pace and magnitude of genetic improvement generally depend on the amount of genetic variability present in a population. Further more, the spectrum of variability in segregating generations largely depend on the genetic diversity of the parents involved in the hybridization. Majority of the economically important characters including yield and its components are amenable to genetic improvisation through *inter-se* breeding among genetically diverse parents. It is, therefore, logical to assess the genetic divergence in the available germplasm, as the importance of genetic diversity for successful selection of parents to be used in hybridization has been emphasized earlier (Bansal *et al*., 1999; Soni *et al*., 1999). To unzip the genetic divergence and identify the character contributing towards the genetic divergence, a study was undertaken in 37 aromatic rice genotypes under Terai Zone of West Bengal.

---

*Author for Correspondence: E-mail: bcroy10@yahoo.com*

## Materials and Methods

The experimental meterial comprised 37 aromatic rice genotypes consisting of 19 aromatic farmers' varieties, one basmati rice, six pure lines isolated from Kalobhog and 11 advanced aromatic lines derived from hybridization involving Kalobhog (Table 1). The experiment was conducted at University Farm, Pundibari, Cooch Behar. Single seedling (30 days old) was transplanted per hill in a plot measuring 3 x 1.5 m in randomized block design with two replications. The experiment was conducted for two years during rainy (*kharif*) season of 2010 and 2011. The inter- and intra-row spacing was 30 and 25 cm, respectively. Standard agronomic practices compatible to the humid sub-tropic of Terai Zone were adopted to ensure good crop growth. Observations were recorded for days to 50% flowering, plant height (cm), number of panicles/plant, panicle length (cm), number of fertile seeds/panicle, 100-seed weight (g), 100-kernel weight (g), seed length (mm), seed width (mm), seed thickness (mm) and seed yield (t/ha). The mean performance over two years was pooled and used for statistical analysis.

Data were subjected to multivariate analysis following Mahalanobis' $D^2$ statistics (Mahalanobis, 1928 and 1936) to measure the genetic divergence followed by the clustering of genotypes based on above mentioned 11 characters. $D^2$ statistics were performed using GenRes Statistical Software, (c) 1994 Pascal Intl Software Solutions, Version 3.01.

## Results and Discussion

Analysis of variance showed highly significant mean sum of square for all the characters used in this study (Table 2). Based on the relative magnitude of $D^2$ values, 37 genotypes were grouped into 10 clusters (Table 3). Twelve genotypes were accommodated in cluster I, while clusters II, III, IV, V, VI and IX had two genotypes in each, clusters VIII contained three genotypes, finally the clusters VII and X retained five genotypes in each. Most of the aromatic farmers' varieties were accommodated in clusters I, VI, VII and VIII. Clusters II, III, IV and V retained only advanced lines derived from Kalobhog, whereas, the clusters VI, VII, VIII, IX and X contained both the advanced lines and farmers' varieties. The pattern of distribution of genotypes from diverse geographical region into different clusters was random, such as, Kalturey, Kagui, Jhapaka, Fudugey and Munimahnanri were collected from Kalingpong of Darjeeling district, distributed in cluster I and VII. It

**Table 1. Place of collection or parentage of 37 genotypes of aromatic rice**

| Genotype | Place of collection or parentage | Genotype | Place of collection or parentage |
|---|---|---|---|
| Mohanbhog | Nadia, W.B. | KNS-5 | Kalobhog/Pusa basmati-1 |
| Kalojeera | Cooch Behar, W.B. | KNS-3-9(N) | Pure line of Kalobhog |
| Kalojeera-1 | Nadia, W.B. | KNS-3 | Kalobhog/Pusa basmati-1 |
| Radhunipagal | Cooch Behar, W.B. | KNS-6 | Kalobhog/Pusa basmati-1 |
| Kalobhog | Cooch Behar, W.B. | KNS-2-1 | Pure line of Kalobhog |
| Khasha | Maldah, W.B. | KNS-1(N) | Pure line of Kalobhog |
| Badshabhog | Maldah, W.B. | KNS-3-1 | Kalobhog/Pusa basmati-1 |
| Kalturey | Kalingpong, W.B. | KNS-4 | Kalobhog/Pusa basmati-1 |
| Kagui | Kalingpong, W.B. | KNS-2 | Kalobhog/Pusa basmati-1 |
| Jhapaka | Kalingpong, W.B. | KNS-2(N) | Pure line of Kalobhog |
| Chinikamani | Nadia, W.B. | KNS-1-2B | Kalobhog/Pusa basmati-1 |
| Fudugey | Kalingpong, W.B. | KNS-5-1 | Kalobhog/Pusa basmati-1 |
| Munimahnanri | Kalingpong, W.B. | KNS-1-1 | Kalobhog/Pusa basmati-1 |
| Chakhao Poireiton | Imphal, Manipur | KNS-1-3(N) | Pure line of Kalobhog |
| Tulaipanji | Maldah, W.B. | KNS-1-2 | Kalobhog/Pusa basmati-1 |
| Gobindobhog | Nadia, W.B. | KNS-6/2 | Kalobhog /IET4786 |
| Radhunipagal-1 | Nadia, W.B. | Chini Atap | Siliguri, W.B. |
| Pusa Basmati-1 | IARI, New Delhi | Nunia | Kalingpong, W.B. |
| KNS-1 | Pure line of Kalobhog | | |

**Table 2. Pooled analysis of variance for grain yield and yield component character in 37 genotypes of aromatic rice**

| Source | d.f. | Mean sum of square | | | | | |
|---|---|---|---|---|---|---|---|
| | | Days to 50% flowering | Plant height | No. of panicles/plant | Panicle length | No. of fertile seed/panicle | |
| Total | 73 | 147.669 | 406.121 | 38.164 | 5.004 | 1778.194 | |
| Replication | 1 | 0.216 | 0.379 | 0.039 | 0.026 | 5.085 | |
| Treatment | 36 | 299.051** | 817.280** | 70.289** | 8.457** | 3385.351** | |
| Error | 36 | 0.382 | 6.232 | 7.099 | 1.598 | 220.291 | |
| | | 100-seed weight | 100-kernel weight | Seed length | Seed breadth | Seed thickness | Seed yield |
| Total | 73 | 0.116 | 0.082 | 1.319 | 0.006 | 0.026 | 0.813 |
| Replication | 1 | 0.001 | 0.002 | 0.006 | 0.008 | 0.003 | 0.466 |
| Treatment | 36 | 0.234** | 0.165** | 2.673** | 0.105** | 0.050** | 1.529** |
| Error | 36 | 0.003 | 0.001 | 0.003 | 0.067 | 0.003 | 0.107 |

**Table 3. Cluster pattern, size and constituents of clusters involving 37 aromatic genotypes of rice through $D^2$ statistics**

| Cluster | No. of genotypes | Genotypes |
|---|---|---|
| I | 12 | Mohanbhog, Kalojeera, Kalojeera-1, Radhunipagal, Kalobhog, Khasha, Badshabhog, Kalturey, Kagui, Jhapaka, Chinikamani, KNS-1(N) |
| II | 2 | KNS-1, KNS5-1 |
| III | 2 | KNS-3-9(N), KNS-2-1 |
| IV | 2 | KNS-5, KNS-6 |
| V | 2 | KNS-4, KNS-1-1 |
| VI | 2 | Chakhao Poireiton, KNS-1-2B |
| VII | 5 | Fudugey, Munimahnanri, Tulaipanji, KNS-3-9(N), KNS-1-2B |
| VIII | 3 | Gobindobhog, Radhunipagal-1, KNS-2(N) |
| IX | 2 | KNS-6/2, Chini Atap |
| X | 5 | Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1, Nunia |

showed that genotypes collected from same geographic region got distributed in several clusters. It might be due to selection differential or genetic drift under diverse environmental conditions within the same geographical region (Roy *et al*., 2002). Similarly, genotypes collected from different places coexisted in the same cluster, such as, cluster I. Mohanbhog, Kalojeera-1, Radhunipagal and Chiakamani were collected from southern parts of West Bengal; Kalobhog and Kalojeera were collected from Cooch Behar; Khasha and Badshabhog were collected from Madah and Kalturey and, Kagui and Jhapaka were collected from Darjeeling. Thus, the distribution of genotypes into different clusters was not associated with their geographical origin. Roy and Panwar (1993), Mehera *et al*. (1998) and Roy *et al*. (2002) reported the non-correspondence of genetic divergence with geographic diversity in rice. This tendency of genotypes occurring in the same cluster cutting across the geographical boundaries demonstrated that geographical isolation is not the only factor causing genetic diversity in rice (Bansal *et al*., 1999). Sinha *et al*. (1991) reported that geographical diversity might not always be a useful index in assessing genotypic diversity in rice.

The relative divergence (Table 4) of each cluster from other clusters displayed higher order of divergence between cluster VIII and X (D = 84.548) followed by clusters VII and VIII (D = 80.403), clusters IX and X (D = 77.329), and clusters III and IX (D = 70.210). Highly divergent genotypes deem to produce wide variability that may help further selection for genetic improvement (Rahaman *et al*., 1997). Hybrid developed from the genotypes within the limit of compatibility of those clusters may manifest high heterosis or desirable transgressive segregants, which would be beneficial for

**Table 4. Average intra- and inter-cluster $D^2$ and D values among 37 aromatic genotypes of rice**

| Clusters | I | II | III | IV | V | **VI** | **VII** | **VIII** | **IX** | **X** |
|---|---|---|---|---|---|---|---|---|---|---|
| **I** | **1992.598**<br>**(44.639)** | 1768.943<br>(42.059) | 2379.483<br>(48.780) | 1667.057<br>(40.830) | 1743.835<br>(41.759) | 1489.898<br>(38.599) | 3636.560<br>(60.304) | 2741.397<br>(52.358) | 2354.313<br>(48.521) | 4656.813<br>(68.421) |
| **II** | | **75.337**<br>**(8.680)** | 253.903<br>(15.934) | 522.461<br>(22.587) | 189.184<br>(13.754) | 542.287<br>(23.287) | 2256.036<br>(47.498) | 2842.288<br>(53.313) | 3767.885<br>(61.383) | 2808.486<br>(52.995) |
| **III** | | | **108.291**<br>**(10.406)** | 560.588<br>(23.677) | 276.144<br>(16.618) | 1002.625<br>(31.664) | 2207.437<br>(46.983) | 3651.724<br>(60.429) | 4929.434<br>(70.210) | 2553.670<br>(50.534) |
| **IV** | | | | 111.645<br>(10.566) | 284.129<br>(16.856) | 436.655<br>(20.896) | 3037.185<br>(55.111) | 1989.237<br>(44.601) | 3566.569<br>(59.721) | 3779.634<br>(58.988) |
| **V** | | | | | **121.552**<br>**(11.026)** | 524.309<br>(22.898) | 2372.981<br>(48.713) | 2565.899<br>(50.655) | 3561.843<br>(59.681) | 2688.152<br>(51.847) |
| **VI** | | | | | | **165.408**<br>**(12.861)** | 3330.538<br>(57.711) | 1656.536<br>(40.701) | 3191.938<br>(56.497) | 4194.745<br>(64.767) |
| **VII** | | | | | | | **3080.236**<br>**(55.500)** | 6464.682<br>(80.403) | 5040.680<br>(70.998) | 3238.605<br>(56.909) |
| **VIII** | | | | | | | | **2533.656**<br>**(50.335)** | 3342.030<br>(57.810) | 7148.374<br>(84.548) |
| **IX** | | | | | | | | | **1117.012**<br>**(33.422)** | 5979.820<br>(77.329) |
| **X** | | | | | | | | | | 4028.527<br>(63.471) |

genetic improvement. Dey *et al.* (2011) also suggested the use of divergent genotypes for development of lines with high yielding potential and better adaptability. Hybridization between genetically divergent parents to generate high heterotic segregants reported promising (Roy and Panwar, 1993; Vivekanandan and Subramanian, 1993; Sharma *et al.*, 1997).

Maximum intra-cluster distance was observed among the genotypes, viz., Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1, Nunia in cluster X, indicating existence of wide genetic divergence among the constituent genotypes in it. High degree of divergence among the genotypes within a cluster would produce more segregating breeding materials and selection within such cluster might be executed based on maximum mean value for the desirable characters. Intra-cluster distance among the genotypes, viz., KNS-1 and KNS5-1, in cluster II was minimum. This indicates that unidirectional selection, which might have been practiced, could lead to uniformity with less divergence between the genotypes.

Considerable variation in cluster mean values was observed for all the characters (Table 5), except, seed thickness (mm) which did not show much variation among different clusters. In respects of days to 50% flowering, the genotypes (Pusa Basmati-1, KNS-3-1, KNS-2, KNS-5-1 and Nunia) in the cluster X were early maturing, had comparatively shorter plant height and moderate number of fertile seeds per panicle. The genotypes (Fudugey, Munimahnanri, Tulaipanji, KNS-3-9(N) and KNS-1-2B) of cluster VII showed maximum number of panicles per plants along with high 100-seed weight, high seed length and high yield. Highest number of fertile seeds per panicle was observed for the genotypes (KNS-6/2 and Chini Atap) in the IX along with highest yield. Maximum number of panicles per plant was observed among the genotypes [Mohanbhog, Kalojeera, Kalojeera-1, Radhunipagal, Kalobhog, Khasha, Badshabhog, Kalturey, Kagui, Jhapaka, Chinakamani and KNS-1(N)] of cluster I along with tallest plants, moderate number of fertile seeds per panicle and moderate yield. Since the genotypes of clusters IX (KNS-6/2 and Chini Atap) and III (KNS-3-9(N) and KNS-2-1) possessed high seed yield, they may be directly used for adoption or used in hybridization programme for yield improvement. The genotypes with high mean value in any cluster for particular character may be directly used for adoption or in hybridization programme for improvement of that particular character.

The contribution of characters towards the total genetic divergence is important in deciding the characters for selection. Seed length, seed thickness, seed breadth, panicle length and seed yield were major contributing characters towards the total genetic divergence among the genotypes (Table 6). Whereas, number of panicles

**Table 5. Cluster mean for 11 characters in 37 aromatic genotypes of rice**

| Clusters | Days to 50% flowering | Plant height (cm) | No. of panicles/ plant | Panicle length (cm) | No. of seeds/ panicle | 100 seed weight (g) | 100-kernel weight (g) | Seed length (mm) | Seed breadth (mm) | Seed thickness (mm) | Seed yield (t/ha) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 177.07 | 126.66 | 28.23 | 26.63 | 150.72 | 1.291 | 0.839 | 6.220 | 2.066 | 1.753 | 2.128 |
| II | 173.80 | 136.25 | 26.45 | 27.90 | 143.60 | 1.489 | 1.351 | 7.009 | 2.148 | 1.781 | 1.800 |
| III | 175.00 | 139.50 | 26.30 | 27.85 | 148.50 | 1.507 | 1.122 | 7.319 | 1.993 | 1.697 | 2.662 |
| IV | 170.85 | 140.00 | 27.30 | 26.35 | 124.30 | 1.247 | 0.676 | 6.392 | 2.045 | 1.679 | 2.025 |
| V | 160.85 | 137.25 | 20.35 | 25.70 | 95.050 | 1.377 | 1.045 | 6.813 | 2.008 | 1.791 | 1.119 |
| VI | 172.40 | 135.50 | 23.47 | 24.90 | 82.85 | 1.716 | 1.003 | 5.964 | 2.288 | 1.731 | 1.325 |
| VII | 174.62 | 123.60 | 29.74 | 26.92 | 116.04 | 1.800 | 1.115 | 7.826 | 2.272 | 1.827 | 1.906 |
| VIII | 159.50 | 136.33 | 27.50 | 26.56 | 137.05 | 1.110 | 0.717 | 5.073 | 1.950 | 1.603 | 2.200 |
| IX | 149.02 | 113.00 | 24.92 | 26.15 | 172.55 | 0.934 | 0.776 | 5.884 | 1.969 | 1.771 | 2.775 |
| X | 145.92 | 127.60 | 24.13 | 26.02 | 157.14 | 1.554 | 1.135 | 8.091 | 2.126 | 1.791 | 1.845 |
| CV (%) | 1.49 | 0.48 | 9.98 | 4.77 | 10.73 | 3.790 | 3.850 | 0.780 | 3.850 | 3.150 | 16.350 |

**Table 6. Contribution of different characters to total genetic divergence**

| **Characters** | **No. of first rank** | **Contribution (%)** |
|---|---|---|
| Days to 50% maturity | 4 | 0.601 |
| Plant height (cm) | 79 | 11.862 |
| Number of panicles/plant | 1 | 0.150 |
| Panicle length (cm) | 1 | 0.150 |
| Number of fertile seeds/panicle | 9 | 1.351 |
| 100- seed weight (g) | 20 | 3.003 |
| 100-kernel weight (g) | 27 | 4.054 |
| Seed length (mm) | 167 | 25.075 |
| Seed breadth (mm) | 114 | 17.117 |
| Seed thickness (mm) | 138 | 20.720 |
| Seed yield (t/ha) | 106 | 15.916 |

per plant and panicle length were the characters, whose contributions were least in creating the total genetic divergence. These findings revealed that the seed shape was the major contributing factor towards total genetic divergence. The characters having high contribution towards the total genetic divergence may be used in selecting genetically diverse parents, particularly to exploit maximum heterosis or to execute efficient selection in highly segregating generations.

## Acknowledgement

I am thankful to Shri Ayub Ali Khan for his continuous support during field work, crop supervision and data collection.

## References

Anonymous (2009) Agricultural statistics at a glance. Directorate of economics and statistics, Department of Agriculture and Co-operation, Ministry of Agriculture, Government of India. p 359.

Bansal VK, RG Saini, NS Rani and A Kaur (1999) Genetic diversgence in quality rice. *Oryza* **36:** 20-23.

Dey SS, SR Sharma, Chander Prakash, RN Barwal and R Bhatia (2011) Genetic divergence in snowball cauliflower (*Brassica oleracea* var. *botrytis* L.). *Indian J. Plant Genet. Resour.* **24:** 49-52.

Mahalanobis PC (1928) A statistical study of Chinese heads measurement. *J. Asiatic Soc. Bengal* **25:** 301-317.

Mahalanobis PC (1936) On the generalized distance in statistics. In: Proceedings of National Institute of Science, India **12:** 49-55.

Mehetre SS, PA Patil, CR Mahajan and DH Hajare (1998) Genetic divergence in upland rice. *Oryza* **35:** 219-222.

Rahaman M, V Acharya, SN Sukla and K Pandi 1(997) Genetic divergence in low land germplasm. *Oryza* **34:** 209-212.

Roy A and DVS Panwar (1993) Genetic divergence in rice. *Oryza* **30:** 1997-801.

Roy B, AK Basu and AB Mandal (2002) Genetic diversity in rice (*Oryza sativa*) genotypes under humid tropics of Andaman based on grain yield and seed characters. *Indian J. Agric. Sci.* **72:** 84-87.

Sharma MK, RK Agarwl and AK Richaria (1997) Genetic diversity in rice under rainfed upland and integrated ecosystem. *Oryza* **34:** 19-24.

Sinha PK, VS Chauhan, K Prasad and JS Chauhan (1991) Genetic divergence in indigenous upland rice. *Indian J. Genet. Plant Breed.* **51:** 47-50.

Soni DK, AK Sarawagi and NK Rastogi (1999) Genetic diversity in traditional rice accession of Madhya Pradesh, India. *Oryza* **36:** 118-120.

Vivekanandan P and S Subramanian (1993) Genetic divergence in rainfed rice. *Oryza* **30:** 60-62.