GENETIC DIVERSITY ANALYSIS IN NON-BASMATI AROMATIC RICE

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ABSTRACT

The experiment was conducted during two Kharif seasons (June-November) at the Agriculture Farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan to determine the genetic diversity among twenty-eight aromatic non-basmati rice genotypes which were originated in different eco-geographical region of eastern India, collected from different research stations and institutions belonging to West Bengal and Bihar. The genotypes were grouped into 5 clusters based on Mahalanobis's D^2 statistics. Cluster-I consisted of the highest number of genotypes (16), followed by a cluster-II (6), cluster-V (3), cluster-III (2) and cluster-IV was solitary clusters. The clustering, pattern of genotypes indicated the little relation of genetic divergence with geographical differential. Average intra cluster distance was highest 13.3 in cluster V and maximum intercluster distance 77.22 was found between cluster V and II followed by cluster V and III (70.42), cluster V and I (44.54) and so on. This indicated the considerable amount of divergence within and between clusters. Cluster V played an important role in the inter-cluster distance. Cluster V exhibited highest mean value for days of 50% flowering, plant height, and flag leaf area. Cluster II was characterized by the lowest mean value of days to 50% flowering and high value of panicle length and test weight. The genotypes from these clusters with desirable characters may be used as a potential donor for future hybridization program to develop high yielders.

KEYWORDS: Aromatic Rice, Divergence, D2 Analysis, Intra Cluster & Inter Cluster

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INTRODUCTION

India has had an immense wealth of non-Basmati aromatic rice. The aromatic rice is preferred over non-aromatic rice due to special occasions and for export, and thus they command a higher market price. Rice production will be required to increase by more than 30% to meet the staple food requirement by 2030 (Sharma *et al.*, 2012). Crop improvement mainly depends upon the amount of genetic variability present in the population. In any crop, germplasm serves as a valuable source of base population and providing scope for wide variability. Knowledge of genetic diversity among existing cultivars of any crop is essential for long-term success of the breeding program and maximizes the exploitation of the genetic resources (Belaj *et al.*, 2002). Hybridization is one of the major tools for the improvement of a crop that needs the analysis of genetic diversity in the selection of parents (Singh, 1983). Moreover, evaluation of genetic diversity is important for the source genes of particular traits within the available germplasm (Roy and Panwar, 1993). Genetic diversity assessment between and within groups or clusters is very important for the proper selection of parents for the better search of heterosis (Murty and Arunachalam, 1966). Multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of several characters and assesses the relative contribution of different components to the total divergence (Zahan *et al.*, 2008). This study was undertaken to

determine the genetic diversity in non-basmati aromatic rice for the maximum utilization of the genetic resources and proper selection of donor parents.

MATERIALS AND METHODS

The experiment was conducted during two *Kharif* seasons (June-November) at the Agriculture Farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan. The farm is situated at 23°29' N latitude and 87°42' E longitudes with an average altitude of 58.9 meters above mean sea level under sub-humid, subtropical, lateritic belt of West Bengal. Twenty-eight aromatic non-basmati rice genotypes (Table 4) were sown in seedbed on *Kharif* seasons. In each genotype, one seedling per hill was transplanted in the main field after 35 days. All the genotypes were grown in a Randomized Complete Block Design (RCBD) with 3 replications during the two growing seasons (i.e. *Kharif* 2015 and 2016). The experimental plot of each genotype consisted of 5 rows of 1.5-meter length keeping plant-to-plant and row-to-row spacing of 15 cm and 20 cm apart. All recommended package of practices was followed during the crop season for raising a healthy crop.

The experiment was conducted to explore the extent of divergence in 28 rice genotypes for ten quantitative characters, viz., days to 50% flowering, plant height, flag leaf area, number of panicle/plant, panicle length, primary branch, secondary branch, number of filled grain per panicle, test weight and grain yield. Data were recorded on 5 randomly selected competitive plants from the 3 rows except for 2 border rows. The analysis of genetic divergence was done using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters, inter and intracluster distances and mean performances of characters were also computed.

RESULTS AND DISCUSSIONS

The analysis of variance of twenty-eight genotypes pooled over two seasons with respect to ten quantitative characters is presented in Table 5. The analysis of variance showed significant difference among genotypes for all the ten characters. Wilk's Lambda criterion ($\lambda = 0.7370 \times 10^{-11}$ and $V = 1268.86$, with 220 df) revealed highly significant differences among the genotypes for the pooled effect of all the characters. The D^2 values ranged from 18.04 (between Subhasita and Seetasail) to 6149.95 (between Kalikhasa and BM-1). Majority of D^2 values are significant. Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationships. The multivariate analysis by means of Mahalanobis's D^2 statistic for estimating genetic divergence has been emphasized by many workers (Anand and Murty, 1968; Arunachalam, 1981; Anand and Rawat, 1984). The more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining a higher amount of heterotic expression in the F_1 and the broad spectrum of variability in segregating generations (Ananda and Murty, 1968). The objective of this work is to group a set of twenty-eight genotypes into different clusters according to the genetic divergence and such grouping would help to initiate crossing programme between diverse groups. Based on the relative magnitude of D^2 values, the genotypes were grouped into five clusters (Table 1).

Table 1: Distribution of Twenty Eight Genotypes into Various Clusters

Cluster	No. of Genotypes	Name of Genotypes
I	16	Kaminibhog, Radhunipagal, Radhatilak, Gobindabhog, Chinakamini, Sheetabhog, Bahadurbhog, Tulsimukul, Kalikasha, Subhasita, Subhasita, Dudhaswar, Krishnabhog, Seetasail, Danaguri, Deheradoongandeswari, 124(17)10
II	6	BM 34, BM 35, BM 1, BM4, Rajendrasubhasini, BM-7
III	2	33(9)17, 88(8)3
IV	1	KeralaSundori
V	3	Shantibhog, Manipuri Black Rice, Gopalbhog

Cluster I comprised a maximum number of sixteen genotypes representing Kaminibhog, Radhunipagal, Radghatilak, Govindabhog, Chinakamini, Sheetabhog, Bahadurbhog, Tulsimukul, Kalikasha, Subhasita, Dudhaswar, Krishnabhog, Seetasail, Danaguri, Deheradoongandeswari and 124(17)10 (mutant of Gobindabhog). Genotypes in this cluster were mostly local aromatic landraces/farmers varieties of erstwhile Bengal of pre-independence India and neighboring areas. Cluster-II comprised six genotypes representing BM-34, BM-35, BM-1, BM-4, BM-7 (from Bidhan Chandra Krishi Viswavidyalaya) and Rajendrasubhasini (from RAU, Bihar), lines/varieties developed using hybridization with Basmati types. Cluster-III had two genotypes 33(9)17 and 88(8)3, mutants of popular aromatic rice of northern parts of West Bengal, Tulaipanja. Cluster-IV was solitary and was represented by Keralasundori genotypes. Cluster- V had three genotypes, Shantibhog, Manipuri black rice, and Gopalbhog.

The distribution pattern of genotypes in different cluster indicated that genetic divergence was not exclusively related to geographical differentiation. Many genotypes of close geographic proximity fell into different clusters (Clusters-I, II and V) and vice-versa. Clustering of genotypes from the different eco-geographic location into a single cluster (cluster I, II and V) could be attributed to the possibility of free exchange of breeding materials. Similar findings were reported by Nayak *et al.* (2004). However, unidirectional selection, practiced for a particular trait or a group of a linked trait (*e.g.* aroma and associated quality characters) in several places may produce similar phenotypes, which can aggregate into one cluster irrespective of their geographic region (Singh and Gupta, 1968), as observed in Cluster-II. Therefore, the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to the difference in adoption, selection criteria, selection pressure and environmental conditions (Vivekananda and Subramanian, 1993). The formation of solitary clusters may be due to the total isolation, preventing the gene flow or intensive natural/human selection for diverse adaptive complexes.

The study revealed that the average intracluster distance varied from 4.72 in cluster III to 13.3 in cluster V (Table 2).

Table 2: Average Intra-and Inter-Cluster $\sqrt{D^2}$ Values

Cluster	I	II	III	IV	V
I	7.33	37.7	26.59	17.77	44.54
II		8.28	18.25	23.66	77.22
III			4.72	19.01	70.42
IV				0	28.44
V					13.3

The maximum intercluster distance 77.22 was found between cluster V and II followed by cluster V and III (70.42), cluster V and I (44.54), cluster II and I (37.7), and so on. This indicated a considerable amount of divergence within and between clusters. Cluster V played an important role in the inter-cluster distance. The inter-cluster distances

were greater than intra cluster indicating wide genetic diversity among genotypes. Similar results were reported by Toshimenla *et al.*, (2016), Chamundeswari (2016) and Nirosha *et al.*, (2016).

It would, therefore, be logical to effect crossing between genotypes separated by considerable statistical distance to produce superior hybrids in the F_1 generation and promising recombinants in segregating generations.

The mean performance of different clusters in respect of ten characters is presented in Table 3.

Table 3: Cluster Means of Ten Quantitative Characters in Aromatic Rice

	50% Flowering	Plant Height	Flag Leaf Area	No of Panicle	Panicle Length	Primary Branch	Secondary Branch	No of Filled Grain	Test Weight	Yield
Cluster 1	116.34	146.8	27.05	8.95	25.77	10.01	30.63	128.61	12.59	12.23
Cluster 2	96.53	102.5	27.56	8.84	27.05	9.31	25.64	57.51	17.22	8.66
Cluster 3	116.33	97.54	15.66	13.95	22.89	7.44	13.27	58.85	13.61	9.51
Cluster 4	112.67	130.41	37.98	9.47	24.16	9.98	28.3	122.81	20.28	22.05
Cluster 5	126.56	170.51	49.95	6.82	26.3	10.13	24.39	109.88	29.4	19.52
Relative contribution (%)	17.72%	43.12%	0%	26%	2.38%	26%	1.06%	2.91%	24.07%	8.2%

Cluster I and Cluster IV were characterized by a highest mean value of secondary branch & number of filled grain per panicle and high value for grain yield respectively. Hence, these genotypes could be utilized in yield improvement breeding programmes. Cluster II had a lowest mean value of days of 50% flowering and might be utilized as a suitable source for incorporation of earliness in other genotypes. Cluster III exhibited lowest mean value for most of the characters including plant height. Hence, genotypes from the cluster could be made use in the development of dwarf and semi – dwarf lines or the trait could be transferred into other desirable genotypes. Cluster V exhibited highest mean value for days to 50% flowering, plant height, and flag leaf area. Panicle length and grain yield showed moderate mean value.

None of the clusters contained genotypes with the highest values for all characters. Also, most of the minimum and maximum clusters mean values were distributed in relatively distant clusters. The hybridization between individuals of different clusters would, therefore, be logical for recombining the superior characters for the development of elite genotype(s).

The relative contribution to the total divergence was highest for plant height (43.12%), followed by a number of panicle/plant (26%), the primary branch(26%), test weight(24.07%) and days to 50% flowering (17.72%). These results are in agreement with Dutta and Mani (2003) for plant height; Awasti *et al.*(2005) for plant height and days to 50% flowering; Nayek *et al.*(2004) for days to 50% flowering and test weight; Kole and Chakraborty(2012) for days to 50% flowering, plant height and test weight. Hence, plant height, number of panicle/plant, primary branch, test weight and days to 50% flowering should be given importance during the choice of parents for hybridization and selection in the segregating populations.

Table 4: List of Genotypes of Twenty Eight Aromatic Rice

Serial Number	Name of Genotypes	Serial Number	Name of Genotypes
1	124(17)10	15	Subhasita
2	33(9)17	16	Sheeta bhog
3	Chinakamini	17	Bahadurbhog
4	Dehradoongandeshari	18	Seetasail
5	Danaguri	19	Manipuri Black Rice
6	Dudhaswar	20	Tulsimukul
7	Gobindabhog	21	88(8)3
8	Kalikasha	22	BM 1
9	Kaminibhog	23	BM4
10	Krishnabhog	24	BM 7
11	Radhunipagal	25	BM 34
12	Rajendrasubhasini	26	BM 35
13	Radhatilak	27	Keralasundori
14	Shantibhog	28	Gopalbhog

Table 5: Analysis of Variance for Ten Quantitative Characters in Aromatic Rice

Source	Df	Mean Sum of Square									
		50% Flowe ring	Plant Height (Cm)	Flag Leaf Area (Cm ²)	No. Of Panicle	Panicle Length	Prim ary Branch	Secon dary Branch	No. Of Filled Grain/ Panicle	Test Weig ht	Grain Yield (G)
Season	1	3207* *	1511.5**	194.90* *	89.21 **	21.07**	34.30 **	57.70*	1644.75* *	6.48	4.16**
Replica tion	2	6.38	32.75	1.19	0.95	0.73	0.12	7.22	107.25	4.4	3.12
S × R	2	5.38	59.5	56.72	0.36	1.07	1.02	13.21	54.31	3.45	8.03
Genoty pes	27	691.8 8**	3939.55* *	592.98* *	26.15 **	24.34**	4.91* *	232.30 **	9044.08* *	218.4 4**	148.36 **
G × S	27	31.27 **	53.54**	112.61* *	4.62* *	5.29**	1.78* *	32.40* *	488.86**	3.64* *	9.69**
Error	108	1.48	17.02	20.94	3.12	1.36	0.35	11.29	159.3	2.19	4.67

*, **: Significant at P=0.05 and 0.01, respectively

CONCLUSIONS

Considering genetic divergence, relative importance of characters in determining the yield in this particular population and performance of the genotypes *per se* as well as cluster means, crossing between the intra-cluster genotypes Dehradoongandeshari × Kaminibhog, Dehradoongandeshari × Kalikhasa, Seetasail × Dudhaswar, Dudhaswar × Radhunipagal of cluster I; BM-7 × BM-35 of cluster II and inter-cluster genotypes Seetasail × Rajendrasubhasini and Seetasail × BM-7 (Cluster I × Cluster II), Gopalbhog × Rajendrasubhasini, Shantibhog × Rajendrasubhasini, Monipuri black rice × BM-7 and BM-7 × Gopalbhog (Cluster II × Cluster V), Shantibhog × 88(8)3 and Shantibhog × 33(9)17

(Cluster V $\times$ Cluster IV) are most likely to yield a considerable amount of heterosis in F_1 generation and to provide a wide spectrum of recombinants in segregating generations.

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