Original Research Article

Agro-morphological Characterization and Genetic Diversity in a mini core collection of Aromatic Rice (*Oryza sativa* L.)

ABSTRACT

Aromatic rice is a special type of rice known in the World. 20 genotypes of aromatic rice were evaluated at the Agricultural Experimental Farm, University of Calcutta Baruipur, West Bengal to characterize and estimate Genetic Diversity in mini core collection of Aromatic Rice (*Oryza sativa* L.). Phenotypic coefficients of variation exhibited a bit higher values but maintained a close relation with a genotypic coefficient of variation for all the traits, indicating low G×E interaction. Additive gene action was prominent for the traits like plant height, panicle length, number of filled grains per plant and 1000 grain weight. A correlation study showed that grain yield per plant was positive and significantly correlated with panicles per plant and total number of filled grains per plant, suggesting the need for more emphasis on these components for increasing the grain yield in aromatic rice. Manhattan cluster analysis based on agro-morphological traits revealed two distinct clusters i.e. Cluster I(A and B) and Cluster II(A and B). Maximum of 15 genotypes were grouped into Cluster II and 5 genotypes in Cluster I. It is also concluded from the present investigation that total number of filled grains per plant and panicle length influenced grain yield. Path analysis revealed that total number of filled grains , panicles per plant and 1000 grain weight has maximum direct effect on grain yield per plant.

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***Key Words**: Agro-morphological traits, Aromatic rice, Cluster, Genetic Diversity.*

1. INTRODUCTION

Rice is the staple food for more than 70% of Indians and more than half the World's population of 8 billion approximately (Worldmeters, 2020). It is prevalent and grown in almost all states and ecologies of India. Due to enhanced rice production, India made a mark in international trade by becoming the fourth exporter of rice in the world. In India, West Bengal is known as the rice bowl of India and is the largest producer of rice.

Aromatic rice is a special class of rice with high market value due to its superior grain qualities and pleasant aroma (Singh *et al.,* 2000). The productivity of aromatic rice is low in comparison to other types of rice. This is due to non-availability of aromatic rice varieties with higher productivity.

India is very rich in rice genetic resource, aromatic rice in particular. Aromatic rice constitutes a small and unique group of rice and is highly priced due to its quality; it is widely grown in different states of North India like Himachal Pradesh, Jammu and Kashmir, Punjab, Haryana and parts of Uttar Pradesh (Nene, 1998). Due to the high demand for aromatic rice in the international market, about two-thirds of aromatic rice produced in our country is exported to different countries and increases every year (Siddiq, 1990). Trade-in aromatic rice has not received considerable attention in India even though scented rice varieties have competitive international prices and the country can earn foreign exchange. Demand for aromatic rice has been increased manyfold in the last two decades in national and international markets. The aromatic rice of

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India is very famous throughout the world. Now, realizing the importance and demand of short grain aromatic rice in the world market, efforts are being started to collect, characterize and evaluate the aromatic short grain rice in India for documentation and to find suitable donors for different traits that are prerequisites for varietal development.

Exploring diversity in the landrace collection is essential for identifying new genes and further improving the germplasm (Thomson *et al*., 2007). Some small and medium-grained aromatic rice landraces could be excellent sources for improving quality in high-yielding varieties as they possess excellent aroma and other quality traits like elongation after cooking, taste, etc. The improvement of aromatic rice landraces requires the collection and evaluation of existing cultivars present in our state. Genetic study of existing aromatic rice landraces is the prerequisite for the development of new varieties. Many researchers have performed studies on genetic diversity with different genotypes of aromatic rice (Siddique *et al*., 2013; Islam *et al*., 2014; Ahmed *et al*., 2016 and Akter *et al*., 2018). Therefore, the present study was done to assess the genetic variation in a mini core collection of 20 aromatic rice genotypes by studying their agro-morphological traits.

2. MATERIAL AND METHODS

Seeds of 20 aromatic rice accessions (Table No.1) were sown in the nursery bed. Twenty-five (25) days old seedlings were transplanted in the field during rainy season (June to December) 2019. The design used was an RBD - randomized block design with three replications. The spacing was 15 x 20 cm. Each genotype was sown in three lines per replication. In our study, the fertilizer dose of N:P:K used was 60:30:30 kg/ha. Agro-morphological characters for randomly selected five plants in each replication were recorded at different crop growth stages and the data were statistically analyzed with the help of SPSS 20. The quantitative characters like Days to flowering, Days to maturity, Plant height (in cms), Tillers per plant, Panicles per plant, Panicle length (in cms), Total number of filled grains per plant, 1000 grain/seed weight (in gms) and Total grain yield per plant (in gms) etc. were recorded.

3. RESULT AND DISCUSSIONS

3.1. Genetic Variation Estimation

The analysis of variance has revealed significant differences among the genotypes for all the traits under the experiment (Table No. 2). In the present study, the Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient Variation (GCV) for all the traits that imply the environment's role. The same findings were reported earlier (Bhadru *et al.,* 2012). The PCV and GCV were high for the characters-panicle length, total number of filled grains per plant, 1000 grain weight and total grain yield per plant, indicating more significant variability in respect of these attributes. Moderate to moderately high PCV and GCV were estimated for the traits plant height and tillers per plant (Table No.3). A narrow difference between PCV and GCV indicated less influence of the environment in the expression of the traits. According to the earlier studies, all the characters except 50% flowering, days to maturity, and yield per plant showed less environmental influences (Sarawag*i et al.,* 2000). In the present investigation, high heritability coupled with moderate to high genetic advances were observed for the traits total number of filled grains per plant and grain yield per plant. This study suggests that these traits were primarily under additive genetic control and selection for the traits can be achieved through their phenotypic performance.

3.2. Correlation between Quantitative traits

Correlations helps in the identification of the measurement of the intensity of association between the traits. Further, the study helps the breeder understand the mutual component

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characters on which selection can be based on genetic improvement. In the present investigation, the association analysis (Table No.4) demonstrated that the trait grain yield per plant was positive and significantly correlated with panicles per plant and total no. of filled grains per plant indicating the importance of these characters for yield improvement in this population. Similar kinds of associations were reported earlier by various researchers like Krishna *et al. (*2008) for panicle number. The associations with other characters are to be considered simultaneously when characters have a direct bearing on yield are selected, as this will indirectly affect yield. Therefore, a judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters under any situation. The results of correlation coefficients implied that plant height, panicle numbers per plant and number of filled grains per plant might be considered for selection for yield improvement. Correlation analysis thus revealed that panicles per plant and total number of filled grains per plant played a vital role in increasing grain yield per plant. Enhancing these traits may hopefully help to obtain a high grain yield. In order to have more close view of relationship between traits it is imperative to provide an effective means of untangling direct and indirect causes of association which would permit a critical examination of the specific forces acting to produce a given correlation.

3.3. Path Analysis

An attempt has been made in the present study to find out the direct effect of each causal factor component and its indirect effect via another factor component on grain yield per plant with the help of path coefficient analysis (Wright, 1934). This method has already been proved to be very useful in plant selection and breeding depending upon one or more causal factor (Dewey and Lu, 1959). A path coefficient is a standardized partial regression coefficient and measures the direct influence of a predictor variable on the response variable (Li, 1975) result showed that the most important agronomic trait determining grain yield in the path coefficient analysis were number of grains per plant which exhibited highest positive direct effect on grain yield per plant (Table No.5). Other traits which contributed positive direct effects were panicles per plant and 1000 grain weight. We have observed in our study that days to maturity had negative correlation. Thus, it appeared that the traits-panicles per plant, filled grains per plant and 1000 grain weight were important yield components. Plant breeders are always interested to carry out selection in the field with minimum number of traits. Inter-relationship study exhibited plant height was positively correlated with panicles per plant and 1000 grain weight. So, selection for improvement with plant height would like to improve panicles per plant and 1000 grain weight through correlated response. More over improving plant height would have positive correlated response in some other traits also like tillers per plant and panicle length etc. Naturally, plant height would have obvious choice rather than tillers per plant which exhibited negative interrelation with 1000 grain weight. So, restructuring plant ideotype in aromatic rice with following traits would like to produce desirable lines in future- 1) plant with more grains per plant 2) plant with taller height.

3.4. Cluster Analysis

SPSS 20 further analyzed all 20 aromatic rice genotypes for grouping. Based on Manhattan clustering, two distinct clusters were found. Cluster I was further divided into Sub Cluster I A and I B, similarly Cluster II was divided into Sub Cluster II A and Sub Cluster II B (Fig. No. 1). Maximum 15 genotypes were grouped into Cluster II consisting of two genotypes in Sub Cluster II A and 13 genotypes in Sub Cluster II B. Whereas, 5 genotypes were grouped into Cluster I with 4 genotypes in Sub Cluster I B and a single genotype in Sub Cluster I A. Investigating the cluster composition revealed that genotypes of different geographic origins are present in the same cluster, indicating that genotypes genetic divergence is independent

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of geographic origin. Similarly, Hossain (2009) and Nascimento *et al.* (2011) found in rice. The highest genetic distance has been observed in Paramanya and Dehradun Basmati, Gobindobhog and Gandeswari and Gobindobhog and Paramanya. (Table No.5). Desirable segregates are expected to produce a crossing between these pair of genotypes with a high dissimilarities coefficient. The crosses consisting of these kind of diverse parents would likely express a considerable amount of heterosis in the F1 generation and provide a wide spectrum of recombinants in segregating generations.

4. CONCLUSION

Aromatic rice genotypes showed considerable genetic variability and divergence. It was found that additive gene action was prominent for the traits like plant height, panicle length, filled grains per plant and 1000 grain weight. A correlation study at phenotypic level revealed that grain yield per plant was positive and significantly correlated with Number of panicles per plant and total number of filled grains per plant, so the selection for high panicles per plant, number of filled grains per panicle and total number of filled grains per plant will lead towards high yield. Path analysis reveals that panicles per plant and 1000 grain weight are positively related to higher grain yield. The cluster analysis that groups the genotypes into different clusters with specific character traits can help select parental lines in future breeding programmes. The highest genetic distance has been observed in Paramanya and Dehradun Basmati, Gobindobhog and Gandeswari and Gobindobhog and Paramanya. Crossing between the above pairs of genotypes would most likely express a considerable amount of heterosis in the F1 generation and provide a wide spectrum of recombinants in segregating generations. Grouping of genotypes based on multivariate analysis was independent of the origin of cultivars. The conventional assumption that was selecting genotypes of different geographical origins will maximize the diversity available to a breeding project does not follow in aromatic rice.

Table 1: List of 20 genotypes.

SERIAL NO.	ENTRY NAME	SERIAL NO.	ENTRY NAME
1	GOBINDOBHOG	11	DEHDRADUN BASMATI
2	PARAMANYA	12	SEETASHAL
3	PUSA BASMATI-I	13	TULAIPANJI
4	KALO NUNIA	14	DADHSAL
5	GANDESWARI	15	KAMAL DHAN
6	RADHUNIPAGOL	16	LAGHU DHAN
7	CHINISHAKKAR	17	JAMAI NADU
8	GOBINDOBHOG (SELECTION)	18	SEETABHOG
9	DANAGURI	19	GOPALBHOG
10	KANAKCHUR	20	KATARIBHOG

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Table 2: Analysis of variance (ANOVA) for the yield and yield attributing traits.

*Significant at 5% probability level.   **Significant at 1% probability level at 0.01%
DF-Degrees of Freedom

Source	DF	DAYS TO 50% FLOWERING	DAYS TO MATURITY	PLANT HEIGHT	TILLERS PER PLANT	PANICLES PER PLANT	TOTAL NO. OF FILLED GRAINS PER PLANT	1000 GRAIN WEIGHT	YIELD PER PLANT
Replications	2	1.26	2.066	14.82**	49.82**	0.216	673.35**	0.13	24.32**
Treatments	19	16.61**	16.93**	591.96**	18.65**	47.293**	7904.03**	44.72**	1096.73**
Error	38	0.58	0.557	22.24**	5.82*	6.199**	595.93**	0.33	50.553**

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Table 3: Estimates of Genetic Parameters.

	CD	C.V	G.C.V(%)	P.C.V(%)	H(%)	GA
DAYS TO 50% FLOWERING	1.2338	0.743	2.25	2.37	90.17	4.2927
DAYS TO MATURITY	1.2675	0.5857	1.83	1.92	90.72	4.3658
PLANT HEIGHT	7.6236	3.8039	11.12	11.75	89.52	25.4125
TILLERS PER PLANT	3.899	14.949	12.82	19.69	42.37	1.80489
PANICLES PER PLANT	4.025	15.9773	23.75	28.62	68.84	5.2489
TOTAL NO. OF FILLED GRAINS PER PLANT	39.465	14.948	30.22	33.72	80.35	81.689
1000 GRAIN WEIGHT	0.9306	3.5974	24.04	24.31	97.81	7.75027
GRAIN YIELD PER PLANT	11.494	17.469	45.88	49.10	87.34	33.598

Table 4: Phenotypic correlation coefficients among yield and its components.

	DF	DM	PH	TP	PP	PL	FGP	GW	GYP
DF	1								
DM	0.87**	1							
PH	.492*	.492*	1						
TP	.266	.266	.262	1					
PP	.333	.333	.318	.585**	1				
PL	-.227	-.227	.017	.144	.266	1			
FGP	.006	.006	-.096	.198	.450*	.398	1		
GW	-.011	-.011	.084	-.137	-.157	-.076	-.439		
GYP	.181	.181	.190	.434	.799**	.437	.716**	.081	1

**.Correlation is significant at 0.01 level (2-tailed). *.Correlation is significant at 0.05 level (2-tailed).

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Table 5: Path Analysis.

	DF	DM	PH	PP	TP	FGP	GW
DF	**0.0991**	0.1019	0.0525	0.0325	0.0251	-0.0072	0.0017
DM	-0.1341	**-0.1305**	-0.0659	-0.423	-0.0316	0.0046	-0.0056
PH	0.0182	0.0173	**0.0343**	0.0124	0.0120	-0.0037	0.0029
PP	0.1696	0.1674	0.1861	**0.5163**	0.4000	0.2641	-0.0910
TP	0.0157	0.0150	0.0217	0.0479	**0.0619**	0.0139	-0.0071
FGP	-0.0491	-0.0239	-0.0730	0.3473	0.1520	**0.6791**	-0.3154

GW	0.0087	0.0209	0.0413	-0.0866	-0.0563	-0.2281	**0.4911**

Residual Value:- 0.1092

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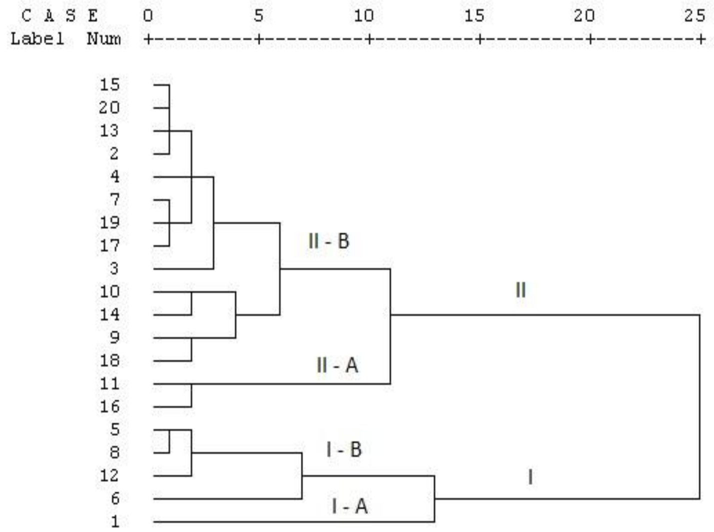
Dendrogram using Average Linkage (Between Groups)

Rescaled Distance Cluster Combine



Refer to Table 1 for name of genotypes.

Figure 1: Dendrogram of 20 aromatic rice genotypes based on morphological data.

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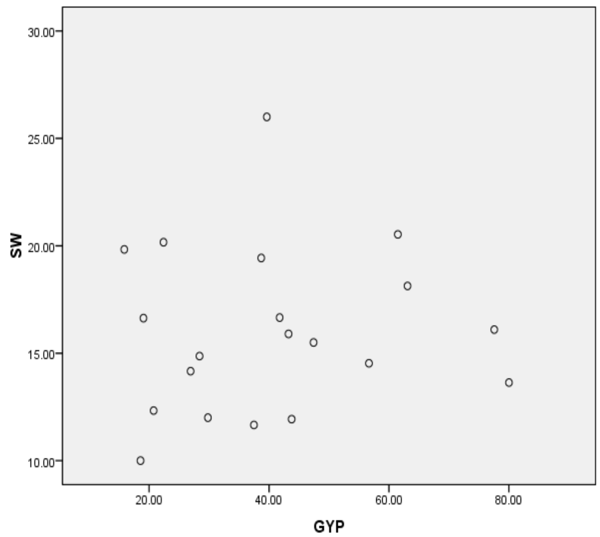

Figure 2 : Plot showing association between Seed Weight and Grain Yield per Plant.

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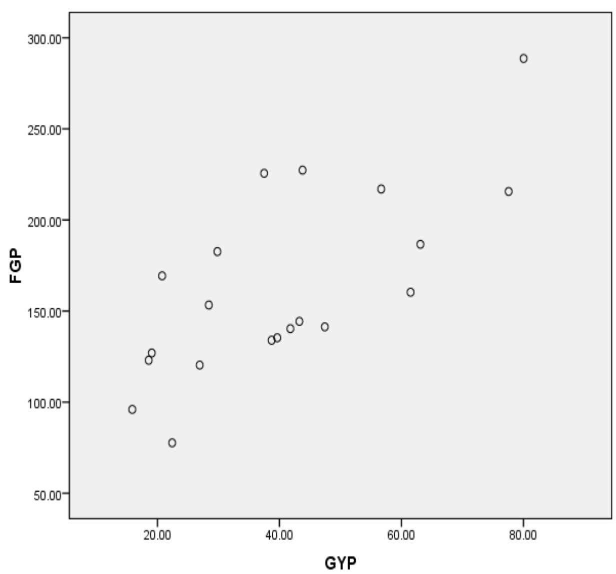

Figure 3: Plot showing association between Filled Grain per Plant and Grain Yield per Plant.

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ABBREVIATIONS

G.C.V- Genetic Coefficient of Variability.

P.C.V-Phenotypic Coefficient of Variability.

H-Heritability.

GA-Genetic Advance.

DF- Days to Flowering

DM- Days to Maturity.

PH-Plant Height.

TP-Tillers per Plant.

PP-Panicles per Plant.

FGP- Filled Grains per Plant.

SW-Seed (Grain) Weight.

GYP- Grain Yield per Plant.